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Dengsheng Zhang

Fundamentals of Image Data Mining

Analysis, Features, Classification and Retrieval

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To my beloved wife Qin

Preface

Due to the rapid development of Internet and digital technology, a mammoth amount of digital data has been created in the world in just a few decades. The processing and management of big data including image data have become one of the greatest challenges facing humankind. Images are a dominant information source and communication method along with text. However, the processing and understanding of image data are far more difficult than dealing with textual data. Tremendous efforts have been made, and a large amount of research work has been carried out around the world in the past few decades to overcome the challenges of efficient management of image data. A significant progress has been achieved in the field of image data mining during this period of intensive research and experiments, highlighted by those breakthrough technologies such as wavelets, MPEG, Google Image search, convolutional neural network, machine learning, ImageNet, Matlab toolboxes, etc.

Given the complexity of image data mining, there is a need for a deep analysis of and insight into the field, especially the latest development, to help researchers understand opportunities and challenges in the field. This book timely captures and presents cutting-edge techniques in the field of image data mining as well as foundational know-how for processing images. The book also provides a complete recipe for image data mining and is a treasure trove of techniques on image analysis, image understanding, feature extraction, machine learning and image retrieval. The book is built upon the author's career-long and high-impact research in the frontier of this exciting research field. Theories and concepts in the book are typically formulated with practical mathematical models which are realized using algorithms and data from actual experiments or working examples. Students and researchers in mathematics and the broader science disciplines will be able to use this book to understand the actual problems in computing world and gain firsthand experience of computing. Students and researchers in many areas of the computing discipline will be able to use this book to understand how to apply fundamental and advanced math tools to solve the variety of computing problems.

Dr. Dengsheng Zhang
Melbourne, Australia
January 2021

About This Book

The book covers the complete know-how on image data mining including math tools, analysis, features, learning and presentation. It has been organized into four parts: fundamentals, feature extraction, image classification and image retrieval.

Part I of the book aims to equip readers with some essential tools for image mining. Specifically, Part I provides a brief and evolutionary journey from the classical Fourier transform (Chap. 1) to Gabor filters (Chap. 2) and to contemporary wavelet transform (Chap. 3). It prepares readers with fundamental math for some of the advanced mining techniques discussed in the book. Apart from the theories, this part also uses Fourier spectra, STFT spectrogram, Gabor filter spectra, DCT spectra and wavelet spectra to demonstrate how key information or features in an image can be captured by these fundamental transforms.

Part II and Part III are the core of the book, which examine and analyze varieties of state-of-the-art models, tools, algorithms/procedures and machines for image mining. In contrast to Part I which is mostly theoretical, these two parts focus on dealing with real image data and real image mining. Part II demonstrates how a variety of features can be mined or extracted from images for image representation, and it covers three chapters which focus on color (Chap. 4), texture (Chap. 5) and shape, respectively (Chap. 6). Each chapter typically begins with simple methods or methods at intro level and moves on to the more advanced methods in a natural flow. Most of the methods in Part II are demonstrated with intuitive illustrations.

If Part II is analogue to raw mining, Part III is about refinery. Specifically, Part III presents readers with four powerful learning machines to classify image data, including Bayesian machine (Chap. 7), SVM (Chap. 8), ANN/CNN (Chap. 9) and DT (Chap. 10). Each chapter in this part begins with an icebreaking and introductory journey to give readers a big picture and a direction to follow. It then navigates to the more advanced topics with illustrations to key concepts and components of the learning machine. The story of each machine learning method is typically told with concise maths, demonstrations, applications and implementations.

After a breathtaking and arduous journey on image mining involving feature extraction and machine learning, readers are soothed with a recovery journey on image retrieval in Part IV. Part IV deals with putting images in order, inspecting the quality of a haul and organizing them for presentation or display. Indexing techniques suitable for image data are first described in details in Chap. 11 followed by the analysis of a number of image ranking techniques in Chap. 12. The part concludes in Chap. 13 with a number of interesting image presentation techniques and powerful image database visualization methods.

Key Features

A shortcut to AI. AI and machine learning are usually intimidating to many who don't have the sophisticated mathematics background. This book, however, offers readers a surprising shortcut to AI on machine learning by introducing four major machine learning tools with gentle and easy to understand mathematics using rich illustrations.

A natural marriage between maths and data. Maths and data can only be understood well when they are well matched. This book brings mathematics and computing into a single display and tells image stories with maths by a trained mathematician.

Visualization of image data mining. With more than 200 illustrations (multiple illustrations in some figures), it can be said that the book is a visualization of image data mining, making it very easy to read and understand for readers.

End of chapter summary. Every chapter of the book is equipped with an end of chapter summary to highlight the key points and connect the dots in the chapter. The summary also gives insights into some of the essentials which can be missed during the reading.

Project-based exercises. High-quality exercises with instructions or Matlab code have been created for each chapter to give readers the opportunities to test their skills learnt from the book. Each exercise is designed as a mini project which helps students to gain skills on solving a real-world problem. Instructors can expand most of them into internship projects and final year projects for undergraduates.

Writing for scanning. The book makes extensive use of powerful writing techniques tailored for modern readers, including inverted pyramid writing, blurbs, bullet lists, plain language, keyword headings, text chunking, analogies, scannable content, etc. Due to the use of a variety of writing for scanning techniques, it makes reading of the book very efficient and a good experience.

New Features of the Second Edition

1. A new section of discrete cosine transform or DCT has been added to Chap. 2. DCT features are widely used in many machine learning methods. Block-based DCT extends the series of windowed FT and shows the power of windowed FT from another perspective.

2. A new section of pre-processing has been added to Chap. 4. Noise removal and contrast enhancement are essential for image processing. The inclusion of techniques such as Gaussian filter, median filter and histogram equalization in the chapter further enhances the power of feature extraction.

3. A new section of statistical testing has been added to Chap. 12. Often researchers need to evaluate their work against existing approaches, hypothesis test provides a tool to verify the performance of their work and make the result more convincing. The additional section equips the readers with essential theories of statistical inference and provides a toolkit on how to conduct hypothesis test. This section offers readers a shortcut to statistical inference which is a complex topic.

4. New exercises have been added to Chaps. 8–13 and more quality exercises have been added to other chapters. Most of the exercises are provided with Matlab code and instructions, making them a valuable resource and experience for readers.

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Part I
Preliminaries

Good beginning is half done

In image analysis and understanding, no other tools is more important than wavelet transform. Wavelet is a remarkable achievement of decades of research on signal processing and analysis. Although many books have been written on wavelet, they are often too focused on theoretical part and too mathematical. This has hindered many researchers especially novice researchers from good understanding and application of this essential and important tool.

Wavelet theory is complex, it is difficult to understand it without rigorous mathematical training. Since wavelet theory is based on Fourier series and Fourier transform, it is impossible to understand how wavelet works without understand how Fourier transform works. On the other hand, a good understanding of Fourier transform will naturally leads to the understanding of wavelet theory.

In this part of the book, we present the wavelet transform theory as an evolution from Fourier transform. We start with Fourier series and Fourier transform by preparing readers with mathematical fundamentals and building a foundation for understanding wavelet. More importantly, the connection between Fourier theory and its application on signal processing is systematically shown to the readers. By finishing the Fourier transform chapter, readers will be able to understand the limitations of Fourier transform and this naturally leads to Short Time Fourier Transform (STFT), Gabor transform and Discrete Cosine Transform (DCT).

Once completing both Chaps. 1 and 2, readers are fully prepared to understand wavelet transform. Wavelet transform is just a natural extension of STFT and Gabor transform. To further strengthen readers understanding, the implementation of wavelet transform is shown by both theoretical illustrations and practical examples.

This part is the foundation of the many techniques discussed in this book. By completing this part, readers will be able to understand those powerful feature extraction methods including the curvelet transform in Part II.

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1. Fourier Transform

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In essence, the world is just elements and compounds.

1.1 Introduction

Fourier transform has played a key role in image processing for many years, and it continues to be a topic of interest in theory as well as application. The fundamental principle behind Fourier transform is that a pattern can be treated as a signal and as such it can be represented by elementary components of the signal. If we can define elementary components to represent or approximate a pattern under analysis, we can determine how significant an elementary component in a given pattern. The elementary components found in the signal can be used to describe the given pattern. Fourier transform is useful for pattern analysis and description because different patterns can be distinguished by the transformed spectra (Fig. 1.1) [1], while similar patterns will have similar transformed spectra even they are affected by noise and other variations. It can be observed that the spectrum of Fig. 1.1a clearly shows patterns of both horizontal and vertical directions, while that in Fig. 1.1b shows patterns of random fashion. They demonstrate the power of Fourier transform in image analysis and understanding.

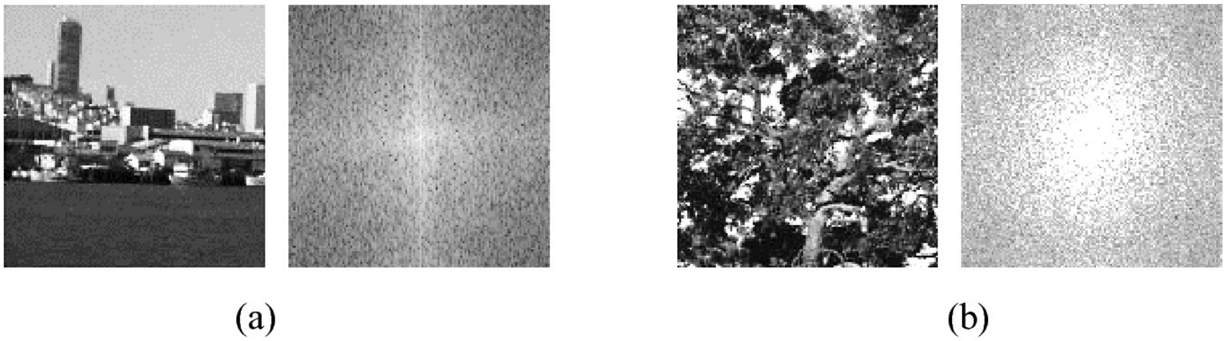

Fig. 1.1 Fourier spectra of different images. **a** A scenic image at the left and its Fourier spectrum at the right; **b** a tree image in the left and its Fourier spectra in the right. The brighter the pixel the higher magnitude of the spectrum

1.2 Fourier Series

1.2.1 Sinusoids

To understand how Fourier transform works, it has to start with understanding how sinusoids work. It is important to understand the relationship between frequency and period. Figure 1.2 shows a sine wave and its harmonic waves. It shows how the change of variable scaling or horizontal stretching affects the sine wave's frequency and periods.

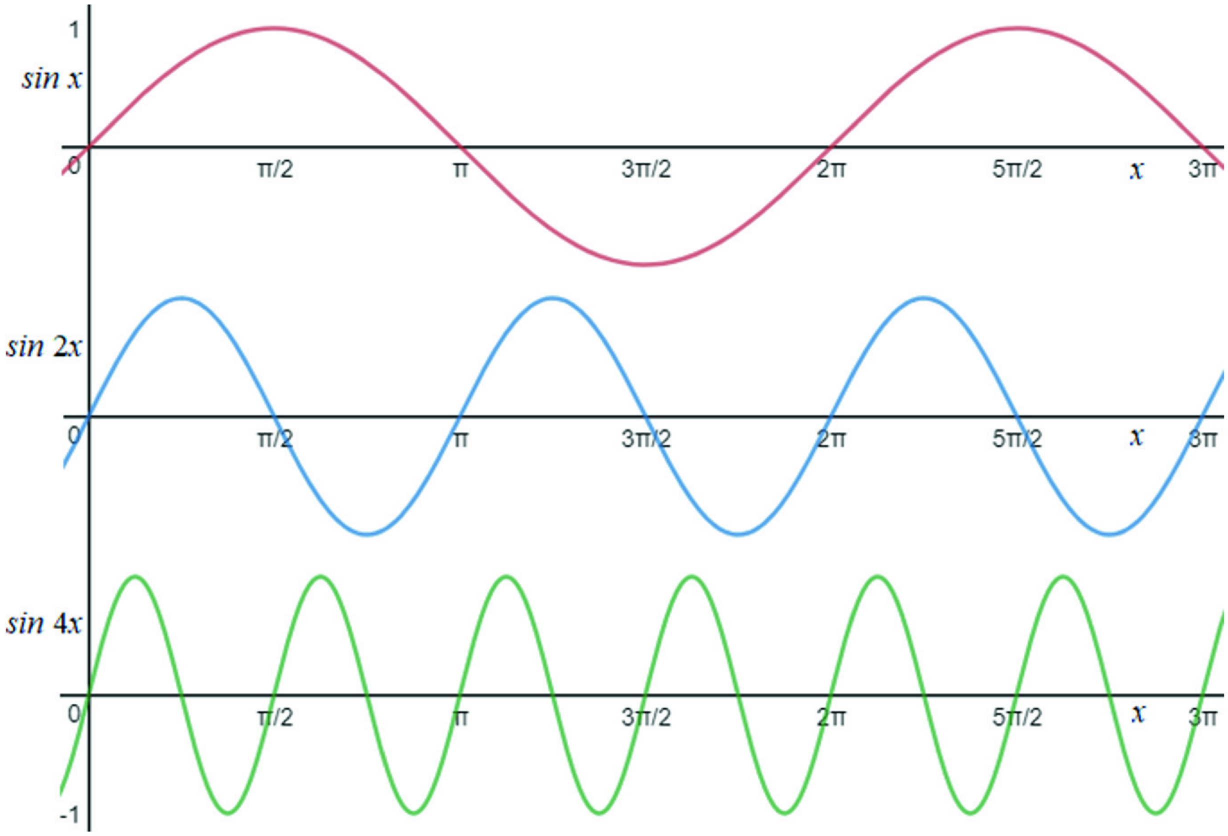

Fig. 1.2 The sine waves sin(nx) with different periods and frequencies

Sine waves	Frequency	Periods
sin x	$\frac{1}{2\pi}$	2π
sin $2x$	$\frac{1}{\pi}$	π
sin $4x$	$\frac{2}{\pi}$	$\frac{\pi}{2}$
…		
sin nx	$\frac{n}{2\pi}$	$\frac{2\pi}{n}$

As can be seen, as the variable scaling factor n increases, the period of sin(nx) becomes shorter and the frequency becomes higher. For example, the period of sin(x) is 2π, while the periods of sin($2x$) and sin($4x$) are π and ½ π, respectively. Consequently, the frequencies of the three sine waves are $1/2\pi$, $1/\pi$ and $2/\pi$, respectively. Similarly, the period and frequency of sin(nx) is $2\pi/n$ and $n/2\pi$, respectively.

The sine waves expressed this way do not have an easy interpretation of the frequency and periods because both of them are in angular terms. Now let's replace n with $2\pi n$ and change the sine function from $\sin(nx)$ to $\sin(2\pi nx)$; see what will happen.

Sine waves	**Frequency**	**Periods**
$\sin(2\pi x)$	1	1
$\sin(4\pi x)$	2	$\frac{1}{2}$
$\sin(8\pi x)$	4	$\frac{1}{4}$
...		
$\sin(2\pi nx)$	n	$\frac{1}{n}$

Now both the periods and frequencies are easier to understand. For example, the period of $\sin(2\pi x)$ is 1, while the periods of $\sin(4\pi x)$ and $\sin(8\pi x)$ are 1/2 and 1/4, respectively. Consequently, the frequencies of the three sine waves are 1, 2 and 4, respectively. Therefore, the period and frequency of $\sin(2\pi nx)$ are $1/n$ and n, respectively. This is much easier to interpret as shown in (Fig. 1.3).

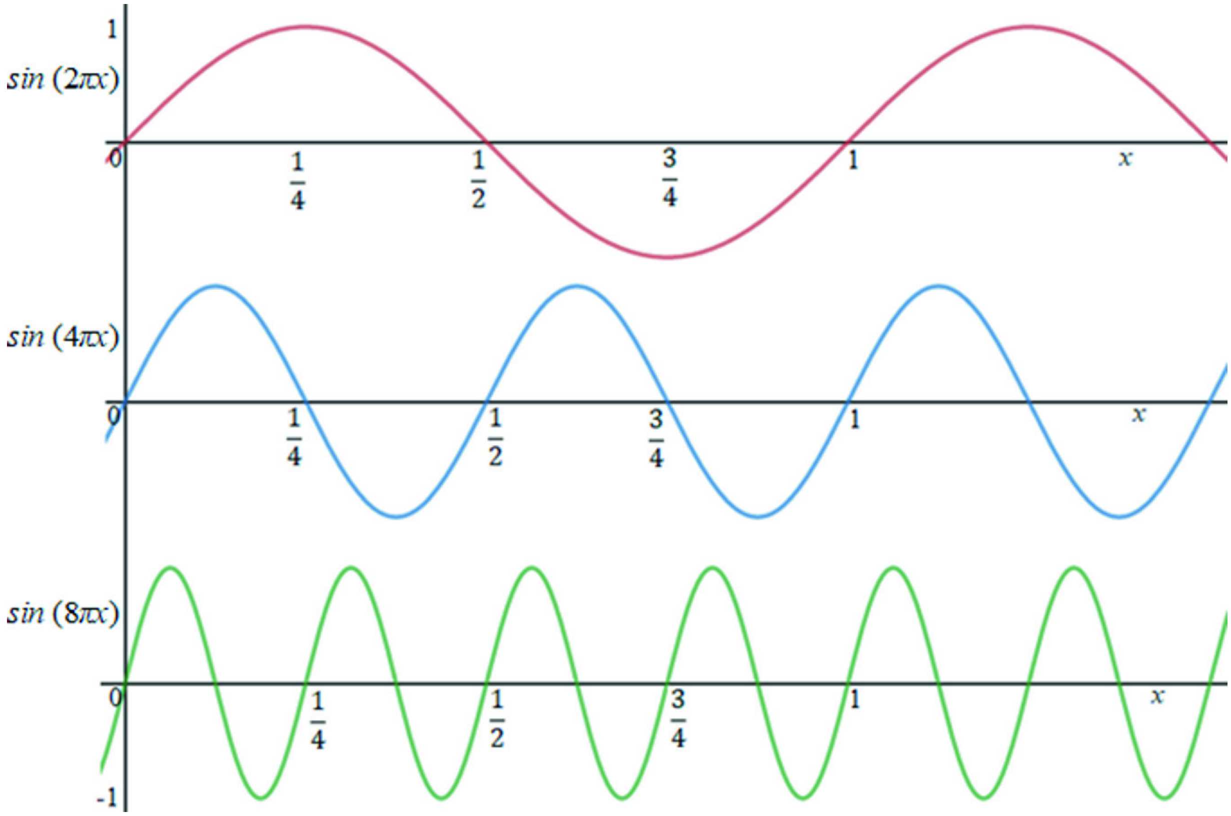

Fig. 1.3 The sine waves $\sin(2\pi n x)$ with different periods and frequencies

A more general form of sine function is expressed as $\sin(2\pi n/L)$, which has a period of L/n and frequency of n/L. This is extremely helpful to analyze signals with arbitrary periodicity and frequencies.

Sine wares	Frequency	Periods
$\sin(\frac{2\pi x}{L})$	$\frac{1}{L}$	L
$\sin(\frac{4\pi x}{L})$	$\frac{2}{L}$	$\frac{L}{2}$
$\sin(\frac{8\pi x}{L})$	$\frac{4}{L}$	$\frac{L}{4}$
...		
$\sin(\frac{2\pi n x}{L})$	$\frac{n}{L}$	$\frac{L}{n}$

1.2.2 Fourier Series

One of the most important and interesting discoveries in mathematics is that any math function can be approximated with a *series of sinusoids* (sine and cosine waves), called *Fourier series*. Now consider a signal function $f(x)$ with period L,

$$f(x) = a_0 + \sum_{n=1}^{\infty} \left(a_n \cos \frac{2\pi n x}{L} + b_n \sin \frac{2\pi n x}{L} \right) \tag{1.1}$$

To determine the Fourier coefficients a_n and b_n, we multiply both sides of the above equation with either $\sin\left(\frac{2\pi n x}{L}\right)$ or $\cos\left(\frac{2\pi n x}{L}\right)$ and do the integral in $[-L/2, L/2]$. It can be shown that sine and cosine waves have the following convenient properties:

$$\int_{-L/2}^{L/2} \cos \frac{2\pi n x}{L} \cos \frac{2\pi m x}{L} \mathrm{d}x = \begin{cases} L/2 & \text{for } n = m \\ 0 & \text{for } n \neq m \end{cases} \tag{1.2}$$

$$\int_{-L/2}^{L/2} \sin \frac{2\pi n x}{L} \sin \frac{2\pi m x}{L} \mathrm{d}x = \begin{cases} L/2 & \text{for } n = m \\ 0 & \text{for } n \neq m \end{cases} \tag{1.3}$$

$$\int_{-L/2}^{L/2} \sin \frac{2\pi n x}{L} \cos \frac{2\pi m x}{L} \mathrm{d}x = 0 \tag{1.4}$$

$$\int_{-L/2}^{L/2} \sin \frac{2\pi n x}{L} \mathrm{d}x = 0 \tag{1.5}$$

$$\int_{-L/2}^{L/2} \cos \frac{2\pi n x}{L} \mathrm{d}x = 0 \tag{1.6}$$

To prove the above properties, we only need to demonstrate that $\int \sin(nx)\sin(mx)\,\mathrm{d}x = 0$ $(m \neq n)$ and $\int \sin(nx)\cos(mx)\,\mathrm{d}x = 0$; the others are obvious due to the symmetry of sine and cosine waves. Without loss of generality, we just need to show $\int \sin x \sin(2x)\,\mathrm{d}x = 0$ and $\int \sin x \cos x\,\mathrm{d}x = 0$.

Figure 1.4 illustrates $\int \sin x \sin(2x)\,\mathrm{d}x$ in one period. We divide the *sum of product* (SoP) of the two functions within one period into four regions: R1–R4, marked with different colors. It's easy to observe that the SoP magnitude of the four regions is exactly the same; however, the signs of the four corresponding SoPs are + , − , − and + respectively, resulting in the total SoP of the period as 0. Applying this to all the other periods, it can be shown $\int \sin x \sin(2x)\,\mathrm{d}x = 0$ on the entire *x*-axis.

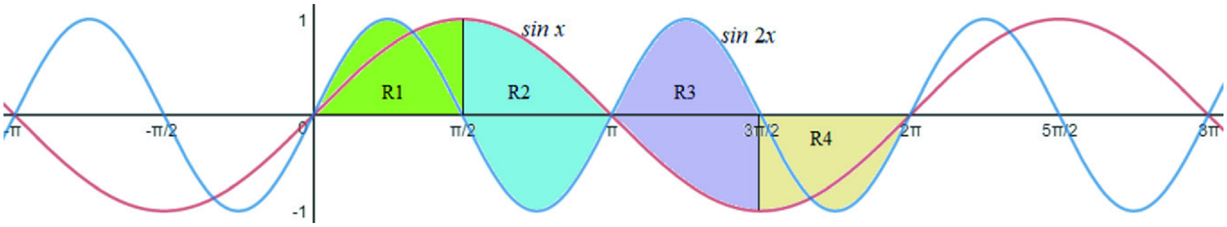

Fig. 1.4 Illustration of $\int \sin x \sin(2x)\,\mathrm{d}x = 0$

Figure 1.5 illustrates $\int \sin x \cos x\,\mathrm{d}x$ in one period. Similar to the above, we divide the sum of product (SoP) of the two functions in the single period into four regions: R1-R4, marked with different colors. Again, it's easy to observe that the SoP magnitude of the four regions is exactly the same; however, the signs of the four corresponding SoPs are + , − , + and −, respectively, resulting in the total SoP of the period as 0. Applying this to all other periods, it can be shown $\int \sin x \cos x\,\mathrm{d}x = 0$ on the entire *x*-axis.

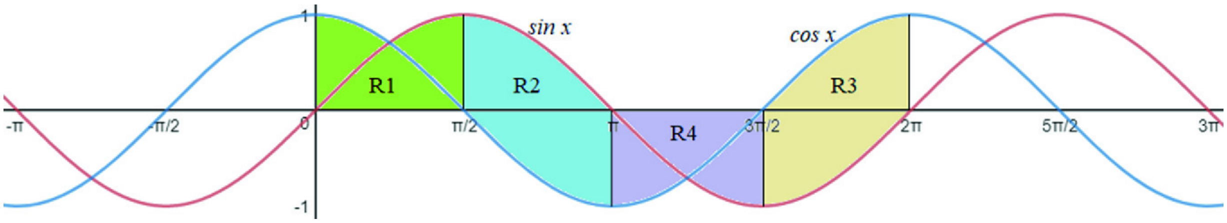

Fig. 1.5 Illustration of $\int \sin x \cos x \, \mathrm{d}x = 0$

By making use of the integral identities and orthogonality of (1.2)–(1.6), the Fourier coefficients are obtained as the following

$$\left.\begin{aligned} a_0 &= \frac{1}{L}\int_{-L/2}^{L/2} f(x)\mathrm{d}x \\ a_n &= \frac{2}{L}\int_{-L/2}^{L/2} f(x)\cos\frac{2\pi n x}{L}\mathrm{d}x \\ b_n &= \frac{2}{L}\int_{-L/2}^{L/2} f(x)\sin\frac{2\pi n x}{L}\mathrm{d}x \end{aligned}\right\} \tag{1.7}$$

$n = 1, 2, \ldots.$

1.2.3 Complex Fourier Series

Using the Euler formula:

$$\mathrm{e}^{ix} = \cos x + i \sin x \tag{1.8}$$

where $i = \sqrt{-1}$. It is easy to work out:

$$\cos(x) = \frac{1}{2}\left(\mathrm{e}^{ix} + \mathrm{e}^{-ix}\right) \tag{1.9}$$

$$\sin(x) = \frac{1}{2i}\left(\mathrm{e}^{ix} - \mathrm{e}^{-ix}\right) = -\frac{i}{2}\left(\mathrm{e}^{ix} - \mathrm{e}^{-ix}\right) \tag{1.10}$$

Now, replace the sinusoids in the Fourier series of (1.1) with the above two equations, we obtain the complex Fourier series:

$$\begin{aligned} f(x) &= \frac{a_0}{2} + \sum_{n=1}^{\infty}\left(a_n \cos\frac{2\pi nx}{L} + b_n \sin\frac{2\pi nx}{L}\right) \\ &= \frac{a_0}{2} + \frac{1}{2}\sum_{n=1}^{\infty} a_n\left(\mathrm{e}^{i\frac{2\pi nx}{L}} + \mathrm{e}^{-i\frac{2\pi nx}{L}}\right) - \frac{i}{2}\sum_{n=1}^{\infty} b_n\left(\mathrm{e}^{i\frac{2\pi nx}{L}} - \mathrm{e}^{-i\frac{2\pi nx}{L}}\right) \quad (1.11) \\ &= \frac{a_0}{2} + \frac{1}{2}\sum_{n=1}^{\infty}(a_n - ib_n)\,\mathrm{e}^{i\frac{2\pi nx}{L}} + \frac{1}{2}\sum_{n=1}^{\infty}(a_n + ib_n)\,\mathrm{e}^{-i\frac{2\pi nx}{L}} \end{aligned}$$

which can be written as the complex Fourier series

$$f(x) = \sum_{n=-\infty}^{\infty} c_n \mathrm{e}^{i2\pi nx/L} \tag{1.12}$$

The exponential form of orthogonality is as follows:

$$\int_{-\frac{L}{2}}^{\frac{L}{2}} \mathrm{e}^{-\frac{i2\pi mx}{L}}\mathrm{e}^{\frac{i2\pi nx}{L}} = \begin{cases} L & \text{for } m = n \\ 0 & \text{otherwise} \end{cases} \tag{1.13}$$

Now, multiplying both sides of the Fourier series (1.12) with $\mathrm{e}^{-i2\pi nx/L}$ and do integral in $[0, L]$, we obtain complex Fourier coefficients:

$$c_n = \frac{1}{L}\int_{-\frac{L}{2}}^{\frac{L}{2}} f(x)\,\mathrm{e}^{-i\frac{2\pi nx}{L}}\mathrm{d}x, \quad n = 0, \pm 1, \pm 2, \ldots \tag{1.14}$$

1.3 Fourier Transform

Equation (1.14) indicates the coefficients of the Fourier series are determined by $f(x)$, while (1.12) indicates that $f(x)$ can be reconstructed from Fourier coefficients c_n. Therefore, the Fourier series establishes a unique correspondence between $f(x)$ and its Fourier coefficients. Now, consider the integral of (1.14):

$$Lc_n = \int_{-\frac{L}{2}}^{\frac{L}{2}} f(x)\, \mathrm{e}^{-j\frac{2\pi nx}{L}} \mathrm{d}x \tag{1.15}$$

where $j = \sqrt{-1}$. If we let $L \to \infty$, n/L becomes continuous and $n/L \to u$, (1.15) becomes:

$$F(u) = \int_{-\infty}^{\infty} f(x) \exp(-j2\pi ux)\, \mathrm{d}x \tag{1.16}$$

Now, substituting (1.6) into (1.12) and replacing the sum with an integral by using $n/L \to u$ and $1/L \to \mathrm{d}u$, (1.12) becomes

$$f(x) = \int_{-\infty}^{\infty} F(u) \exp(j2\pi ux)\, \mathrm{d}u \tag{1.17}$$

The $F(u)$ of (1.16) is called the forward *Fourier transform* or FT and (1.17) is called the *inverse Fourier transform* or FT^{-1}.

1.4 Discrete Fourier Transform

1.4.1 DFT

Discrete Fourier transform (DFT) is particularly useful for digital pattern analysis because digital patterns exist in discrete form. To define DFT from Fourier series, $f(x)$ is first discretized into N samples in $[0, L]$:

$$f(0), f(\Delta x), f(2\Delta x), \ldots, f((N-1)\Delta x) \tag{1.18}$$

where Δx is the sample step in spatial domain and $L = N\Delta x$, then $f(x)$ can be expressed as

$$f(k) = f(k\Delta x), \quad k = 0, 1, 2, \ldots, N-1 \tag{1.19}$$

Now consider the Fourier coefficients (1.14):

$$\begin{aligned} c_n &= \frac{1}{L}\int_{-L/2}^{L/2} f(x)\,\mathrm{e}^{-j\frac{2\pi nx}{L}}\mathrm{d}x \\ &= \frac{1}{L}\int_{0}^{L} f(x)\,\mathrm{e}^{-j\frac{2\pi nx}{L}}\mathrm{d}x \end{aligned} \tag{1.20}$$

By substituting $L = N\Delta x$, $f(x) = f(k)$, $x = k\Delta x$ and $dx = \Delta x$ into the above equation, it yields:

$$\begin{aligned} c_n &= \frac{\Delta x}{N\Delta x}\sum_{k=0}^{N-1} f(k)\,\mathrm{e}^{-j\frac{2\pi nk\Delta x}{N\Delta x}} \\ &= \frac{1}{N}\sum_{k=0}^{N-1} f(k)\,\mathrm{e}^{-j\frac{2\pi nk}{N}} \quad n = 0, 1, 2, \ldots, N-1 \end{aligned} \tag{1.21}$$

Therefore, the DFT of $f(x)$ is given as:

$$F(u) = \frac{1}{N}\sum_{x=0}^{N-1} f(x)\exp(-j2\pi ux/N) \quad u = 0, 1, 2, \ldots, N-1 \tag{1.22}$$

By substituting (1.22) into (1.12), the inverse DFT is obtained as:

$$f(x) = \sum_{u=0}^{N-1} F(u)\exp(j2\pi ux/N) \quad x = 0, 1, 2, \ldots, N-1 \tag{1.23}$$

1.4.2 Uncertainty Principle

Assume $f(x)$ is a signal in a time period of $\Delta T = [0, L]$, the sampling step Δu in frequency domain and the sampling step Δx in spatial domain are related by the following expression:

$$\Delta u = \frac{1}{\Delta T} = \frac{1}{N\Delta x} \tag{1.24}$$

Basically, (1.24) tells that the frequency sampling step is inversely proportional to the spatial sampling step. This is known as the *uncertainty principle*, which means that increasing spatial resolution (reduce Δx) reduces frequency resolution and vice versa. In another words, higher spatial resolution and higher frequency resolution cannot be achieved simultaneously. This is the key reason behind the multi-resolution analysis such as wavelets which will be discussed later on in Chap. 3.

Since the Δx depends on the sampling rate f_s, and the relationship between Δx and f_s is given by $\Delta x = 1/f_s$, the above inequality becomes:

$$\Delta u \geq \frac{f_s}{N} \tag{1.25}$$

and the uth frequency is given by:

$$f_u = u \cdot \frac{f_s}{N} \tag{1.26}$$

It should be noted that the uth frequency computed from (1.22) is not the actual frequency; instead, the uth frequency is the uth *bin* of frequency. In other words, u is the bin number, and the actual frequency is given by (1.26): $f_u = u \cdot \Delta u$, and Δu is called the bin size of DFT. If $f_s = N$, $\Delta u = 1$, this is often the assumption in DFT. However, this is not always the case. When $f_s \gg N, \Delta u \gg 1$, this will be demonstrated in Sect. 2.2. Equation (1.25) is another form of the *uncertainty principle*. Given a sampling rate, in order to increase the frequency resolution (reduce Δu), it has to increase the sample or window size N, which reduces the spatial resolution. This is called the *trade-off* between spatial resolution and frequency resolution.

It should also be noted that any window size of a DFT is relative according to (1.25). Specifically, a window size is relative to the sampling rate or sampling frequency. A window of N samples is smaller in a signal with faster sampling rate than that in a signal with slower sampling rate. For example, in a signal with 44,000 Hz sampling rate, a window of 128 samples has a duration of 128/44,000 = 0.0029 s. However, in a signal with 22,000 Hz sampling rate, the duration of a 128 samples window is 128/22,000 = 0.0058 s, which is twice the size as that in the first signal. This indicates that a bin number (u) of a DFT computed from windows of different sizes or different signals means different frequency.

The inverse relationship between frequency resolution and spatial resolution (window size) can be demonstrated using the following example. Suppose there are two sine waves with very small frequency difference [2]:

$$\text{Sine wave one: } \sin(2\pi \times 0.05x)$$
$$\text{Sine wave two: } \sin(2\pi \times 0.0501x)$$

In this case, $\Delta u = 0.0001$. If we plot the two sine waves in one graph (Fig. 1.6), one in red and the other in blue, the two signals do not show difference in the first 100 samples, means a small window cannot discern the difference of the two signals. However, if we show the two signals in a very large window (5000 samples), at the end of the window, they are 180 degrees out of phase. This is because the periods of the two sine waves are 20 and 19.96, respectively. Assume a sampling frequency of 1 Hz. For a 100 samples window, the difference between the two signals is just 5.01 − 5 = 0.01 period, which is almost indiscernible. However, with a 5000 samples window, the difference between the two signals is 250.5 − 250 = 0.5 period, which is more than sufficient to distinguish the two signals. It’s more convenient to explain this case using (1.25) because the smallest frequency difference can be detected in a 100 samples window is $\Delta u = 1/100 = 0.01$, while in a 5000 samples window, $\Delta u = 1/5000 = 0.0002$, which is able to distinguish the two signals.

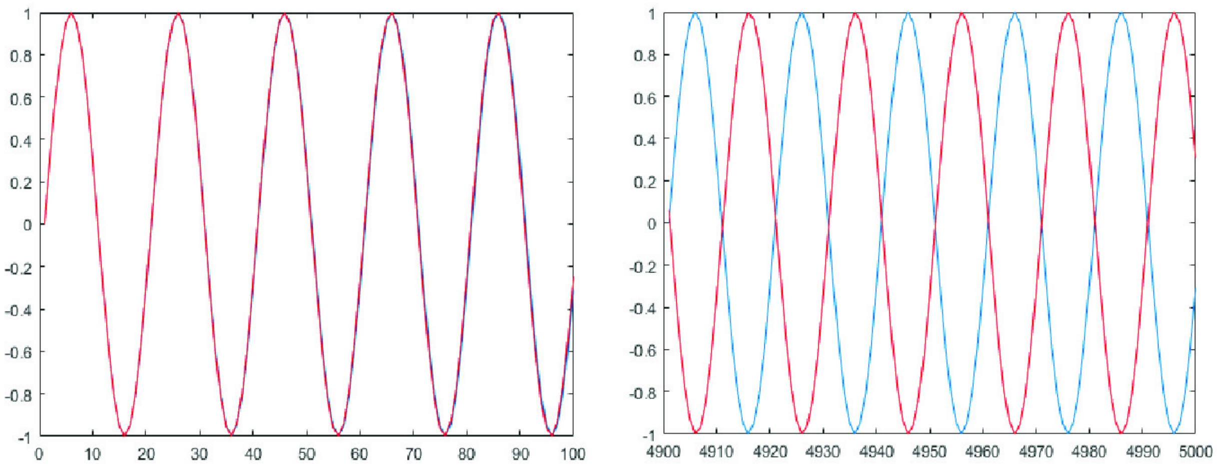

Fig. 1.6 Inverse relationship between spatial and frequency resolution. Left: the first 100 samples of the two sine waves; Right: the last 100 samples of the two sine waves

It demonstrates that a smaller window gives poor frequency resolution, while a larger window gives higher frequency resolution. This is because the larger the window, the more samples and the more low frequencies can be computed.

1.4.3 Nyquist Theorem

Because frequency is measured by the number of cycles in a period of time, and the smallest cycle consists of two samples, for a signal of size N, only $N/2$ frequencies can be computed from the DFT. This is called the *Nyquist theorem*.

Another way to express the *Nyquist theorem* is that in order to reconstruct/recover a signal appropriately (‘appropriately’ means recover the ‘essence’ or low frequency while ignore the ‘nuance’ or high frequency), the sampling rate of the signal must be at least twice the highest frequency in the signal. Figure 1.7 demonstrates this fact. The figure shows three signals of 1 s length. The top signal is a sine wave with one cycle/period (frequency = 1) which can be recovered or reconstructed appropriately by at least two samples (marked with red dots). The middle signal is a sine wave with two cycles/periods in a second (frequency = 2); it needs at least four samples to recover the signal appropriately. The bottom signal is a sine wave with four cycles/periods in a second (frequency = 4); it needs at least eight samples to recover the signal appropriately and so on so forth.

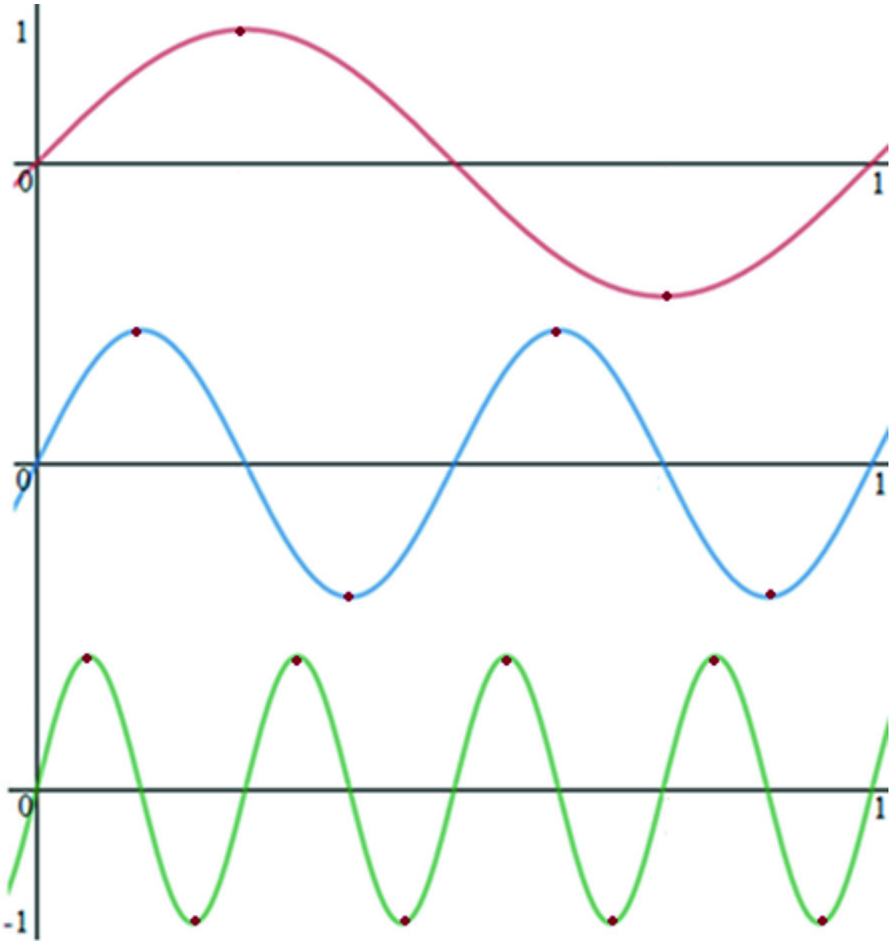

Fig. 1.7 Illustrations of different sampling rates for three signals of the same time length

In the case of images, frequency is related to structure size and small structures are known to have high frequency. Because the smallest structure in an image requires two pixels to discern, the highest frequency which can be captured in an image is 1/2pixels.

1.5 2D Fourier Transform

For a two variable function $f(x, y)$ defined in $0 \le x, y < N$, its Fourier transform pair is given by

$$F(u,v) = \frac{1}{N}\sum_{x=0}^{N-1}\sum_{y=0}^{N-1} f(x,y)\exp[-j2\pi(ux+vy)/N] \tag{1.27}$$

for $u, v = 0, 1, 2, \ldots, N-1$, and $j = \sqrt{-1}$.

$$f(x,y) = \frac{1}{N}\sum_{u=0}^{N-1}\sum_{v=0}^{N-1} F(u,v)\exp[j2\pi(ux+vy)/N] \tag{1.28}$$

for $x, y = 0, 1, 2, \ldots, N-1$.

Although the number of $F(u, v)$ resulted from Fourier transform is usually large, the number of significant $F(u, v)$ (or $F(u)$) (large magnitude) is usually small. This is because the higher frequencies only represent finest pattern details which are not so useful in many applications. This means that a meaningful approximation of original pattern $f(x, y)$ (or $f(x)$) can be constructed from a small number of $F(u, v)$ (or $F(u)$). This forms the basis of Fourier signal processing and Fourier pattern analysis.

1.6 Properties of 2D Fourier Transform

Fourier transform has the following important properties which are useful for image analysis.

1.6.1 Separability

The discrete Fourier transform can be expressed in the separable form

$$\begin{aligned} F(u,v) &= \frac{1}{\sqrt{N}}\sum_{x=0}^{N-1}\left[\frac{1}{\sqrt{N}}\sum_{y=0}^{N-1} f(x,y)\exp\left(-\frac{j2\pi vy}{N}\right)\right]\exp\left(-\frac{j2\pi ux}{N}\right) \\ &= \frac{1}{\sqrt{N}}\sum_{x=0}^{N-1} F(x,v)\exp\left(-\frac{j2\pi ux}{N}\right) \\ &= \mathrm{FT}_x\left\{\mathrm{FT}_y\left[f(x,y)\right]\right\} \end{aligned} \tag{1.29}$$

where FT_x and FT_y are the 1D FTs on row and column, respectively.

The advantage of the separability is that $F(u, v)$ can be obtained in two steps by successive applications of 1D FT which can be computed using the *fast Fourier transform* (FFT).

1.6.2 Translation

The translation property of the Fourier transform is given by

$$\mathrm{FT}\left[f(x-x_0,y-y_0)\right] = F\left(u,v\right)\cdot\exp\left[-j2\pi\left(ux_0+vy_0\right)/N\right] \tag{1.30}$$

It indicates that a shift in spatial domain results in phase change in frequency domain. That means the magnitude of Fourier transform is invariant to translation. This is a desirable feature because in many applications the phase information is discarded which leaves the FT features invariant to translation.

1.6.3 Rotation

To find the relationship between a rotated function $f(x, y)$ and its spectrum, let's assume the function $f(x, y)$ is rotated by an angle θ and the function after the rotation is $f(x', y')$. Then the relationship between two corresponding points of the two functions is as follows:

$$x' = x\cos\theta + y\sin\theta \tag{1.31}$$

$$y' = y\cos\theta - x\sin\theta \tag{1.32}$$

$$x = x'\cos\theta - y'\sin\theta \tag{1.33}$$

$$y = x'\sin\theta + y'\cos\theta \tag{1.34}$$

Substituting (1.33) and (1.34) into (1.27), we have

$$\begin{aligned}
F(u',v') &= \frac{1}{N}\sum_{x'=0}^{N-1}\sum_{y'=0}^{N-1} f(x',y') \\
&\quad \exp\left[-j2\pi\left(\frac{ux'\cos\theta - uy'\sin\theta + vx'\sin\theta + vy'\cos\theta}{N}\right)\right] \\
&= \frac{1}{N}\sum_{x'=0}^{N-1}\sum_{y'=0}^{N-1} f(x',y') \exp\left[-j2\pi x'\left(\frac{u\cos\theta + v\sin\theta}{N}\right)\right] \\
&\quad \exp\left[-j2\pi y'\left(\frac{v\cos\theta - u\sin\theta}{N}\right)\right] \\
&= \frac{1}{N}\sum_{x'=0}^{N-1}\sum_{y'=0}^{N-1} f(x',y') \exp\left[-j2\pi\left(\frac{x'u' + y'v'}{N}\right)\right]
\end{aligned} \tag{1.35}$$

where

$$u' = u\cos\theta + v\sin\theta \tag{1.36}$$

$$v' = v\cos\theta - u\sin\theta \tag{1.37}$$

Therefore, rotating $f(x, y)$ by an angle of θ in spatial domain rotates $F(u, v)$ by the same angle in frequency domain.

The rotation property can be proved more conveniently by considering $f(x, y)$ and FT in either complex domain or polar space. A point (x, y) in complex domain can be expressed as:

$$z = x + jy \tag{1.38}$$

By using Euler’s formula, it is simple to show that

$$\begin{aligned}
z\mathrm{e}^{-j\theta} &= (x + jy)\cdot(\cos\theta - j\sin\theta) \\
&= x\cos\theta + jy\cos\theta - jx\sin\theta + y\sin\theta \\
&= (x\cos\theta + y\sin\theta) + j(y\cos\theta - x\sin\theta) \\
&= x' + jy'
\end{aligned} \tag{1.39}$$

Equation (1.39) shows that a point z rotated by an angle θ is equivalent to z times $e^{-j\theta}$. In other words, the following is true:

$$f(x', y') = f(x, y) \cdot e^{-j\theta} \tag{1.40}$$

Equation (1.40) is a more concise and convenient rotation formula than (1.31) and (1.32). By substituting (1.40) into (1.27), we obtain the FT of the rotated function $f(x', y')$:

$$\begin{aligned} F(u', v') &= \frac{1}{N} \sum_{x=0}^{N-1} \sum_{y=0}^{N-1} f(x', y') \exp\left[-j2\pi\left(\frac{ux + vy}{N}\right)\right] \\ &= \frac{1}{N} \sum_{x=0}^{N-1} \sum_{y=0}^{N-1} f(x, y) e^{-j\theta} \exp\left[-j2\pi\left(\frac{ux + vy}{N}\right)\right] \\ &= F(u, v) \cdot e^{-j\theta} \end{aligned} \tag{1.41}$$

Therefore, we obtain the same result as shown in (1.35).

If we consider both $f(x, y)$ and $F(u, v)$ in polar space, they can be expressed as $f(r, \theta)$ and $F(\rho, \phi)$, respectively, where

$$x = r\cos\theta, y = r\sin\theta; \; u = \rho\cos\phi, \; v = \rho\sin\phi \tag{1.42}$$

(r, θ) is the polar coordinates in image plane and (ρ, ϕ) is the polar coordinates in frequency plane. The differentials of x and y are:

$$\left.\begin{aligned} dx &= \cos\theta dr - r\sin\theta d\theta \\ dy &= \sin\theta dr - r\cos\theta d\theta \end{aligned}\right\} \tag{1.43}$$

The Jacobian of (1.43) is r. Therefore, by substituting both (1.42) and (1.43) into 2D continuous FT, the 2D FT in polar space is given by the following:

$$\begin{aligned} F(\rho,\phi) &= \int_0^{\infty}\int_0^{2\pi} f(r,\theta)\mathrm{e}^{-j2\pi(rcos\theta\ \rho cos\phi + rsin\theta\ \rho sin\phi)} r\mathrm{d}r\mathrm{d}\theta \\ &= \int_0^{\infty}\int_0^{2\pi} f(r,\theta)\mathrm{e}^{-j2\pi r\rho\cos(\theta-\phi)} r\mathrm{d}r\mathrm{d}\theta \end{aligned} \tag{1.44}$$

Suppose $f(r, \theta)$ is rotated for an angle of θ_0 to $f(r, \theta + \theta_0)$. Let $\theta' = \theta + \theta_0$; then

$$\theta = \theta' - \theta_0 \quad \text{and} \quad \mathrm{d}\theta = \mathrm{d}\theta' \tag{1.45}$$

Now, in (1.44), substituting $f(r, \theta)$ with $f(r, \theta')$ and substituting θ with (1.45), we obtain:

$$F(\rho,\phi') = \int_0^{\infty}\int_0^{2\pi} f(r,\theta')\mathrm{e}^{-j2\pi r\rho\cos[\theta'-(\phi+\theta_0)]} r\mathrm{d}r\mathrm{d}\theta' \tag{1.46}$$

Equation (1.46) means:

$$\mathrm{FT}[f(r,\theta+\theta_0)] = F(\rho,\phi+\theta_0) \tag{1.47}$$

Again, this yields the same result as (1.35) and (1.41). Equation (1.47) also tells that in polar domain the rotation of an image causes a translation or shift on its FT spectrum. This property is useful for feature normalization.

1.6.4 Scaling

For two scalars a and b, the scale property of Fourier transform is given by

$$\mathrm{FT}[f(ax,by)] = \frac{1}{ab}F\left(\frac{u}{a},\frac{v}{b}\right) \tag{1.48}$$

It indicates the scaling of $f(x, y)$ with a and b in x and y directions in spatial domain (time domain in 1D case) causes inverse scaling of magnitude of $F(u, v)$ in frequency domain. That means, if you stretch

$f(x, y)$ in spatial domain, you shrink $F(u, v)$ in frequency domain, and vice versa. This proves the *uncertainty principle* from another perspective. In general terms, enlarging an object in an image gives rise to lower frequencies in spectral domain while shrinking an object in an image gives rise to higher frequencies in spectral domain. This property is useful in dealing with image scaling.

1.6.5 Convolution Theorem

The *convolution theorem* states that the FT of a convolution between two functions is equal to the product of two FTs. Specifically, given two function f and g, the following are true:

$$\mathrm{FT}[f * g] = \mathrm{FT}[f] \cdot \mathrm{FT}[g] \tag{1.49}$$

$$f * g = \mathrm{FT}^{-1}\{\mathrm{FT}[f] \cdot \mathrm{FT}[g]\} \tag{1.50}$$

where $f * g$ means convolution. Because of the separability property of 2D FT, we only need to prove the 1D case.

$$\begin{aligned}
\mathrm{FT}\left[f * g\right] &= \sum_{n}\sum_{m} f(m) g(n-m)\, \mathrm{e}^{-\frac{j2\pi nu}{N}} \\
&= \sum_{m} f(m) \sum_{n} g(n-m) \mathrm{e}^{-\frac{j2\pi nu}{N}} \\
&= \sum_{m} f(m) \mathrm{FT}\left[g\right] \mathrm{e}^{-\frac{j2\pi mu}{N}} \text{ (translation property)} \\
&= \mathrm{FT}\left[g\right] \sum_{n} f(m) \mathrm{e}^{-\frac{j2\pi mu}{N}} \\
&= \mathrm{FT}[f] \cdot \mathrm{FT}[g]
\end{aligned} \tag{1.51}$$

Convolution theorem shows that convolution in spatial domain can be done by a FT (FFT in practice) and a product. This is a useful feature because both FFT and product are much more efficient than spatial convolution.

1.7 Techniques of Computing FT Spectrum

The magnitude image of a Fourier transform is called an FT spectrum. The intensity of an FT spectrum has a very large dynamic range; it is impossible to display this large range in a gray-level image. For example, the dynamic range of spectral values of the Lena image [3] is [0, 31744], and Fig. 1.8a shows the FT spectrum without scaling. It can be seen that the spectral image reveals little information about the input image. Conventional *thresholding* (Fig. 1.8b) and *linear scaling* (Fig. 1.8c) do not work well for such a large range of values.

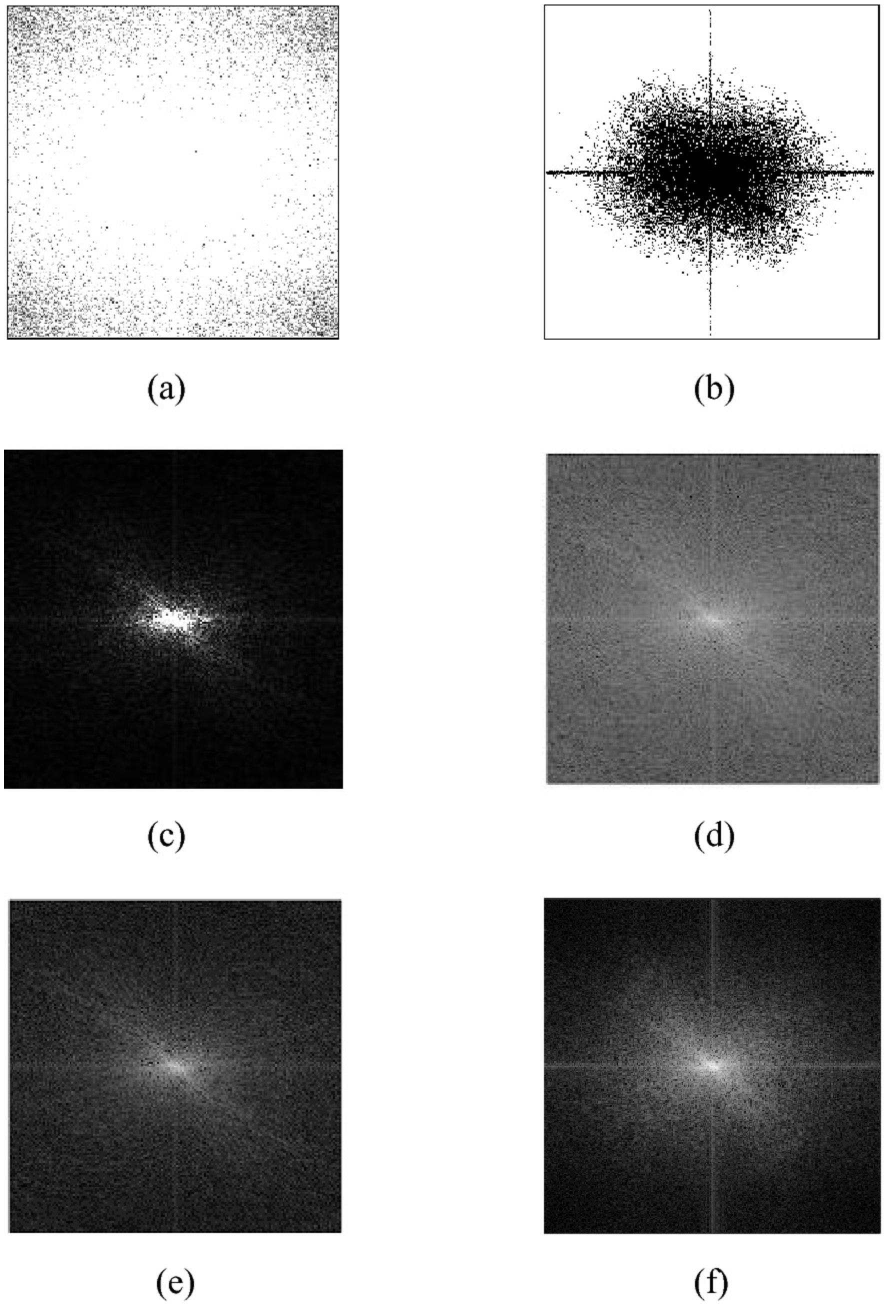

Fig. 1.8 FT spectra with different methods. **a** FT spectrum without scaling; **b** FT spectrum with thresholding value 10; **c** FT spectrum with linear scaling; **d** FT spectrum with log transform; **e** FT spectrum with both log and linear transform; **f** FT spectrum with enhanced contrast from (**e**)

The common practice of displaying an FT spectrum is to do a *logarithmic* transformation of the spectral values to bring down the large spectral values to well within the display range of 255 and raise the lower spectral values in the meantime. However, the logarithm transformed spectrum does not have sufficient contrast between lower frequency and higher frequency spectral values as shown in Fig. 1.8d. A more effective way to display FT spectrum is to apply a logarithm transform on the spectral values followed by a linear scaling to map the spectral magnitudes to [0, 255] using (1.52):

$$F'(u,v) = 255 \times \frac{\log\left(1 + |F(u,v)|\right)}{\log\left[1 + \max\left(|F(u,v)|\right)\right]} \tag{1.52}$$

Figure 1.8e shows the FT spectrum using (1.52). It can be seen from Fig. 1.8e that there are three directional features in the FT spectrum: horizontal, vertical and diagonal. The strong horizontal feature is due to the vertical pole on the left-hand side of the input image, while the vertical and diagonal features are due to the rim of the hat and the black arch on the right-hand side of the input image.

The logarithmic transformation, however, enhances the low magnitude values, while compressing high magnitude values into a relatively small pixel range. Therefore, if an image contains some important high magnitude information, this may lead to loss of information. An alternative solution to further increase the spectral contrast is to decrease the compression rate by scaling down the spectrum image intensity before applying the logarithmic transform. This is because the logarithmic function has a less degree of compression at places close to the origin. Figure 1.8f shows the FT spectrum with enhanced contrast, which is equivalent to highlighting the low-frequency area with a spot light.

The FT spectrum reveals key information about an image if displayed properly. Figure 1.9 shows three different types of homogenous patterns and their FT spectra on the right-hand side of the patterns. It can be seen that the FT spectra have generally accurately captured the three types of texture features: regularity, randomness and directionality. This is the primary motive for the development of short time FT and wavelets, which attempt to capture local and changing patterns.

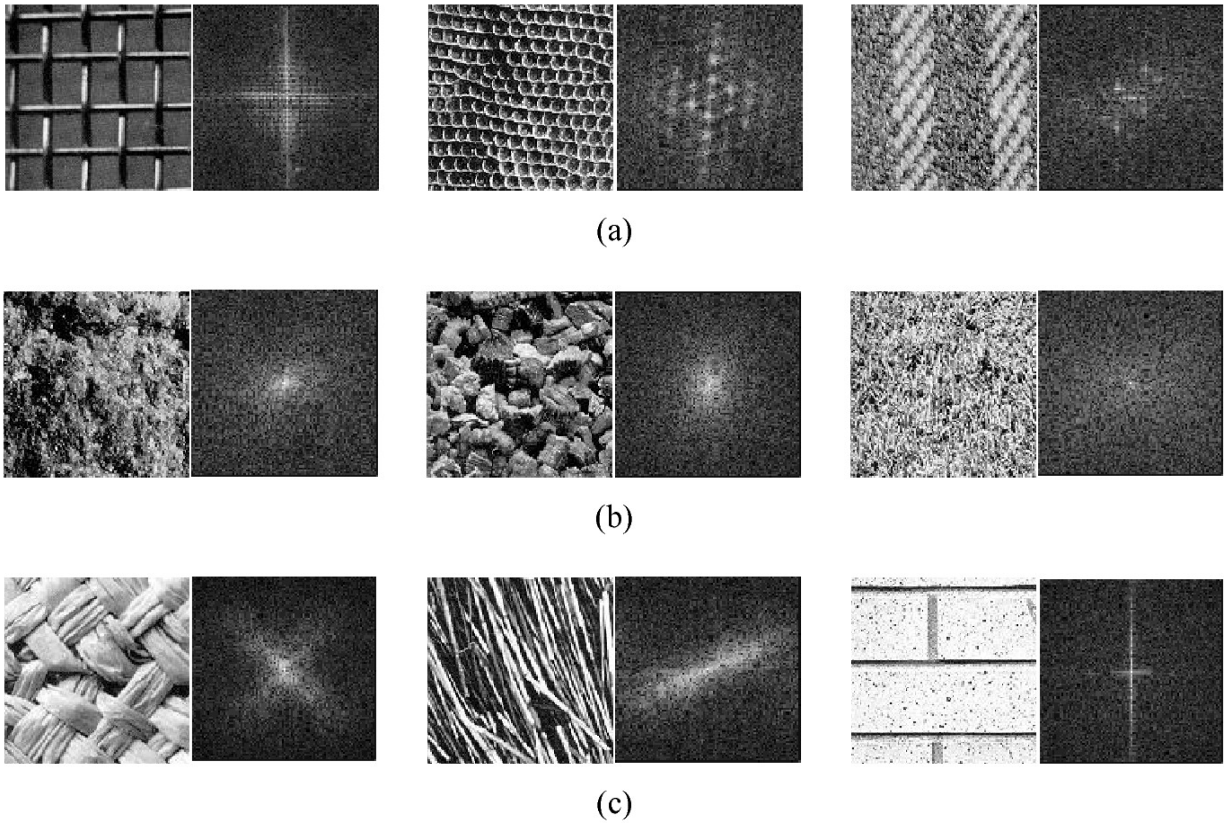

Fig. 1.9 FT spectra of different types of patterns. **a** Regular patterns and their FT spectra on the right; **b** random patterns and their FT spectra on the right; **c** directional patterns and their FT spectra on the right

1.8 Summary

In this chapter, FT, the most fundamental theory in signal and image analysis is formally introduced and described systematically. The idea of decomposing a signal or function into sinusoids is equivalent to breaking down a compound into element. This idea has been demonstrated using Fourier series and complex Fourier series.

Particularly important is the DFT and its properties including rotation, translation, separability and convolution theorem. For example, due to the separability property, FT on an image can be computed on rows first and then on columns, instead of on rows and columns simultaneously; this makes FT very efficient. Another example is that the convolution theorem turns convolution into multiplication in FT domain. Again, this makes convolution very efficient. These properties have been used frequently in the following five chapters.

Another important point is the trade-off between frequency resolution and time/spatial resolution.

FT spectrum is the visualization of FT; it is used to demonstrate what types of patterns are in the image (e.g., random, directional, regular, etc.) and which directions the patterns are aligned. Unfortunately, FT cannot tell where the patterns are located in an image; this is the topic of next two chapters.

1.9 Exercises

1. Download the stripe image from https://homepages.inf.ed.ac.uk/rbf/HIPR2/images/stp1.gif, apply FT to it and show the FT spectrum of this image. The Matlab function for 2D FT is available from https://au.mathworks.com/help/matlab/ref/fft2.html.

2. Now apply logarithm transform to the above FT spectrum and show the FT spectrum image again. Explain the difference.

3. Apply thresholding to the above log FT spectrum with a threshold value 10 and display the FT spectrum image again. Try different threshold values to see the results.

4. Now multiply the FT spectrum from problem 1 by a circle with a radius of 30 pixels and set the pixels outside the circle with 0 (1 if inside the circle); apply the inverse FT to the truncated spectrum and show the reconstructed image. Explain the difference between the reconstructed stripe image with the original stripe image. Try circles with smaller radius, e.g., 10, 5; explain the results.

5. Repeat Exercises 1 and 4 on different images, write a short report on your findings of FT and FT^{-1}; e.g., why some images can be reconstructed well with just a few FT coefficients while some images need high number of FT coefficients to be reconstructed reasonably well.

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2. Windowed Fourier Transform

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It’s a changing world, static is not an option.

2.1 Introduction

2D Fourier transform is a powerful tool to capture the frequency information of an image. The frequency information tells how frequent a pattern changes. This frequency of changes reflects the structural or textural features which are observed by human beings during pattern analysis. The frequency information is crucial to understand the content of an image.

However, Fourier spectrum is captured using the entire image as the window, and it is a global information. In other words, we know there is a frequency in the image, but we cannot tell where the frequency is in the pattern. This is not a problem if the pattern has a homogenous structure across a pattern. For non-homogenous patterns, however, Fourier spectrum is not an effective representation, because different patterns can have similar Fourier spectrum. Figure 2.1 shows this phenomenon [1]; although the two images are very different, however, their FT spectra are quite similar. This is a problem for image classification and retrieval. Therefore, we need better tools to let us have a closer look at the patterns inside the images.

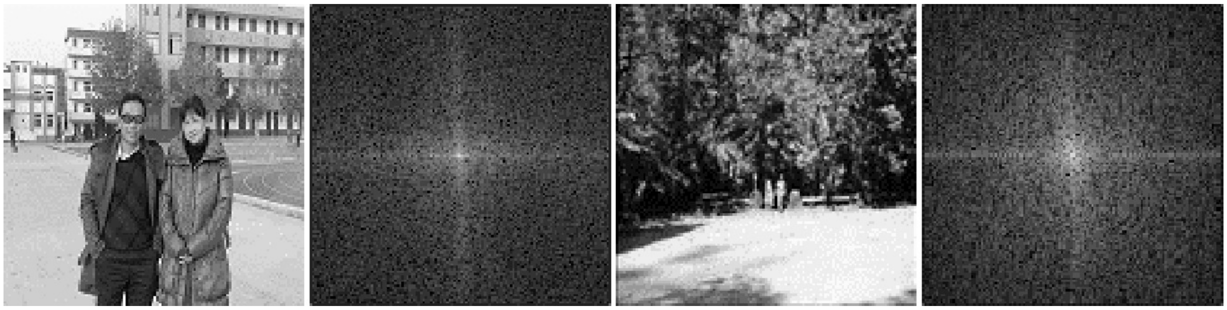

Fig. 2.1 Two images and their corresponding Fourier spectra on the right

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2.2 Short-Time Fourier Transform

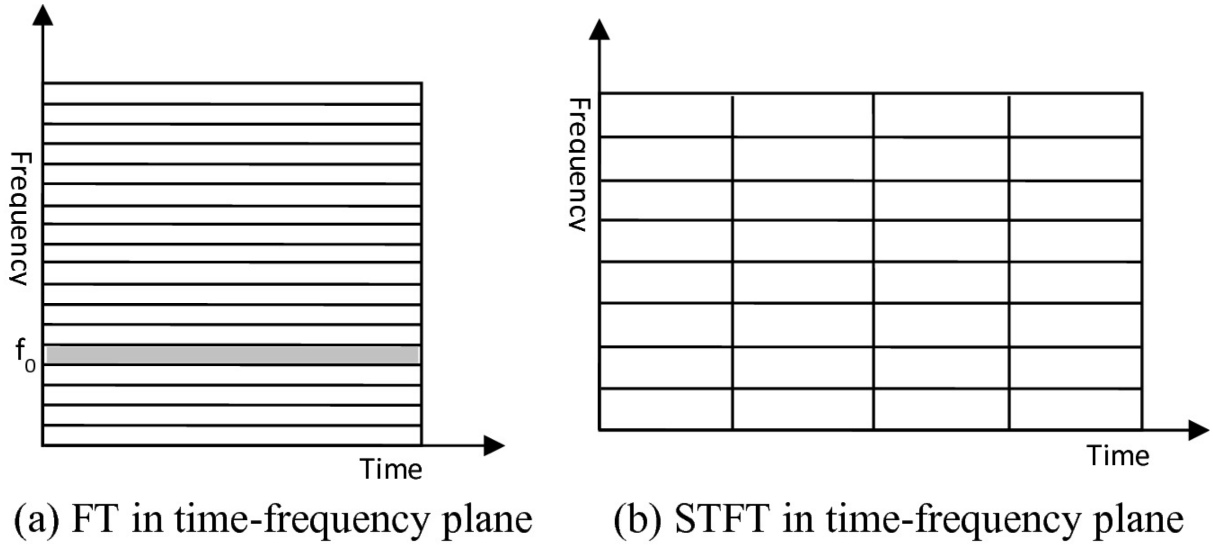
The natural way to overcome this problem is to analyze the signal section by section or window by window. This is short-time Fourier transform (STFT) which provides a way to analyze the signal in both time and frequency. In STFT, a window function is chosen in such a way that the portion of a non-stationary signal which is covered by the window function seems stationary. This window function is then convoluted with the original signal so that only the part of the signal covered by the window is selected. FT is then applied to the newly generated stationary signal. The window is then moved to the next slot of signal, and FT is applied repeatedly until the whole signal is completely analyzed. For a signal $f(x)$, its STFT is defined as:

$$\mathrm{STFT}\left(\tau,\omega\right)=\sum_{x=0}^{N}f\left(x\right)*W\left(x-\tau\right)\mathrm{e}^{-j2\pi\omega x} \tag{2.1}$$

where $W(x)$ is the window, $*$ means convolution, τ represents the spatial position of the window and ω represents the frequency captured at time τ. Similarly, the 2D STFT is given as:

$$\mathrm{STFT}\left(\tau_1,\tau_2,\omega\right)=\sum_{x=0}^{N}\sum_{y=0}^{N}f\left(x,y\right)*W\left(x-\tau_1,y-\tau_2\right)\mathrm{e}^{-j2\pi\omega x} \tag{2.2}$$

Figure 2.2 shows the different spectrum layouts of FT and STFT on a 1D signal. The FT is applied on the entire signal which is equivalent to a single big window, and it can be seen the frequency resolution is higher than that of STFT. STFT is applied on 4 smaller windows; as can be expected, the frequency resolution is lower than that of FT; however, the spatial resolution is higher than that of FT, because we can now examine the signal at different 4 locations. Therefore, STFT achieves a *trade-off* between frequency resolution and spatial resolution.



(a) FT in time-frequency plane (b) STFT in time-frequency plane

Fig. 2.2 Time–frequency illustration for FT and STFT

2.2.1 Spectrogram

When a signal $f(x)$ ($x\epsilon[0, T]$) is analyzed by STFT, instead of a single FT spectrum, it results in a series of STFT spectra. Each of the STFT spectra is a windowed analysis of the signal $f(x)$ in a particular time slot $t\epsilon[0, T]$. By concatenating the series of the STFT spectra vertically (in column) on the time line, it creates a *spectrogram*. Figure 2.3 shows a spectrogram of a short sound wave. It can be observed that most of the energy is concentrated at the low frequencies; however, there are a number of particular high frequencies at different times of the sound, which are marked by the bright horizontal stripes.

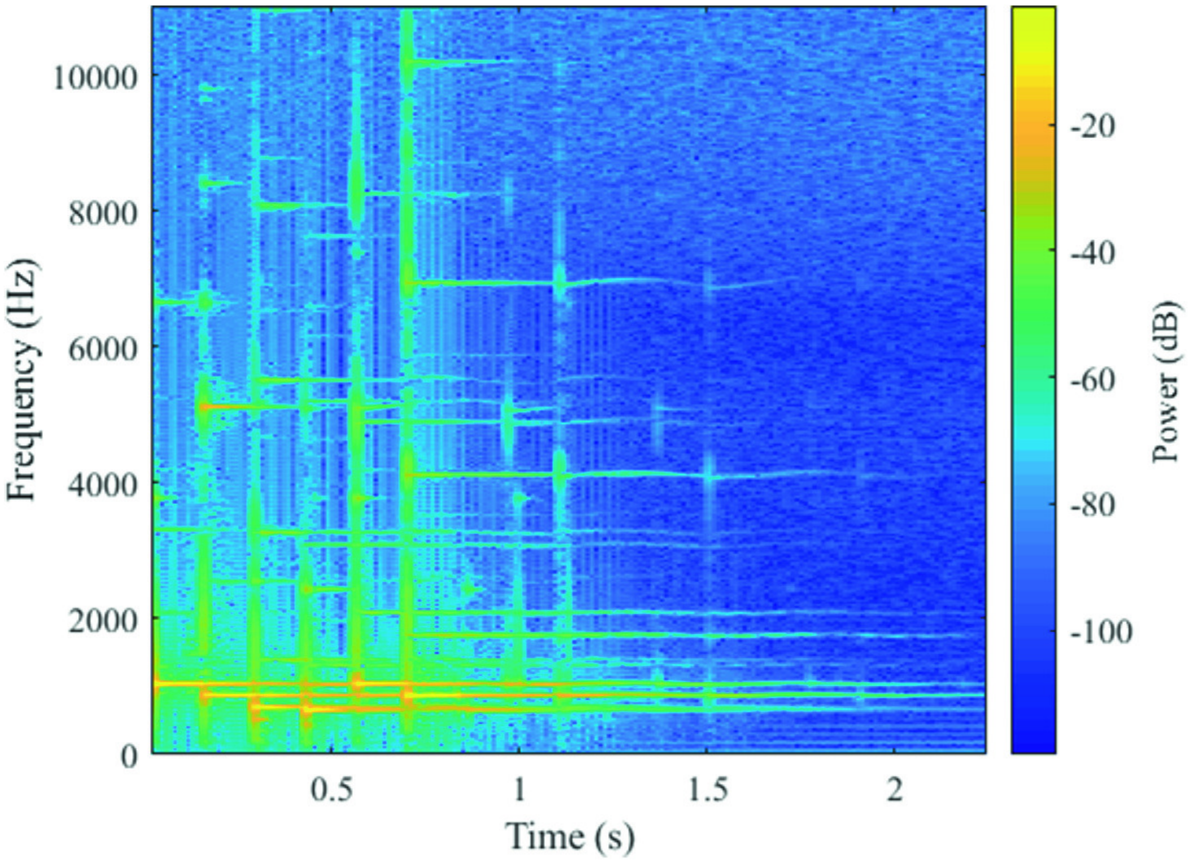


Fig. 2.3 Spectrogram of a sound wave

Although STFT lets us do time–frequency analysis, the usually square windowing causes several side effects. First, the windowing causes the loss of low frequencies which are the most important information for signal representation. This is because low-frequency signals have longer periods/cycles, and in order to capture the low frequency, a signal must complete at least one full cycle within the window. Therefore, a window can only capture frequencies up to a certain limit.

For example, given a signal with a Nyquist sampling rate of 44,800 Hz,

- A window of 128 samples is equivalent to a period of 128/44,800 = 0.00285 s.
- Therefore, the lowest frequency the window can capture is 1/0.00285 s = 350 Hz.
- In other words, the lowest frequency you can analyze with a window size of 128 samples at a sample rate of 44.8 kHz is 350 Hz.

- The second frequency which can be fit into the window is a two-cycle sine wave or a sine wave with period of half of the window size; therefore, the second frequency a 128 window captures is 2 × 350 = 700 Hz.
- Similarly, the third frequency a 128 window captures is 3 × 350 = 1050 Hz, so on so forth.
- In other words, the step size of the windowed frequency resolution (bin size Δu) is 350 Hz for a 128 window instead of 1 Hz for an ordinary FT. This has been shown in (1.25).
- Similarly, for a window of 64 samples, $\Delta u = 700$ Hz, while for a window of 256 samples, $\Delta u = 175$ Hz, so on so forth.
- Therefore, with STFT, we not only lose low frequencies, but also lose frequency resolution, due to using only a single-sized window.

Another issue with STFT is the shape of the window. The typical rectangular window causes severe frequency leakage, that is, a burst of high frequencies at both sides of the window. This is undesirable for signal or image representation which requires a compact spectrum. These issues related to STFT can be overcome to certain extent by using non-rectangular and overlapping windows.

2.3 Gabor Filters

2.3.1 Gabor Transform

This leads to the use of Gaussian window which attenuates high frequencies at both sides of the window. The STFT with Gaussian window is called Gabor transform.

$$G(\tau_1, \tau_2, \omega) = \sum_{x=0}^{N} \sum_{y=0}^{N} f(x, y) * g(x - \tau_1, y - \tau_2)\, \mathrm{e}^{-j2\pi\omega x} \tag{2.3}$$

where $g(x, y)$ is the Gaussian function:

$$g(x, y) = \frac{1}{2\pi\sigma_x\sigma_y} \exp\left[-\frac{1}{2}\left(\frac{x^2}{\sigma_x^2} + \frac{y^2}{\sigma_y^2}\right)\right] \tag{2.4}$$

and σ_x, σ_y are the horizontal and vertical standard deviations which determine the size of the window. The window size can be varied to achieve the optimality between time and frequency.

Because convolution in spatial domain is equivalent to multiplication in frequency domain; in practice, STFT is computed by multiplying the Fourier transforms of $f(x, y)$ and $g(x, y)$.

It is found that the frequency response or Fourier transform of $g(x, y)$ is also a Gaussian $G(u, v)$, and the window size of $G(u, v)$ is inversely proportional to that of $g(x, y)$, that is,

$$\sigma_u = \frac{1}{2\pi\sigma_x} \tag{2.5}$$

$$\sigma_v = \frac{1}{2\pi\sigma_y} \tag{2.6}$$

This relationship can be used to determine the window size in spatial domain. It is known that lower frequencies are more important than higher frequencies for signal analysis and representation. Therefore, in the frequency plane, lower frequencies are given higher resolution than higher frequencies. This is achieved by giving the lower frequencies narrower bandwidth while giving the higher frequencies wider bandwidth. Typically, the bandwidths are arranged in *octave*.

2.3.2 Design of Gabor Filters

Because both Gabor function and its frequency response are Gaussians, and the relationship of the two Gaussians is given by (2.5) and (2.6), Gabor filters are designed on frequency domain. Because a 2D Gaussian function extends to infinity, there is too much overlap or redundancy between two adjacent Gaussian functions. To remove the redundancy, the 2D Gaussian functions in Gabor filters are cut at the half height and the top half of the function is used as the Gaussian window. For a Gaussian function with standard deviation of σ, the full width at half maximum (FWHM) is $2\sqrt{2\ln 2}\sigma$ (Fig. 2.4).

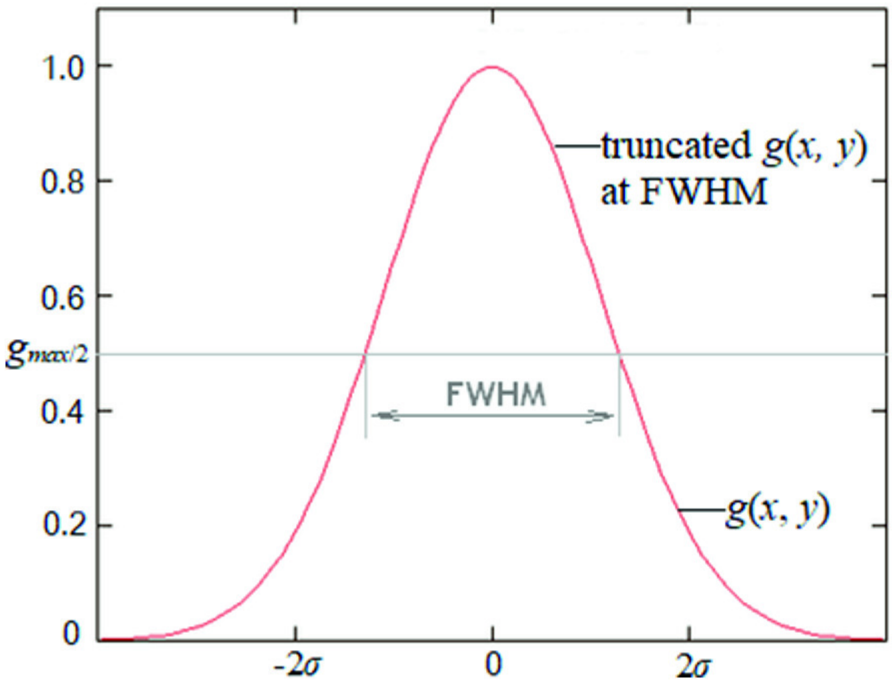


Fig. 2.4 Full width at half maximum of a Gaussian function

Based on the above discussions, the half-amplitude of Gabor filters tiling of the spectrum plane is given in Fig. 2.5.

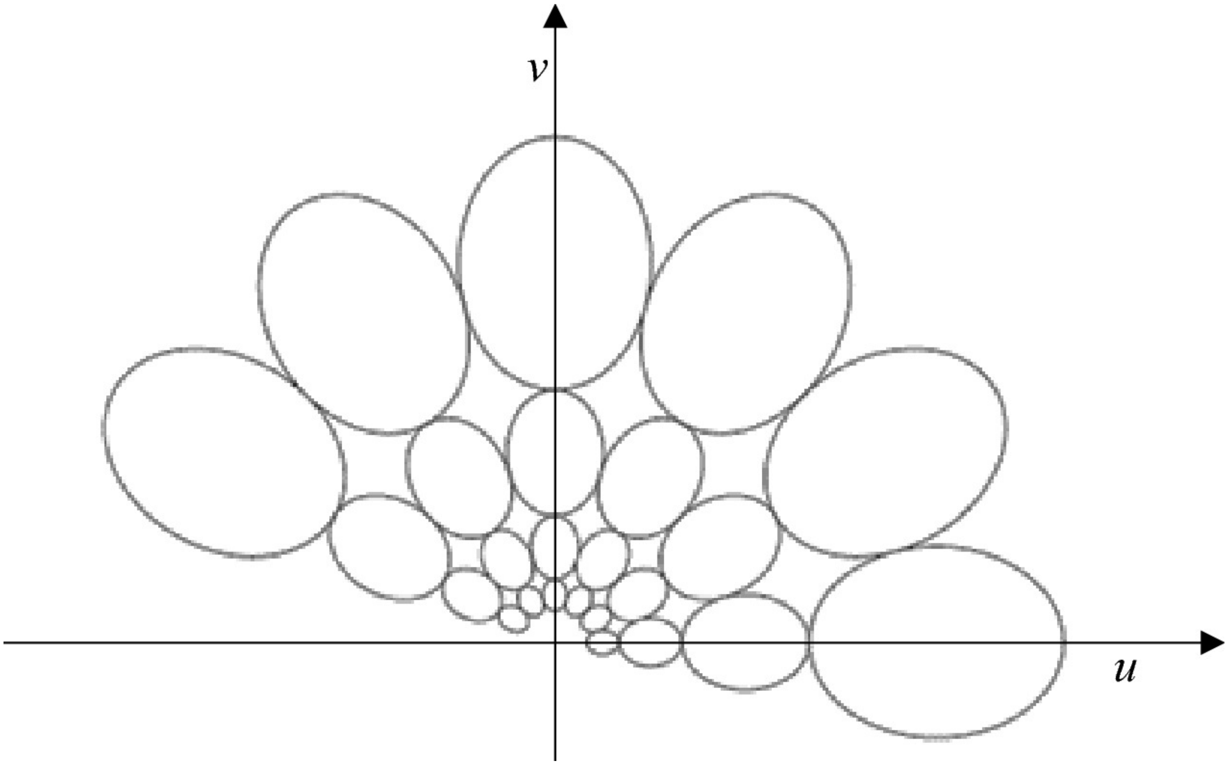


Fig. 2.5 Half-amplitude of Gabor filters in the frequency domain using four scales and six orientations

- Suppose the lowest and highest horizontal frequencies are U_l and U_h, respectively.
- The window at U_l has the smallest width (bandwidth) σ_l.
- The next window at aU_l has a width of $a\sigma_l$.
- The mth window at $a^m U_l$ has a width of $a^m \sigma_l$.
- The width of the window at $U_h = a^{M-1} U_l$ is $a^{M-1} \sigma_l$.
- The octave is then rotated at an interval of $\theta = \pi/k$ to tile the half frequency plane (Fig. 2.6).

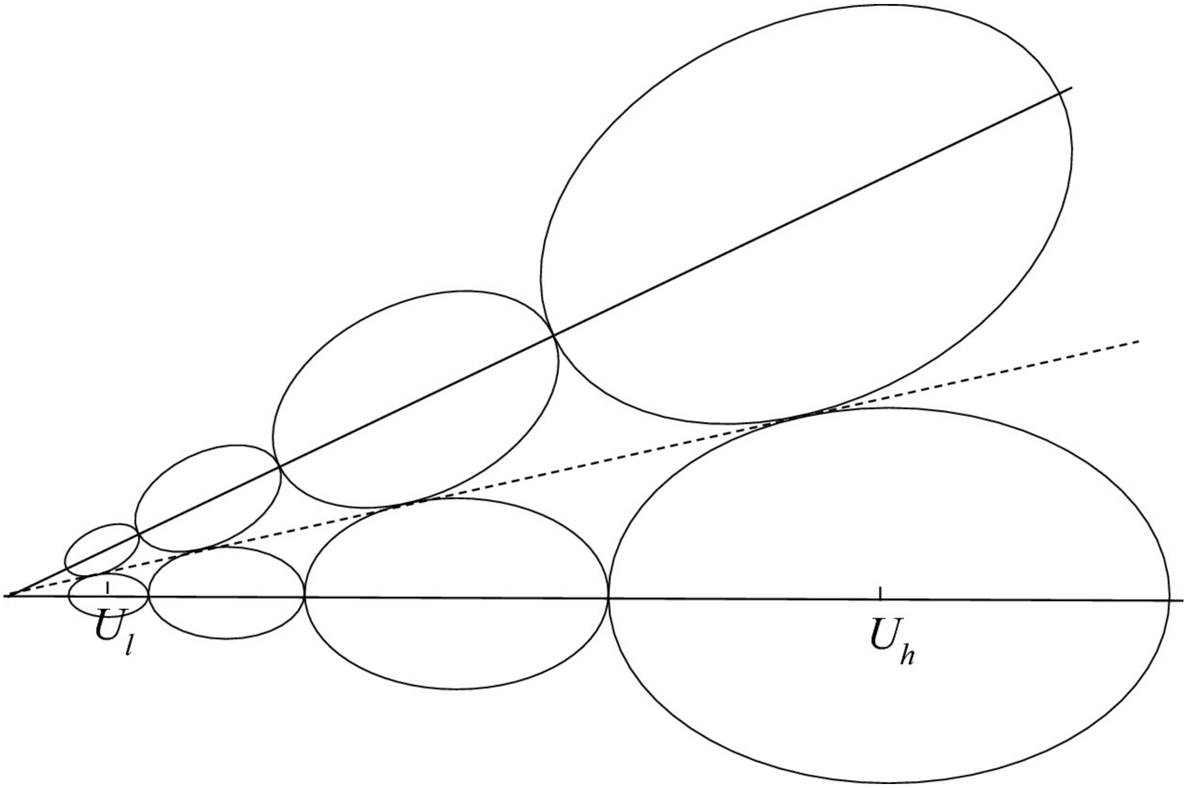


Fig. 2.6 Bandwidth tiling in frequency plane using Gaussian windows

With this arrangement, the parameters of the window are obtained as follows [2]:

$$\sigma_u = \frac{a-1}{a+1} \cdot \frac{U_l}{\sqrt{2ln2}} \tag{2.7}$$

$$\sigma_v = \tan\left(\frac{\pi}{2k}\right)\sqrt{\frac{U_h^2}{2ln2} - \sigma_u^2} \tag{2.8}$$

The Gabor transform lets us do a better time and frequency analysis than STFT, due to the use of Gaussian and overlapping windows. However, because the Gabor function is an infinite window, there is much overlap between Gabor windows. This translates to redundancy in the extracted information from the transformed coefficients. Although the FWHM truncation reduces the redundancy, it causes missing spectral information in frequency plane. Neither case is desirable for image analysis and representation. To overcome this issue, orthogonal wavelets with multiresolution are introduced in the following section.

2.3.3 Spectra of Gabor Filters

Based on the above design, each Gabor filter is determined by two parameters: scale (σ or bandwidth) and orientation; therefore, by changing the scales and orientations, various Gabor filters are generated. Figure 2.7 shows the real components of Gabor filters at different scales and orientations. On 2D plane, each Gabor filter is oval shaped and the center of the filter is given higher weight. The scale determines the granularity, with lower-scale filters capturing rough features of an image and higher-scale filters capturing fine features of an image. The orientation let the filters capturing image profiles and edges from different angles. The combination of both scales and orientations provides Gabor filters, a powerful capability on image analysis.

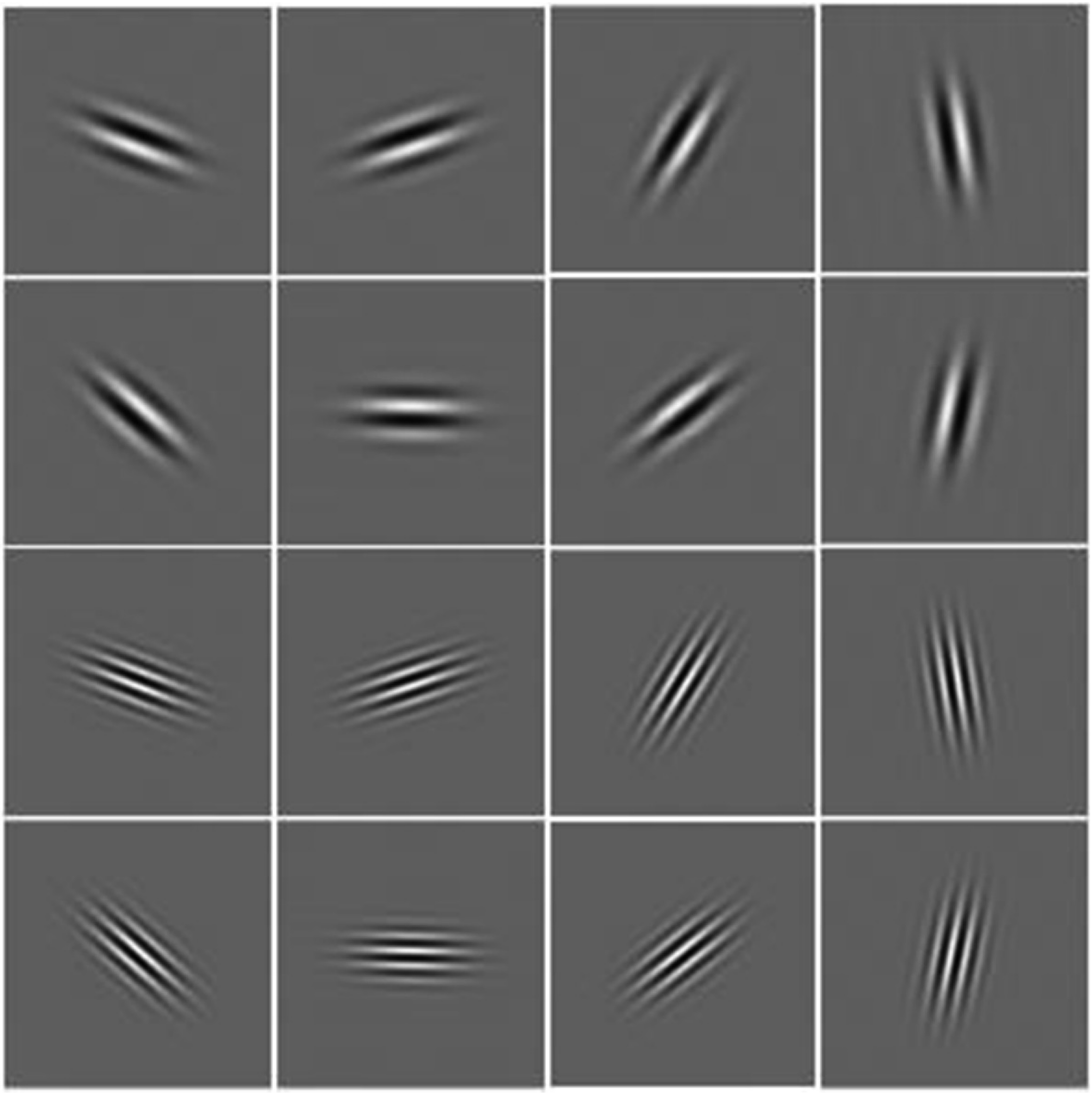


Fig. 2.7 Spectra of Gabor filters at different scales and orientations

2.4 Discrete Cosine Transform

2.4.1 1D DCT Model

The DFT introduced in Chapter 1 is a transform on complex signal, and it results in a complex spectrum with both real and imaginary components. Unless phase information is needed, the imaginary component is actually redundant for real signals or data such as time series and images. Based on the DFT definition, if a signal is symmetric or the signal is an even function, the imaginary component would be 0 and we would be able to remove half the data from the DFT spectrum. For real signals, they can be easily extended to symmetric or even functions so that the DFT on these signals becomes *discrete cosine transform* or DCT.

DCT made its name for making a major contribution the JPEG standard, which marks a milestone in the development of WWW and this multimedia world. Nowadays, DCT is also used as a common tool for image analysis and feature extraction. Because DCT is typically applied on blocks or windows of an image, it can also be regarded as a windowed FT.

Let's start with introducing 1D DCT [3].

- In order to convert a DFT into DCT, the signal under transform needs to be symmetric so that the function representing the signal is an even function.
- Suppose we have a discrete dataset $y = f(t)$, $t = 0, 1, 2, \ldots, N - 1$. $f(t)$ is essentially a discrete function which is shown as blue dots in Fig. 2.8.

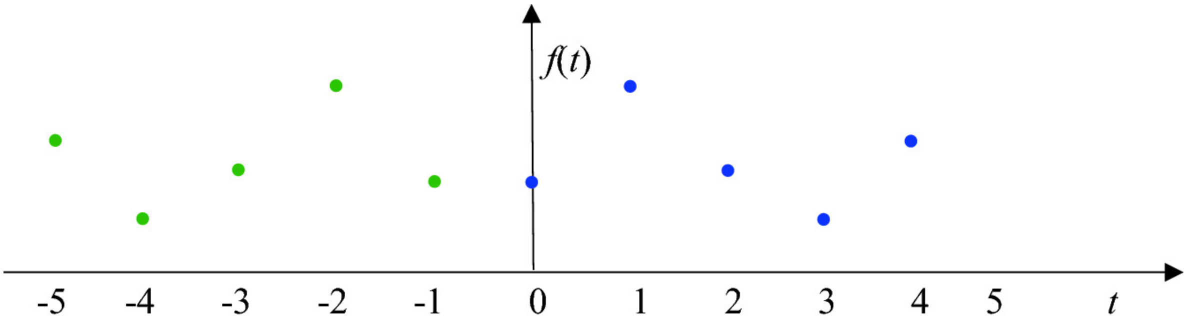


Fig. 2.8 A signal in blue and the mirrored data in green

- To make this discrete function even, we first mirror the data to the left of the origin (Fig. 2.8, green), and the extended function becomes: $f'(t)$, $t = -N, \ldots, -1, 0, 1, 2, \ldots, N - 1$.
- Because we will just use the right side of $f'(t)$, which is the same as $f(t)$, we will simply refer $f'(t)$ as $f(t)$.
- We then shift the extended function to the right by 1/2. This results in Fig. 2.9. The extended function of Fig. 2.9 is an even function: $f(t - 1/2)$, $t = -(N - 1/2), \ldots, -1/2, 0, 1/2, 1.5, \ldots, N - 1/2$.

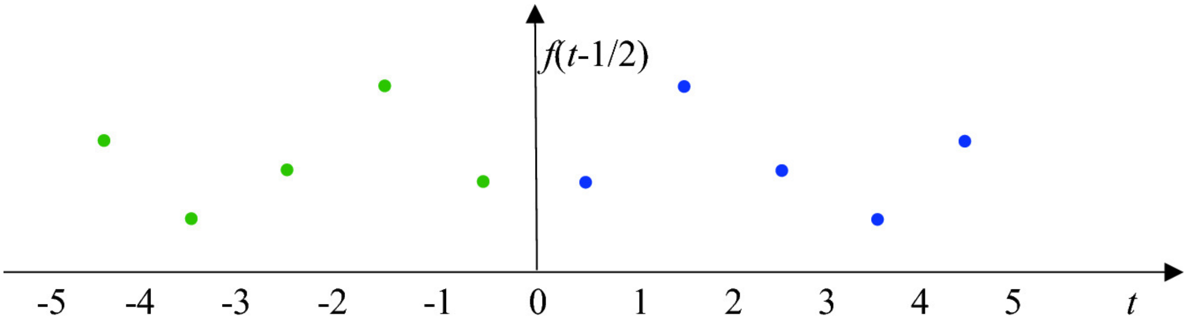


Fig. 2.9 A symmetric signal after the extension from the original blue data

Next, we are going to apply a 1D DFT on $f(t - 1/2), t \in [-(N - 1/2), N - 1/2]$. Because $f(t - 1/2)$ is an even function, $f(t - 1/2) * \cos(nx)$ is also an even function and the sum of $f(t - 1/2) * \cos(nx)$ in $[-(N - 1/2), N - 1/2]$ is twice the sum of that in $[1/2, N - 1/2]$. It also means that $f(t - 1/2) * \sin(nx)$ is an odd function and the sum of $f(t - 1/2) * \sin(nx)$ in $[-(N - 1/2), N - 1/2]$ is zero. Bearing the above in mind, we have the following:

$$\begin{aligned} F(n) &= \frac{1}{\sqrt{2N}} \sum_{t=-\left(N-\frac{1}{2}\right)}^{N-\frac{1}{2}} f\left(t-\frac{1}{2}\right) \exp\left(-\frac{j2\pi tn}{2N}\right) \\ &= \frac{1}{\sqrt{2N}} \sum_{t=-\left(N-\frac{1}{2}\right)}^{N-\frac{1}{2}} f\left(t-\frac{1}{2}\right) \cos\left(\frac{2\pi tn}{2N}\right) \\ &= \frac{2}{\sqrt{2N}} \sum_{t=\frac{1}{2}}^{N-\frac{1}{2}} f\left(t-\frac{1}{2}\right) \cos\left(\frac{2\pi tn}{2N}\right) \\ &\xrightarrow{k=t-1/2} \sqrt{\frac{2}{N}} \sum_{k=0}^{N-1} f(k) \cos\left(\frac{(2k+1)\pi n}{2N}\right) \end{aligned} \tag{2.9}$$

where $n = 0, 1, 2, \ldots, N - 1$ is the nth frequency and the scalar $\frac{1}{\sqrt{2N}}$ is the result of splitting the full weight $\frac{1}{2N}$ between FT and FT^{-1}. The magnitude total of the cosine coefficients in (2.9) is given in (2.10):

$$\left(\sum_{k=0}^{N-1}\cos^2\left(\frac{(2k+1)\,\pi n}{2N}\right)\right)^{\frac{1}{2}} = \left(\sum_{k=0}^{N-1}\frac{\cos\left(\frac{(2k+1)\pi n}{N}\right)+1}{2}\right)^{\frac{1}{2}}$$

$$= \left(\frac{1}{2}\sum_{k=0}^{N-1}\left(\cos\left(\frac{(2k+1)\,\pi n}{N}\right)+1\right)\right)^{\frac{1}{2}} \tag{2.10}$$

$$= \begin{cases} \sqrt{N} & n = 0 \\ \sqrt{\frac{N}{2}} & n = 1,\ 2, \ldots, N-1 \end{cases}$$

Therefore, if we define a scalar as (2.11) and include it in $F(n)$:

$$\alpha_n = \begin{cases} \frac{1}{\sqrt{2}} & n = 0 \\ 1 & n = 1, 2, \ldots, N-1 \end{cases} \tag{2.11}$$

The $F(n)$ in (2.12) becomes an orthonormal transform:

$$F\,(n) = \alpha_n \sqrt{\frac{2}{N}} \sum_{k=0}^{N-1} f\,(k) \cos\left(\frac{(2k+1)\,\pi n}{2N}\right) \tag{2.12}$$

2.4.2 DCT Bases

For computation efficiency, DCT bases are created before the transformation. Because the actual number of data N is just half of the sampling window $2N$, the N data only samples half the number of cycles of each cosine wave in the window. Therefore, the DCT bases effectively increase half a cosine cycle (instead of a full cosine cycle) for every increase of frequency n. The first 8 continuous cosine bases are shown in Fig. 2.10, and the 8 DCT bases are shown in Fig. 2.11.

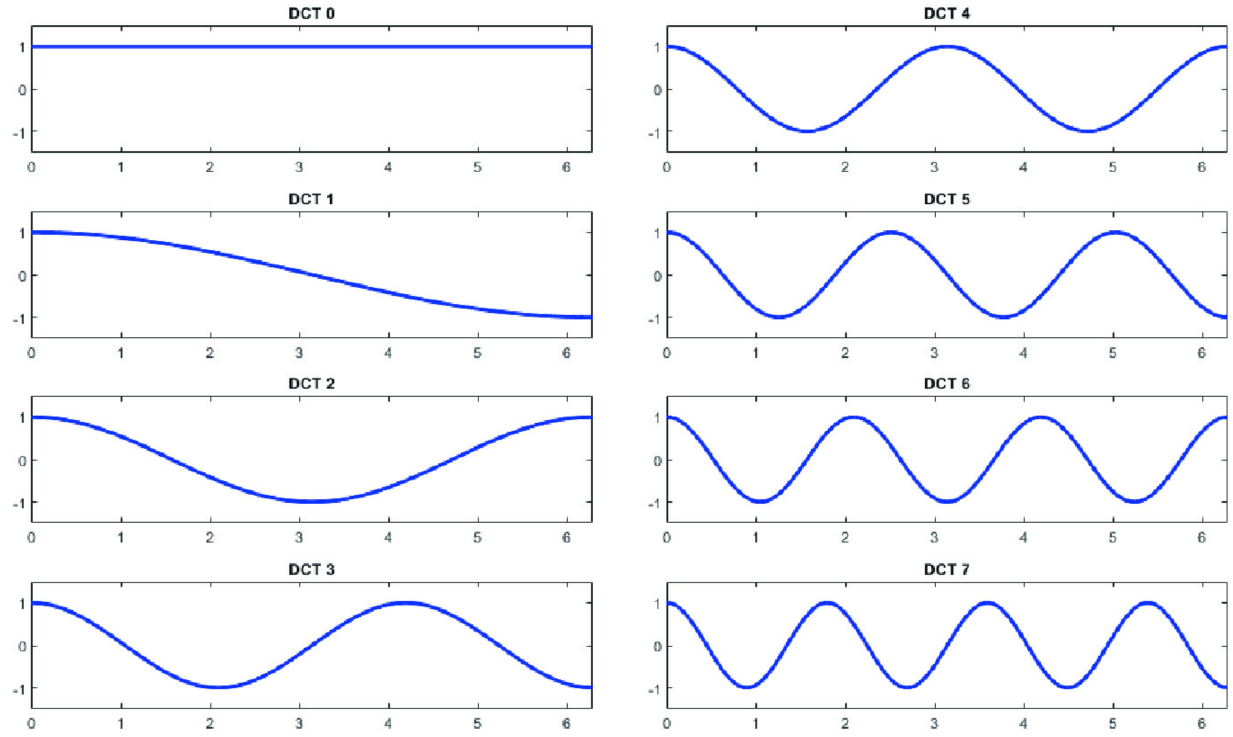

DCT 0
DCT 1
DCT 2
DCT 3
DCT 4
DCT 5
DCT 6
DCT 7

Fig. 2.10 First 8 continuous cosine bases

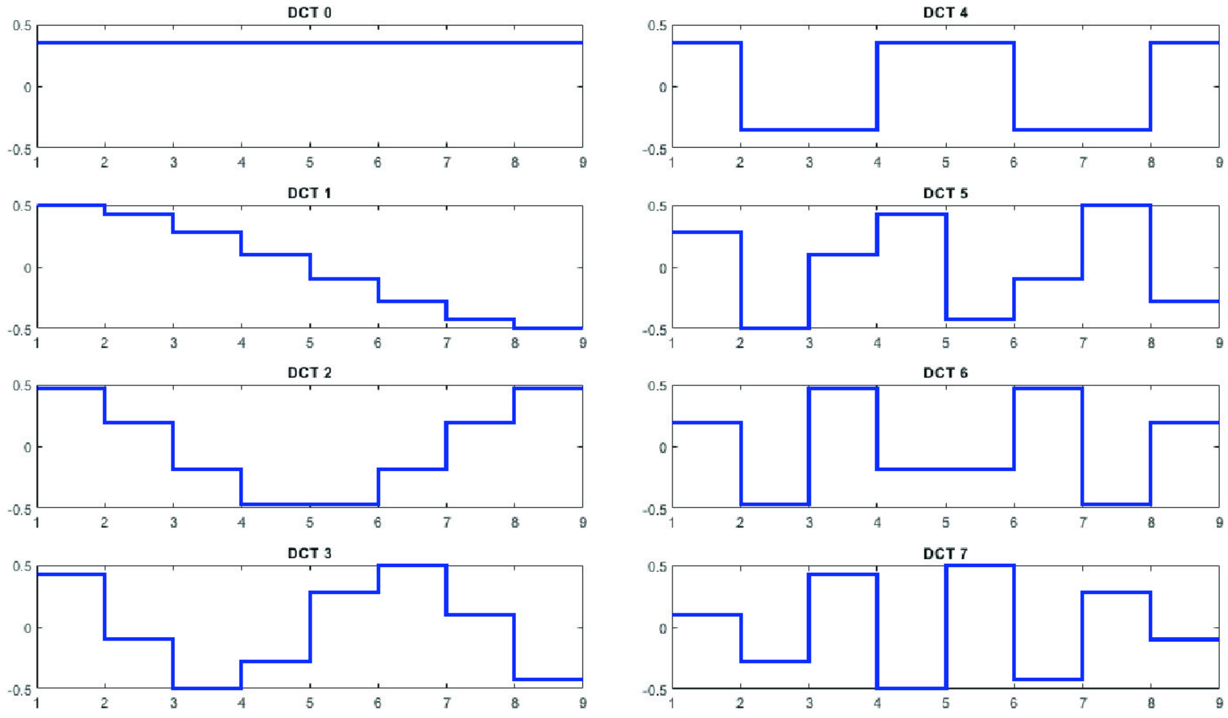

DCT 0
DCT 1
DCT 2
DCT 3
DCT 4
DCT 5
DCT 6
DCT 7

Fig. 2.11 First 8 DCT bases

Each DCT basis is an N element vector: **DCTn** = $d_n[k]$, $k = 0, 1, 2, \ldots,$ $N - 1$. Given a signal $\mathbf{x} = x[k]$, $k = 0, 1, 2, \ldots, N - 1$, the nth DCT coefficient

$F(n)$ is computed as the dot product between **x** and **DCTn**:

$$F(n) = \mathbf{x} \cdot \mathbf{DCTn} \tag{2.13}$$

2.4.3 2D DCT

Given an M x N image or matrix $B(i,j)$, its 2D DCT $D(m,n)$ is defined as (2.14).

$$D(m,\ n) = \alpha_m \alpha_n \sqrt{\frac{2}{M}} \sqrt{\frac{2}{N}} \sum_{i=0}^{M-1} \sum_{j=0}^{N-1} B(i,\ j)\ \cos\frac{(2i+1)\pi m}{2M}\ \cos\frac{(2j+1)\pi n}{2N} \tag{2.14}$$

where

- m and n are the mth horizontal frequency and nth vertical frequency, respectively;
- $$a_m = \begin{cases} \frac{1}{\sqrt{2}} & \text{if } m = 0 \\ 1 & \text{otherwise} \end{cases}$$
- $$a_n = \begin{cases} \frac{1}{\sqrt{2}} & \text{if } n = 0 \\ 1 & \text{otherwise} \end{cases}$$

For an $N \times N$ square image $B(i,j)$, the DCT of $B(i,j)$ is simply the following:

$$D(m,n) = \frac{2}{N} \alpha_m \alpha_n \sum_{i=0}^{N-1} \sum_{j=0}^{N-1} B(i,\ j) \cos\frac{(2i+1)\pi m}{2N} \cos\frac{(2j+1)\pi n}{2N} \tag{2.15}$$

For a commonly used 8×8 block $B(i,j)$, the DCT of $B(i,j)$ is given as (2.16):

$$D(m,n) = \frac{1}{4} \alpha_m \alpha_n \sum_{i=0}^{7} \sum_{j=0}^{7} B(i,\ j) \cos\frac{(2i+1)\pi m}{16} \cos\frac{(2j+1)\pi n}{16} \tag{2.16}$$

2.4.4 Computation of 2D DCT

The idea of computing 2D DCT is similar to that of computing 1D DCT, that is, to create 2D DCT bases before the actual transformation. An $N \times N$ 2D DCT basis $\mathbf{DCT}2(m, n)$ can be generated by the multiplication of two 1D DCT bases using the following formula:

$$\mathbf{DCT}2\,(m, n) = \mathbf{DCTm}' * \mathbf{DCTn} \tag{2.17}$$

where

- $\mathbf{DCT}2(m, n)$ is a 2D DCT basis with mth horizontal frequency and nth vertical frequency;
- $\mathbf{DCTm}'$ is the transpose of the mth 1D DCT basis, which is a $N \times 1$ column vector;
- $\mathbf{DCTn}$ is the nth 1D DCT basis, which is a $1 \times N$ row vector;
- $\mathbf{DCT}2(m, n)$ is an $N \times N$ matrix.

Figure 2.12 shows 64 of the 8 × 8 2D DCT bases.

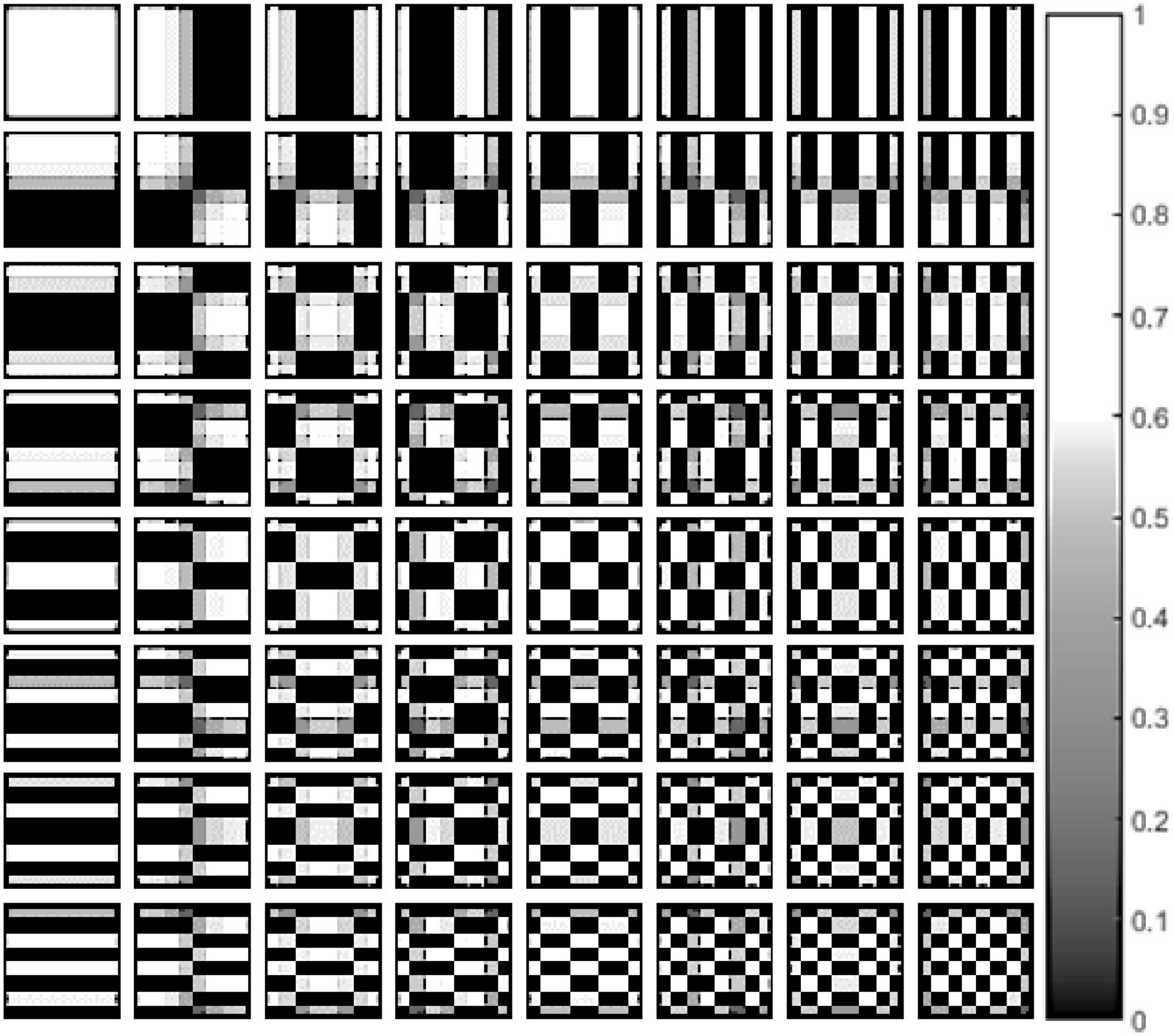


Fig. 2.12 64 2D DCT bases

Once the bases are available, the 2D DCT coefficient $D(m, n)$ can then be computed by multiplying the image matrix $\mathbf{B} = B(i, j)$ with basis $\mathbf{DCT2}(m, n)$ element by element:

$$D\left(m,n\right) = \mathbf{DCT}2\left(m,n\right).*\mathbf{B} \tag{2.18}$$

where .* is the Matlab operator for an *element wise multiplication* of two matrices.

For an $N \times N$ image, a DCT computed using above bases would involve N^2 number of matrix multiplications, and this is very inefficient. In practice, an $N \times N$ DCT matrix $\mathbf{D}$ such as the one shown in Fig. 2.13 is first generated with each row representing a 1D DCT basis. The 2D DCT on an image $\mathbf{B} = B(i,j)$ is then obtained by (2.19):

$$\mathrm{DCT}(\mathbf{B}) = \mathbf{D} * \mathbf{B} * \mathbf{D}' \tag{2.19}$$

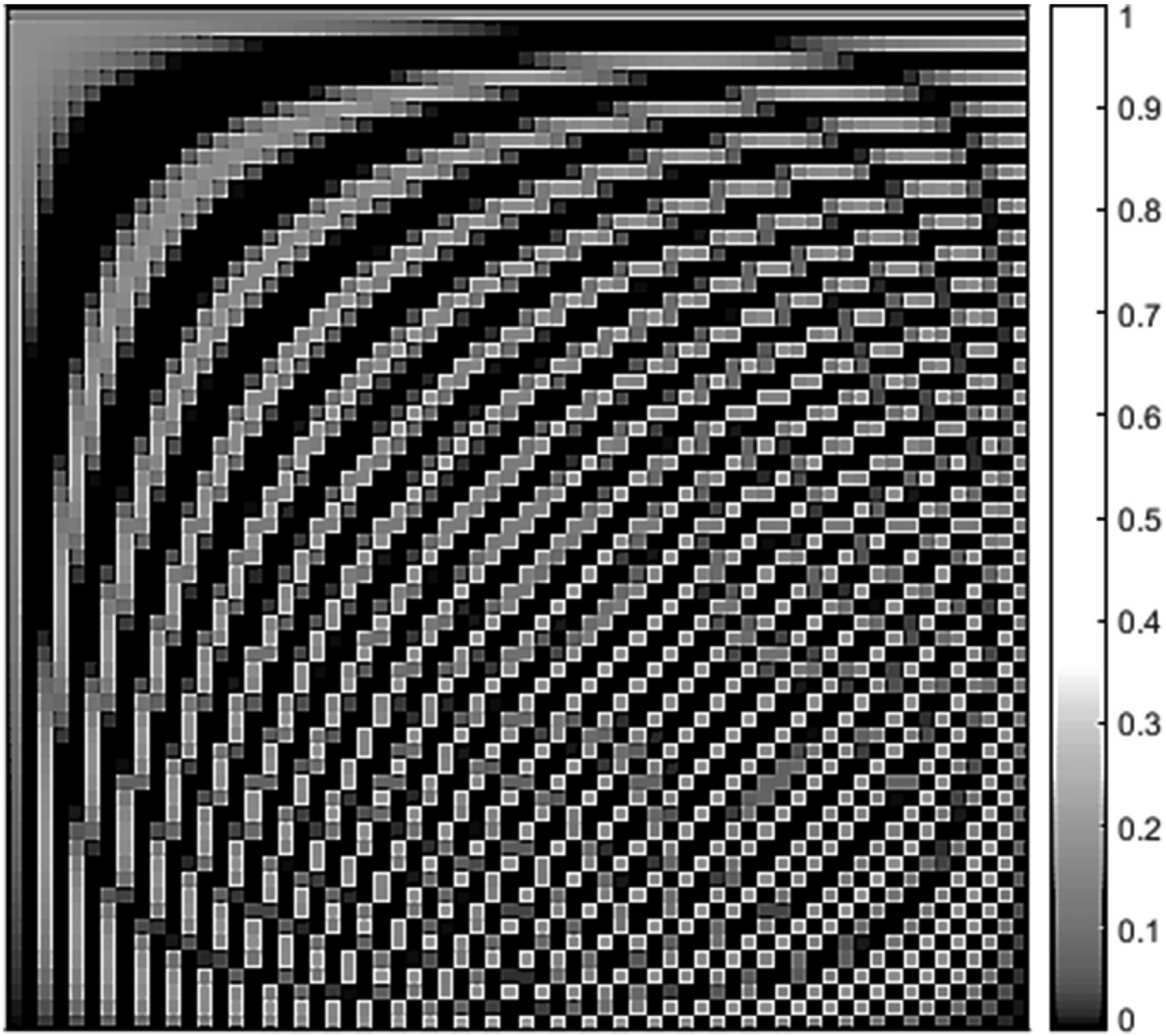
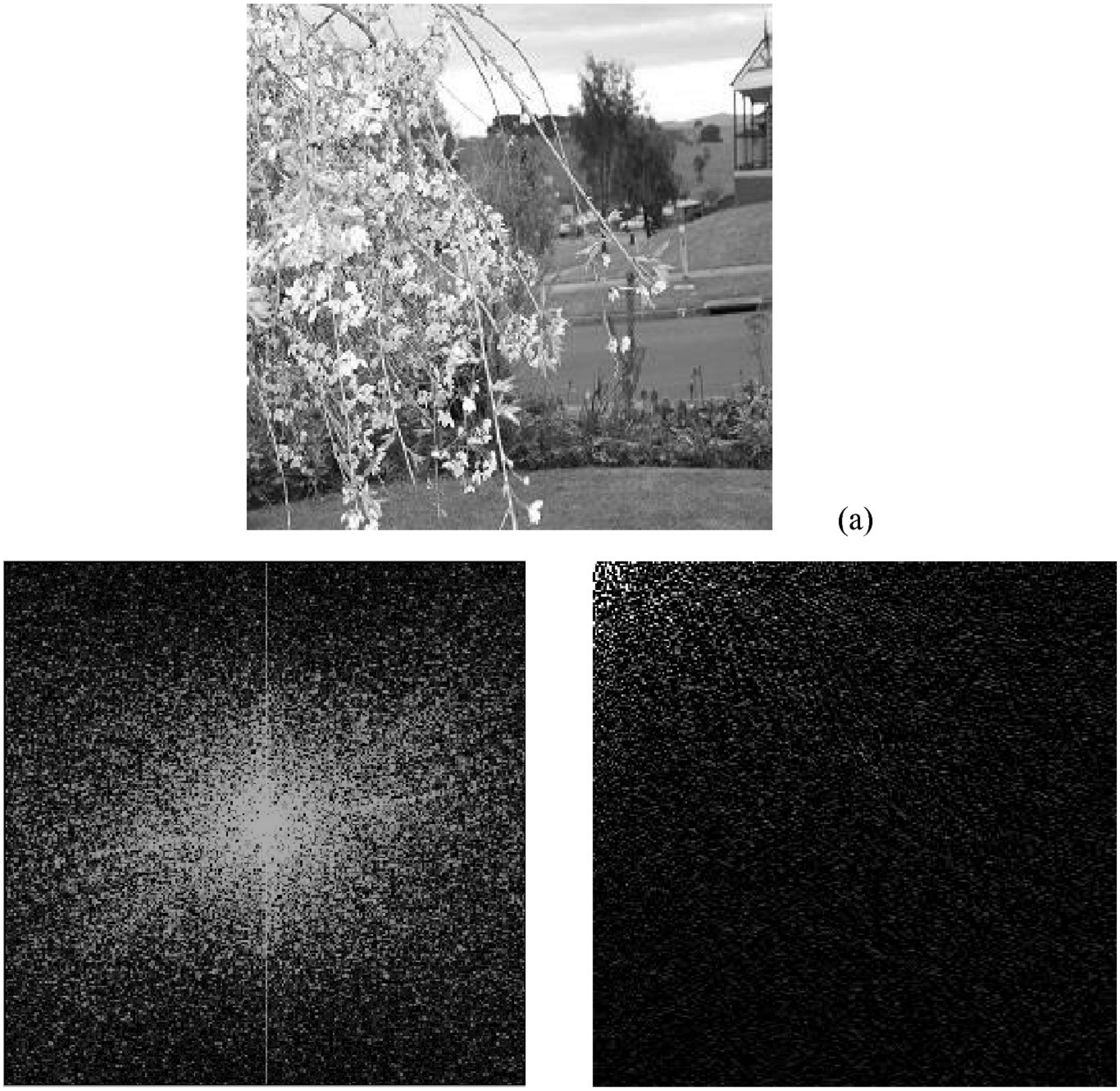


Fig. 2.13 A 64 × 64 DCT matrix. Each row represents a 1D DCT basis

where '$*$' is the normal row times column operator. (2.19) only involves two matrix multiplications. The left multiplication $\mathbf{D} * \mathbf{B}$ is equivalent to N times of 1D DCT on the columns of image $\mathbf{B}$, while the right multiplication of $(\mathbf{D} * \mathbf{B}) * \mathbf{D}'$ is equivalent to N times of 1D DCT on the rows of column-transformed image $\mathbf{D} * \mathbf{B}$.

Figure 2.13 shows the 64 × 64 DCT matrix for a 64 × 64 image transform. An $N \times N$ DCT matrix can be generated similarly for an $N \times N$ image transform.

Figure 2.14a shows a gray-level image, (b) and (c) contrast the DFT spectrum and DCT spectrum of the same image. It can be observed that the DCT spectrum image has much fewer significant coefficients (brighter pixels) than the DFT spectrum image. This phenomenon has significant implication on image compression and representation.



(a)

(b)

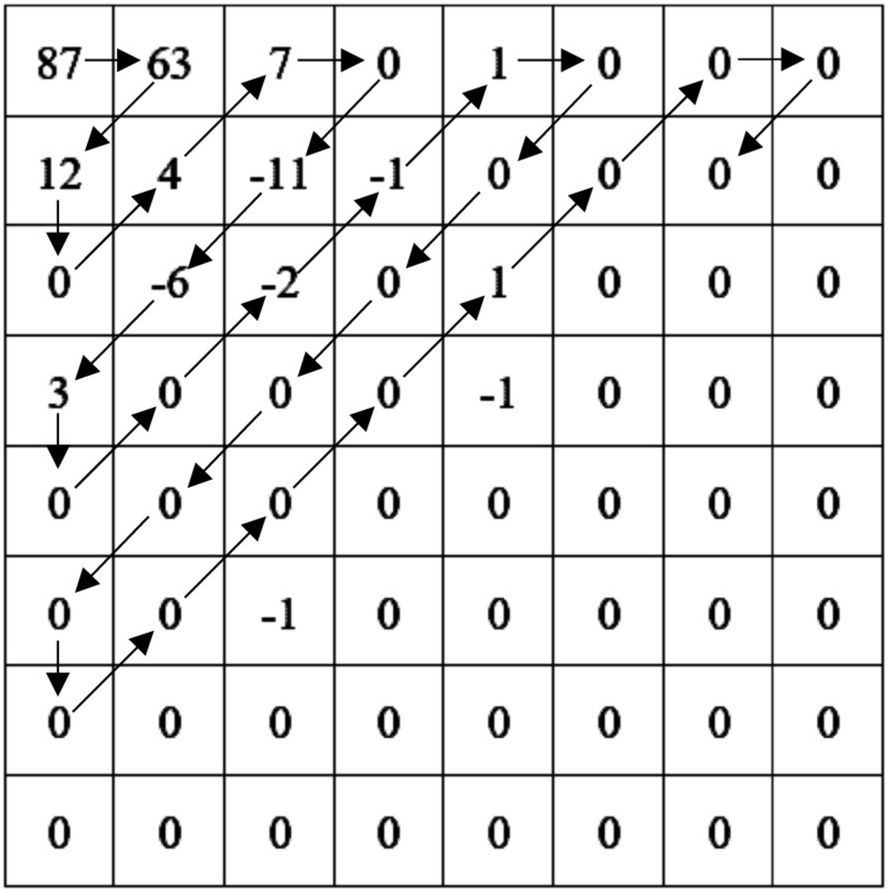
(c)

Fig. 2.14 Contrast of DFT and DCT. **a** An original gray-level image; **b** the DFT spectrum; **c** the DCT spectrum

Another observation is that in a DFT spectrum image, high energy coefficients are concentrated at the center of the spectrum, while in a DCT spectrum image, those high energy coefficients are concentrated at the top left corner of the spectrum.

For image compression and feature extraction, an image I is usually divided into 8 × 8 blocks and each block is transformed using DCT. The reason to divide an image into small blocks is because the features within a small block are most likely to be homogenous, and it usually results in very few DCT coefficients.

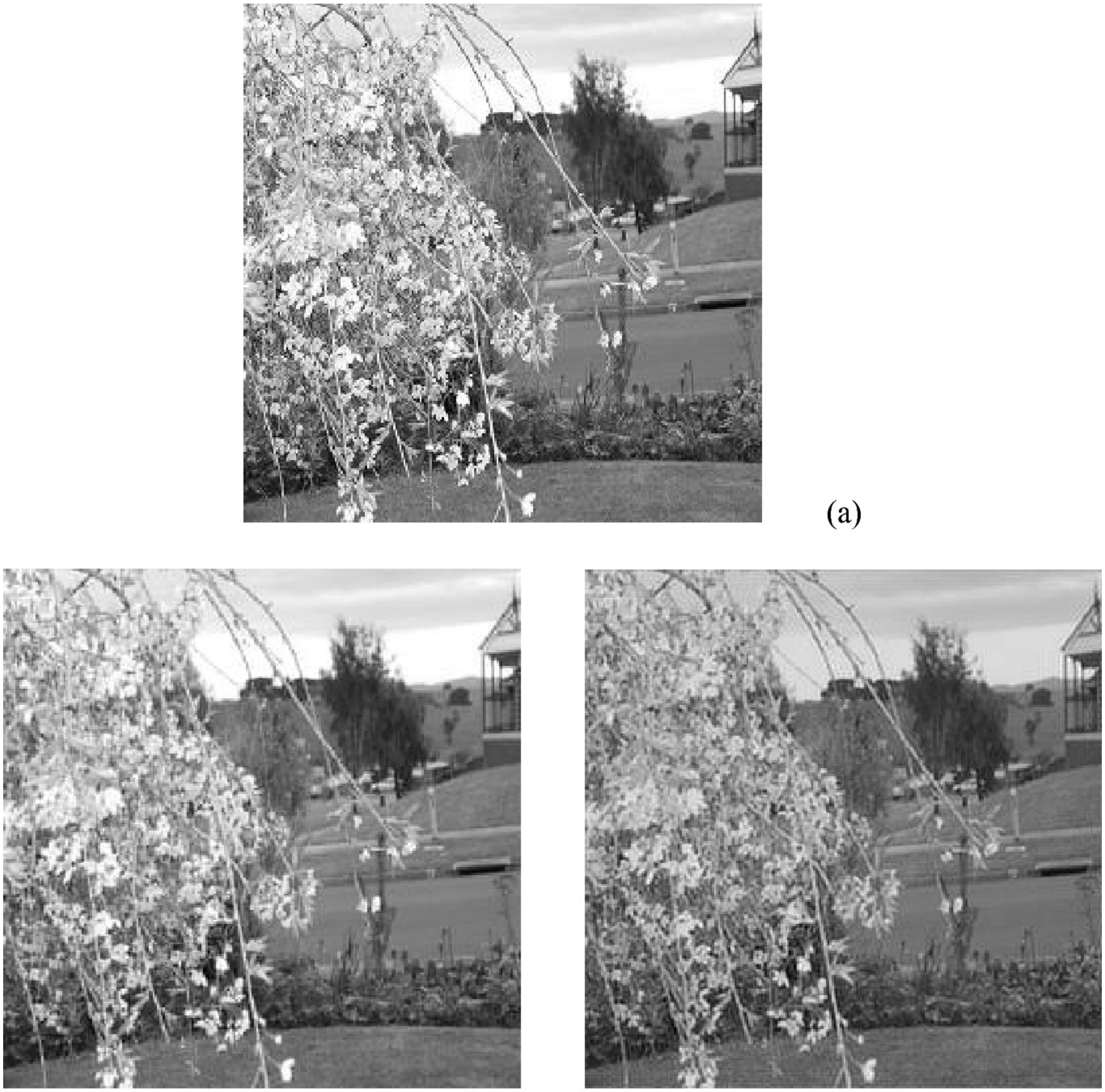
For each block B in the image I, a DCT is applied on B. Because significant DCT coefficients are concentrated at the top corner of B, the coefficients of the DCT on B are collected following a triangularly *zigzag* order starting from the top left corner, which is shown in Fig. 2.15. For example, if 10 coefficients are needed, a 10-element vector is obtained as $\mathbf{x} = [87, 63, 12, 0, 4, 7, 0, -11, -6, 3]$. If the DFT coefficients of every block are collected in the same order, the blocks can be matched and compared properly.



87	63	7	0	1	0	0	0
12	4	-11	-1	0	0	0	0
0	-6	-2	0	1	0	0	0
3	0	0	0	-1	0	0	0
0	0	0	0	0	0	0	0
0	0	-1	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0

Fig. 2.15 Zigzag collection of DCT coefficients from an 8 × 8 image block *B*

Figure 2.16 shows an example of using DCT for image compression. The 512 × 512 Gy-level image in Fig. 2.16a is first divided into 8 × 8 blocks, which result in 64 × 64 = 4096 blocks. Compute the two-dimensional DCT of each block in the image, and discard all but the first 10 of the 64 DCT coefficients in each block. Figure 2.16b shows the compressed image with 40,960 DCT coefficients, which are about 15% of the total number of image pixels (a compression ratio of 6.6). In contrast, the image reconstructed with similar number of DFT coefficients through a low-pass filter is shown side by side with the DCT image in Fig. 2.16c. It can be observed the DCT image has less quality loss than the DFT image.



(a)

(b)

(c)

Fig. 2.16 Image compression using DCT. **a** An original gray-level image; **b** DCT compressed image; **c** DFT compressed image

2.5 Summary

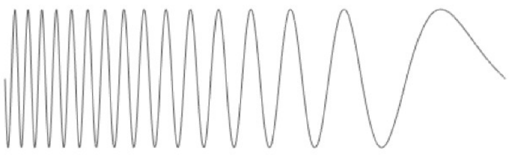
In this chapter, three windowed FT methods are introduced and discussed in detail, namely STFT, Gabor filters and DCT. All of them allow for time/space–frequency analysis. Because of using shifting windows, the output of STFT on a 1D signal is a 2D spectrogram instead of a single 1D FT spectrum. It can be observed that the spectrogram reveals a lot more frequency information than a single FT spectrum. However, due to the use of windows, we sacrifice some frequency resolution. That means, instead of 1 frequency per bin in a FT spectrum, a bin in STFT represents a band of frequencies. The bandwidth of a STFT bin depends on the window size, and the narrow the window, the wider the bin. We also lose some low frequencies due to windowing. Therefore, it is important to learn the trade-off between window size and bin size when using STFT.

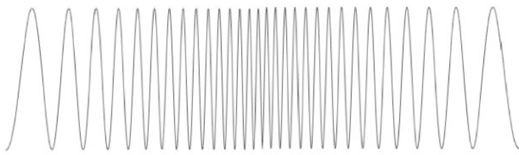
Compared with STFT, Gabor filters provide a better solution in terms of the trade-off, because Gabor filters use multiple filter size and orientations. Furthermore, the use of Gaussian window by Gabor filters produces more desirable results than rectangular window.

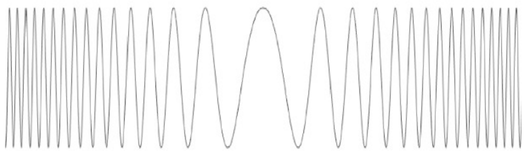
DCT is a variant of STFT by removing the imaginary component of the transform. By removing the imaginary component, DCT is not only more efficient in terms of computation but also more desirable in terms of feature extraction. This is because both DFT and STFT have discontinuity on a signal's boundary or a window's boundary, and this discontinuity causes distortion on the transform. In contrast, DCT removes this discontinuity by mirroring data around the window's boundary.

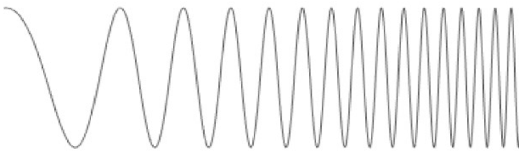
2.6 Exercises

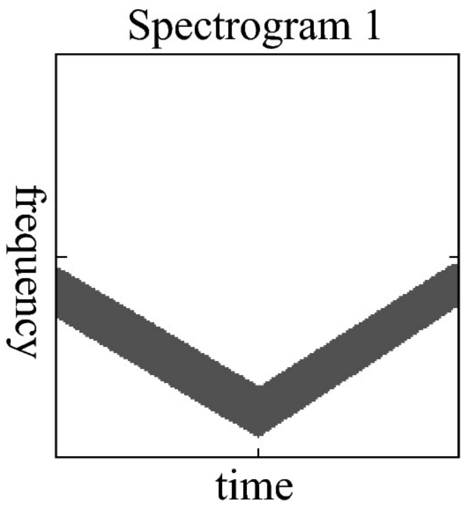
1. Match each of the following signals to its corresponding spectrogram underneath the signals and explain why you match it that way.

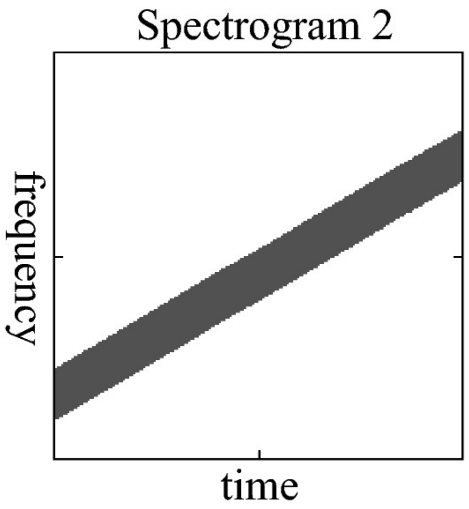

Signal 1

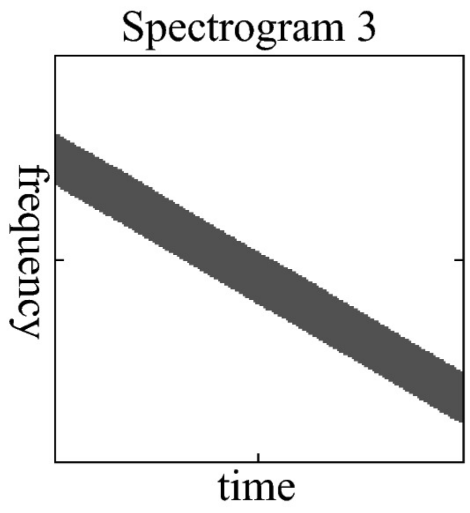

Signal 2

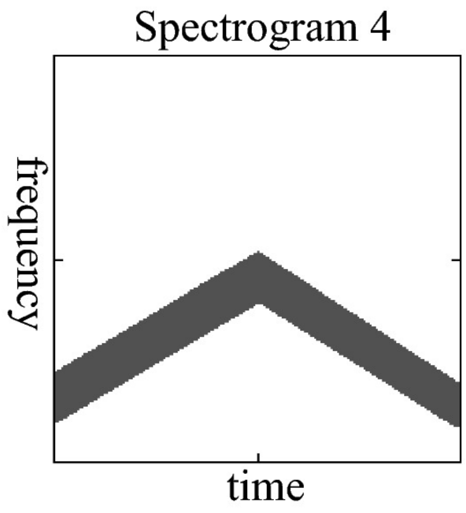

Signal 3


Signal 4


Spectrogram 1


Spectrogram 2


Spectrogram 3


Spectrogram 4

2. Contrast the similarity and difference between STFT and Gabor filtenrs.

3. Explain the different tiling of spectrum plane between STFT and Gabor filters.

4. Use the Matlab code from the following Web page to generate Gabor filters: https://au.mathworks.com/help/images/ref/gabor.html. Try different number of scales and orientations, and explain how they are different and what kind of image feature they capture.

5. Find a texture image, apply the Gabor filters you've generated in Exercise 4 on the texture image, and explain the spectra of the Gabor filtered images. Try more images and report your findings.

6. Find two similar texture images, follow the Matlab code on the following link and apply 2D DCT on each of the two images. Double click the 'J' variable on Matlab Workspace on the right-hand side (or left-hand side) of Matlab editor, collect the first 10 DCT coefficients following the zigzag order shown in Sect. 2.4.4, and put them in a vector. Compare the two vectors collected from the two DCT images, and see if they show similar pattern. Adjust the threshold of J to different values to observe the reconstructed image. Next, find two different texture images and repeat the above procedures. Write a short report to summarize your findings and reflect your understanding of DCT.

https://au.mathworks.com/help/images/ref/dct2.html#d117e35003.

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3. Wavelet Transform

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To understand the real world, zoom in and zoom out.

3.1 Discrete Wavelet Transform

Gabor transform can be written as

$$G_{\sigma_x \sigma_y}(\tau_1, \tau_2) = \sum_{x=0}^{N} \sum_{y=0}^{N} f(x, y)\, g^{*}_{\sigma_x \sigma_y}(x - \tau_1, y - \tau_2) \tag{3.1}$$

where * means complex conjugate and the Gabor function $g_{\sigma_x, \sigma_y}(x, y)$ is given as:

$$g_{\sigma_x \sigma_y}(x, y) = \frac{1}{2\pi\sigma_x\sigma_y} \exp\left[-\frac{1}{2}\left(\frac{x^2}{\sigma_x^2} + \frac{y^2}{\sigma_y^2}\right)\right] e^{j2\pi\omega x} \tag{3.2}$$

The group of Gabor functions $g_{\sigma_x, \sigma_y}(x, y)$ are windowed wave form functions, called wavelets. But the Gabor wavelets are not orthogonal, which means there is correlation between different Gabor wavelets. This correlation results in redundancy in the extracted wavelet features computed from images or signals. The FWHM approach in Sect. 2.3 causes loss of frequency. This is undesirable for image or signal representation. The window size is also an issue similar to that of STFT.

These issues can be overcome by using orthogonal wavelets with varying window size.

The general form of a 2D orthogonal wavelet can be formulated as follows

$$\psi_{a_1 a_2 b_1 b_2}(x, y) = \frac{1}{\sqrt{a_1 a_2}} \psi\left(\frac{x - b_1}{a_1}, \frac{y - b_2}{a_2}\right) \tag{3.3}$$

where a_1, a_2 are the scale parameters and b_1, b_2 are the position parameters. Similar to a 2D FT, a 2D wavelet also has the property of separability:

$$\psi_{a_1 a_2 b_1 b_2}(x, y) = \frac{1}{\sqrt{a_1}} \psi\left(\frac{x - b_1}{a_1}\right) \frac{1}{\sqrt{a_2}} \psi\left(\frac{y - b_2}{a_2}\right) \tag{3.4}$$

The *discrete wavelet transform* (DWT) on a function or image $f(x, y)$ is given as:

$$W^s(k, l) = \frac{1}{s} \sum_n \sum_m f(m, n) \psi\left(\frac{m - k}{s}\right) \psi\left(\frac{n - l}{s}\right) \tag{3.5}$$

where (k, l) is the position of the wavelet and s is the scale. If we compare a wavelet with a magnifying glass, the position vector (k, l) represents the location of the magnifying glass and the scale s represents the distance between the magnifying glass and the image. By adjusting the position and scale, the wavelet can analyze an image the same way as we are analyzing an image using a magnifying glass.

3.2 Multiresolution Analysis

As explained in Sect. 1.4, the window size (time) and the frequency band are inversely proportional. That is, when the window size is halved, the frequency band captured by the window is twice higher. The frequency bandwidth is typically arranged in octave; that is, the next bandwidth is twice the width of the previous one. The inverse relationship between window size and frequency of a DWT can be demonstrated using a 1D signal with a Nyquist sampling rate of 1024 Hz. As can be seen in the following table, as the wavelet decomposition level (scale) and the window size increase, the bandwidth becomes narrower and narrower until it reduces to a single point which is equivalent to a FT frequency.

Decomposition level	Window size	Frequency band
1	2	512–1023
2	4	256–511
3	8	128–255
4	16	64–127
5	32	32–63
6	64	16–31
7	128	8–15
8	256	4–7
9	512	2–3
10	1024	1

The above table can be illustrated using a time–frequency plane. Figure 3.1 shows the time–frequency planes of both DWT and STFT side by side. The wavelet time–frequency plane is shown in Fig. 3.1, left. In contrast, STFT uses one window size for all frequencies as shown in Fig. 3.1, right. Compared with STFT, a DWT yields very high resolution at lower frequencies while sacrifices resolution at higher frequencies. Therefore, a DWT is a multiresolution tool.

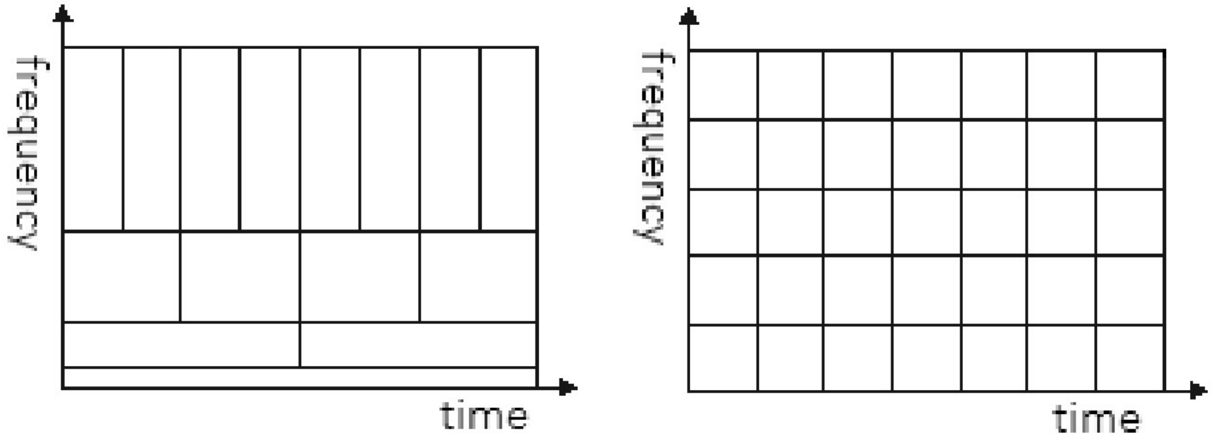


Fig. 3.1 Different frequency tiling of spectral plane. Left: the wavelet spectrum; right: the STFT spectrum

Wavelets analyze and represent a signal with multiresolution. This is extremely useful, because lower resolution represents a summary and higher resolution represents fine details of a signal, and both are essential in signal analysis and representation. The multiresolution representation is done through repeating rounds of scaling (low pass L) and wavelet transform (high pass H) on a signal. The scaling captures the low-frequency information of the signal, and the wavelet captures the high-frequency information of the signal. At each round of the wavelet transform , a low-resolution signal (low frequency L) and a fine details signal (high frequency H) are obtained, and both are half the size of the original signal. Since the information in the fine details signal is usually scarce, most of the information in the original signal is captured by the lower-resolution version, and this achieves great efficiency of signal representation. To recover the signal, the inverse wavelet transform is applied, which is done through repeating rounds of expansion.

3.3 Fast Wavelet Transform

3.3.1 DTW Decomposition Tree

For a 2D image, the rows and columns are treated as 1D signals. Due to the separability property of DWT, the two passes at each round of the DWT are done at the rows and the columns separately. The 2D digital wavelet transform on an image is illustrated in Figs. 3.2, 3.3 and 3.4.

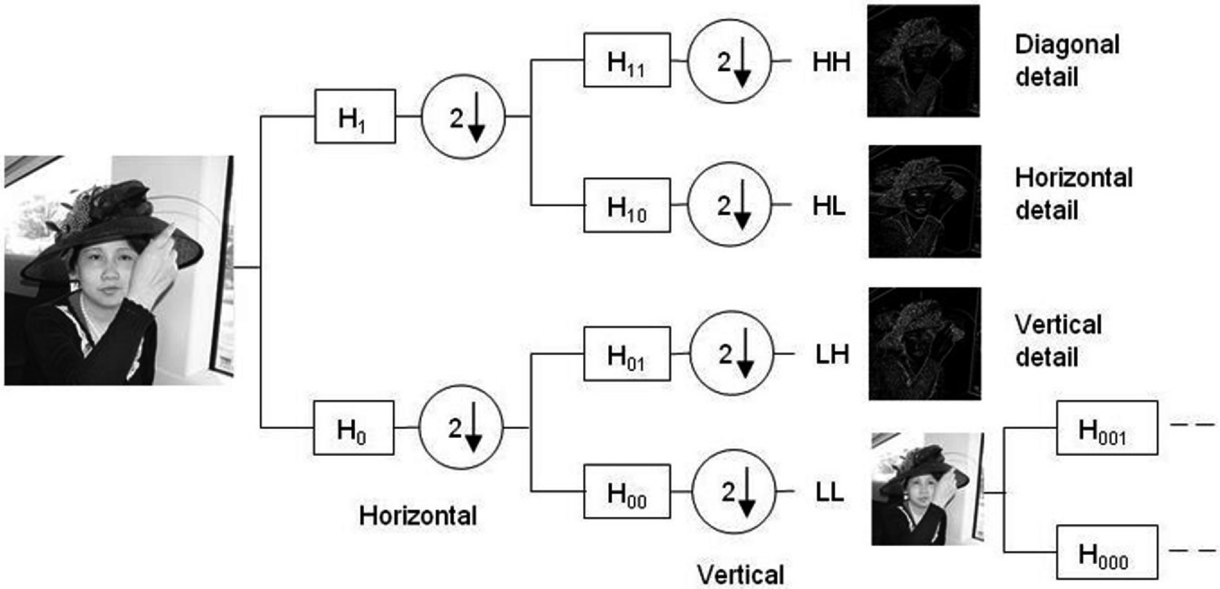

H$_1$
2↓
H$_{11}$
HH
Diagonal detail
H$_{10}$
HL
Horizontal detail
H$_{01}$
LH
Vertical detail
H$_0$
H$_{00}$
LL
H$_{001}$
H$_{000}$
Horizontal
Vertical

Fig. 3.2 2D DWT decomposition tree for a lady image

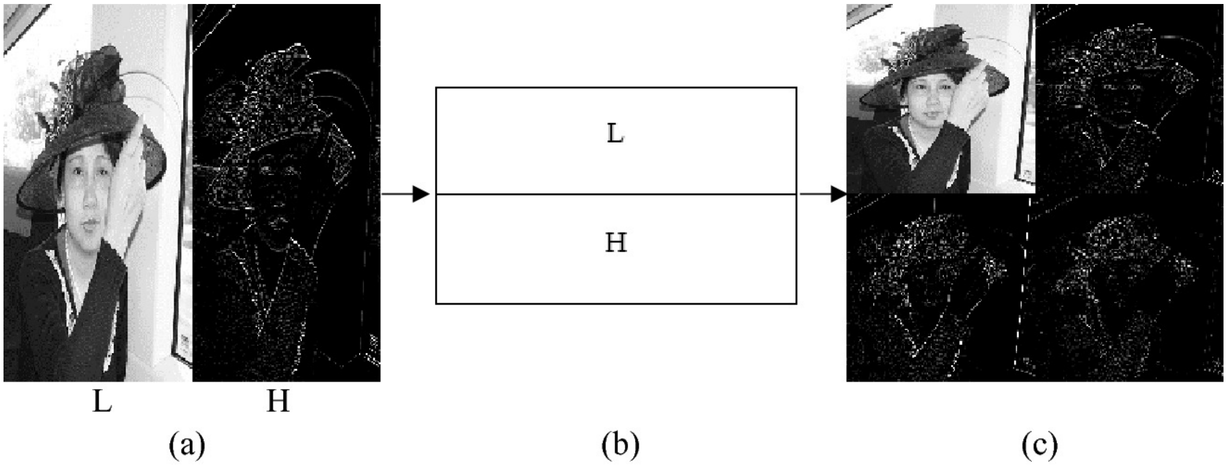
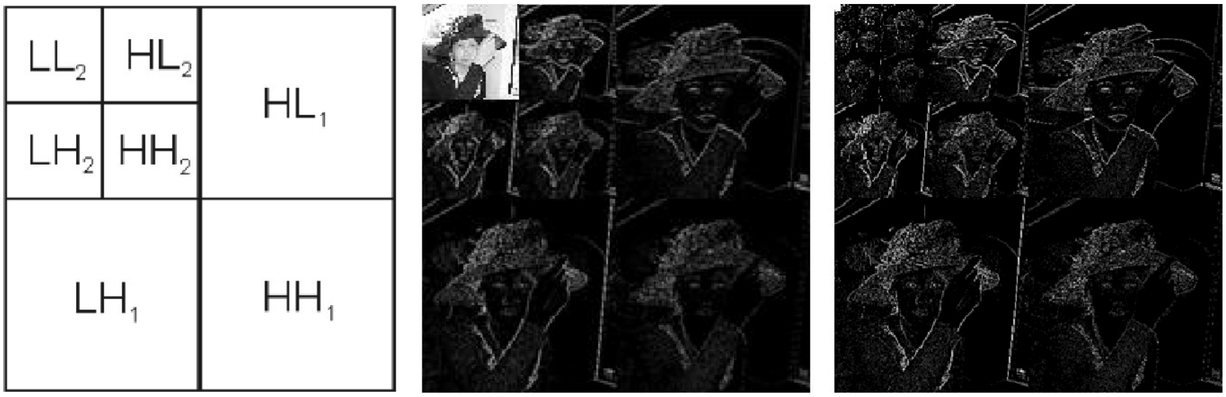


Fig. 3.3 Illustration of 2D DWT process on a lady image. **a** Horizontal transform; **b** vertical transform; **c** spectrum of level 1 2D DWT decomposition



(a) (b) (c)

Fig. 3.4 2 levels of 2D wavelet decomposition. **a** The spectrum plane of two levels of 2D DWT; **b** the spectrum of two levels of 2D DWT on the lady image; **c** the complete decomposition of the lady image

- **Horizontal transform**. At the first step of level 1 decomposition, each row of the image is scaled (weighted average) and wavelet transformed (weighted difference).

  The result from the first step is two half images, one with scaling coefficients (L) and the other with wavelet coefficients (H), and both are half width of the image row (Fig. 3.3a).

- **Vertical transform**. In the next, the scaling (L) and wavelet transform (H) are applied on each column of the two half images from the previous step (Fig. 3.3b).

  The result from the second step is four quarter-sized images, which are: summary (LL, top left), vertical details (LH, bottom left), horizontal details (HL, top right) and diagonal details (HH, bottom right) (Fig. 3.3c).

- **Level 2 decomposition**. The above steps are repeated on the LL image for the next round of DWT (Fig. 3.4b).
- **DWT spectrum**. The level one decomposition process can be repeated until the summary image can no longer be decomposed further, and the final spectrum of the wavelet transform on the lady image is shown in Fig. 3.4c. It can be observed that the DWT spectrum captures the essence of the image while discard all the redundant details. This is very useful for image analysis.

This process can be summarized in mathematical terms. Suppose the scaling and wavelet functions are ϕ and ψ, respectively. At each level of decomposition, the following 4 quarter-sized images are resulted from the DWT by using (3.5): average/summary image $\phi(x, y)$, horizontal difference/details image $\psi^{\mathrm{H}}(x, y)$, vertical difference/details image $\psi^{\mathrm{V}}(x, y)$ and diagonal difference/details image $\psi^{\mathrm{D}}(x, y)$.

$$\phi(x, y) = \phi(x)\phi(y) \rightarrow \mathrm{LL} \tag{3.6}$$

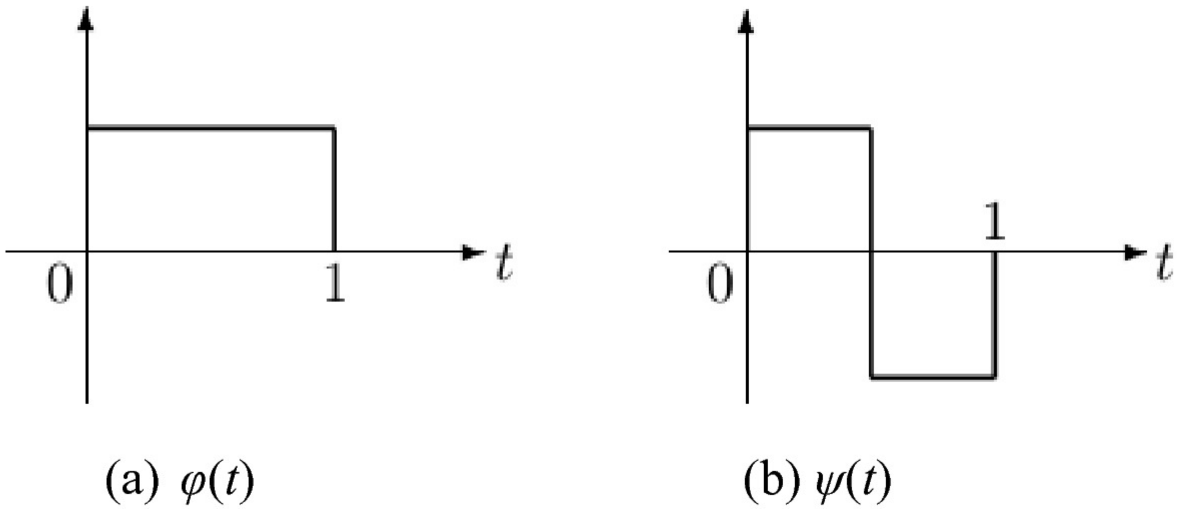
$$\psi^{\mathrm{H}}(x, y) = \psi(x)\phi(y) \rightarrow \mathrm{HL} \tag{3.7}$$

$$\psi^{\mathrm{V}}(x, y) = \phi(x)\psi(y) \rightarrow \mathrm{LH} \tag{3.8}$$

$$\psi^{\mathrm{D}}(x, y) = \psi(x)\psi(y) \rightarrow \mathrm{HH} \tag{3.9}$$

3.3.2 1D Haar Wavelet Transform

The DWT can be demonstrated using Haar wavelet, and the scaling function and wavelet function of Haar transform are shown in Fig. 3.5. Given the unique characteristic or shape of the Haar transform functions, the scaling and wavelet transform of Haar wavelet become simply the *average* and *difference* (or *details*).



(a) $\varphi(t)$ (b) $\psi(t)$

Fig. 3.5 Haar scaling function (**a**) and wavelet function (**b**)

Suppose x and y are two neighboring points, the scaling coefficient and wavelet coefficient are given by s and d, respectively:

$$s = (x + y)/2 \quad \text{and} \quad d = (x - y)/2 \tag{3.10}$$

The inverse Haar transform is then given by *addition* and *subtraction*:

$$x = s + d \quad \text{and} \quad y = s - d \tag{3.11}$$

- Given an even length discrete signal of $(a_0, a_1, \ldots, a_{2n}, a_{2n+1})$.
- It is first organized into pairs $((a_0, a_1), \ldots, (a_{2n}, a_{2n+1}))$.
- By applying the first round of Haar transform, the coefficients of the transform are given by $((s_0, s_1, \ldots, s_n), (d_0, d_1, \ldots, d_n))$.
- The second round of Haar transform can be performed on the sequence of s and so on so forth.

For example, suppose [11, 9, 5, 7] is a 4-point digital signal, the following demonstrates the process of a Haar wavelet transform on the signal.

Resolution	Averages	Details
4	[11, 9, 5, 7]	
2	[10, 6]	[1, −1]
1	[8]	[2]

Therefore, the Haar wavelet transform of [11, 9, 5, 7] is given by [8, 2, 1, −1]. As can be seen, after the wavelet transform, the first value captures the most significant information while the last two values are very small. This is helpful in signal processing and analysis, because more attention can be given to the most significant information.

The wavelet transform can be performed more efficiently by using matrix multiplication. The following is an example of 4 × 4 Haar wavelet transform matrix.

$$H_4 = \frac{1}{4}\begin{bmatrix} 1 & 1 & 1 & 1 \\ 1 & 1 & -1 & -1 \\ 2 & -2 & 0 & 0 \\ 0 & 0 & 2 & -2 \end{bmatrix} \tag{3.12}$$

For the above 4-point signal, using the Haar wavelet transform matrix, the transform coefficients are given by:

$$h_4 = \frac{1}{4}\begin{bmatrix} 1 & 1 & 1 & 1 \\ 1 & 1 & -1 & -1 \\ 2 & -2 & 0 & 0 \\ 0 & 0 & 2 & -2 \end{bmatrix}\begin{bmatrix} 11 \\ 9 \\ 5 \\ 7 \end{bmatrix} = \begin{bmatrix} 8 \\ 2 \\ 1 \\ -1 \end{bmatrix} \tag{3.13}$$

3.3.3 2D Haar Wavelet Transform

For a 2D image, this is done on both the rows and columns separately.

Suppose the following is a 4 × 4 image *I*:

$$\begin{matrix} 102 & 56 & 68 & 152 \\ 24 & 62 & 46 & 32 \\ 52 & 92 & 72 & 84 \\ 76 & 60 & 92 & 60 \end{matrix}$$

Step 1. *Horizontal scaling* of image *I* (horizontal pairwise average, L):

$$\begin{matrix} 79 & 110 \\ 43 & 39 \\ 72 & 78 \\ 68 & 76 \end{matrix}$$

Step 2. *Horizontal wavelet transform* of *I* (horizontal pairwise difference, H):

$$\begin{matrix} 23 & -42 \\ -19 & 7 \\ -20 & -6 \\ 8 & 16 \end{matrix}$$

The image I_c after horizontal transform by combining the results from the above two steps:

$$\begin{matrix} 79 & 110 & 23 & -42 \\ 43 & 39 & -19 & 7 \\ 72 & 78 & -20 & -6 \\ 68 & 76 & 8 & 16 \end{matrix}$$

Step 3. *Vertical scaling* of I_c (vertical pairwise average, LL, HL).

$$\begin{matrix} 61 & 74.5 & 2 & -17.5 \\ 70 & 77 & -6 & 5 \end{matrix}$$

Step 4. *Vertical wavelet transform* of I_c (vertical pairwise difference, LH, HH).

$$\begin{matrix} 18 & 35.5 & 21 & -24.5 \\ 2 & 1 & -14 & -11 \end{matrix}$$

The image after the first round of Haar wavelet transform by combining the results from steps 3 and 4:

LL	61	74.5	2	-17.5	HL
	70	77	-6	5	
	18	35.5	21	-24.5	
LH	2	1	-14	-11	HH

The second round of Haar DWT repeats steps 1–4 on the LL band, and this process can be continued until required levels of decomposition are achieved. Similar to the 1D case, the first quarter of the wavelet-transformed image contains the most significant information.

3.3.4 Application of DWT on Image

Figure 3.6 demonstrates the complete process of computing the Haar wavelet transform on the lady image using the DWT decomposition tree of Fig. 3.2. At each next level of the decomposition, the image is halved; therefore, the DWT is very efficient and fast.

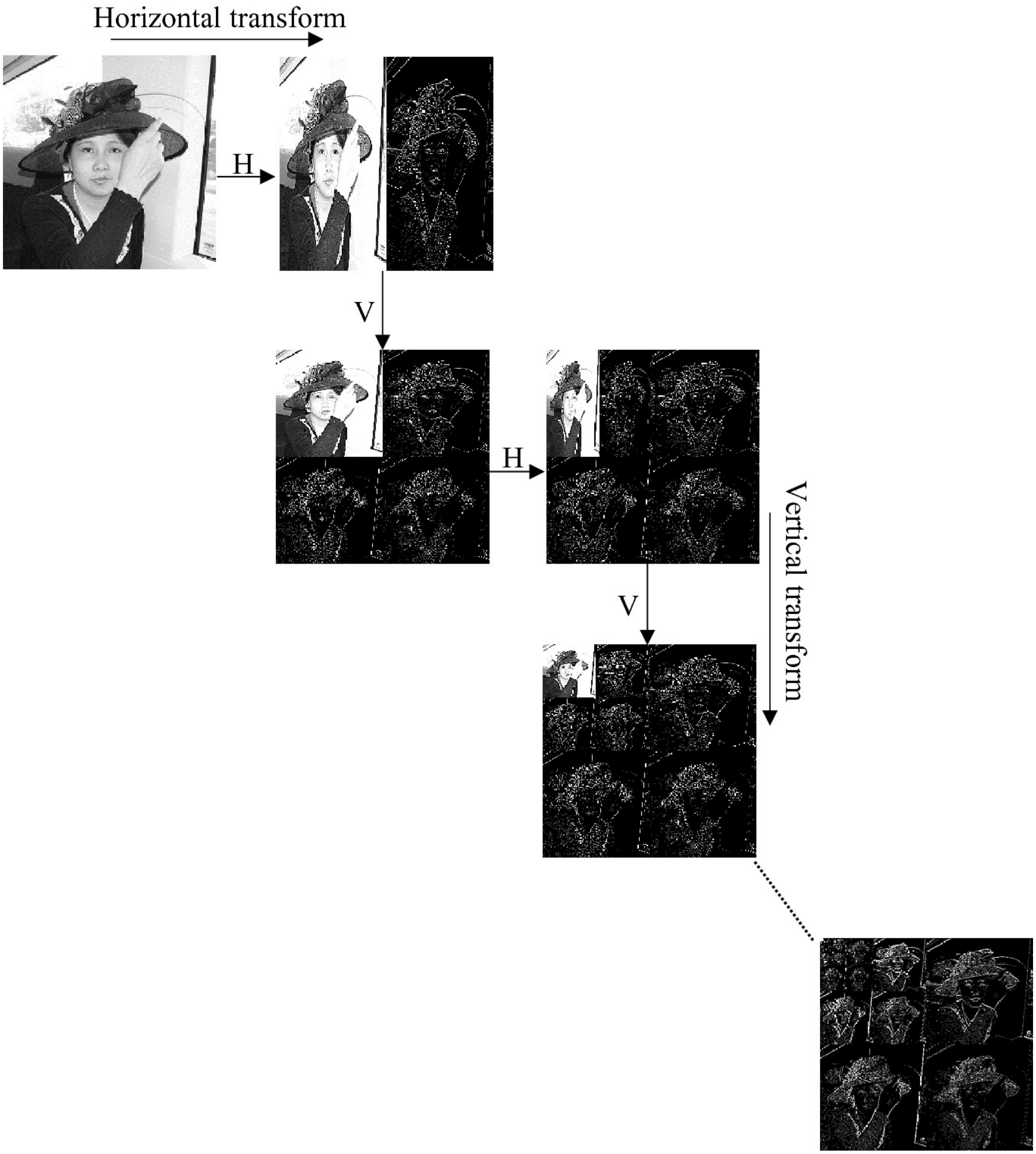

Horizontal transform
H
V
H
Vertical transform
V

Fig. 3.6 Illustration of the computing process of Haar wavelet transform

3.4 Summary

Wavelets are an extension or an improvement to windowed FT in two aspects: *orthogonality* and *multiresolution*. Orthogonality means that there is no redundancy between DWT channels. Multiresolution means to analyze an image by zooming in and zooming out, which is like studying a map with magnifying glass. This is achieved by adapting image resolution to wavelet size/scale.

The contrast between wavelets and windowed FT can be easily understood in frequency plane as shown in Fig. 3.1. Basically, with DWT, we retain higher resolution at very low-frequency band at the cost of losing resolution at high-frequency band. This is sensible because low-frequency information is much more important than high-frequency information to human perception.

The computation of 2D DWT is very efficient due to the separability property of WT. In practice, the computation of 2D DWT follows a decomposition tree or algorithm as shown in Fig. 3.2. Generally, there need just a few rounds of repeat DWT decomposition to transform an image. In terms of understanding the DWT computation process, it is important to understand how Haar wavelet transform works. Once the process of Haar wavelet transform is understood, one can just replace the Haar wavelet with any other wavelet.

3.5 Exercises

1. Given a signal $f = (5, 8, 3, -4, 7, 8, 5, 3)$, compute the Haar wavelet transform of the signal and give all coefficients s and d.

2. Plot all wavelet basis functions ψ_s for all valid scales of the signal computed in problem 1.

3. What is the mathematical concept behind the computation of the Haar coefficients (hint: consider the relationship between Haar, FT and STFT) and why is it important?

4. Choose an image of your own and apply the Haar wavelet transform to the image using the Matlab code shown in this Web page: https://au.mathworks.com/help/wavelet/ref/dwt2.html. Try different images and write a short report on your discovery, e.g., what kind of features it has captured and why.

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Part II

Image Representation and Feature Extraction

Sort the wheat from the chaff

Introduction

A digital color image $I = \{p_{ij}\}$ is a matrix of pixels, each pixel is a three dimensional color vector $p_{ij} = (r_{ij}, g_{ij}, b_{ij})$, representing the three color components of the pixel. E.g., an image with $m \times n$ pixels is represented as an $m \times n$ matrix:

$$I = \begin{bmatrix} p_{11}, p_{12}, \ldots\ldots, p_{1n} \\ p_{21}, p_{22}, \ldots\ldots, p_{2n} \\ \ldots\ldots\ldots \\ p_{m1}, p_{m2}, \ldots\ldots, p_{mn} \end{bmatrix}$$

$$= \begin{bmatrix} (r_{11}, g_{11}, b_{11}), & (r_{12}, g_{12}, b_{12}), & \ldots\ldots, & (r_{1n}, g_{1n}, b_{1n}) \\ (r_{21}, g_{21}, b_{21}), & (r_{22}, g_{22}, b_{22}), & \ldots\ldots, & (r_{2n}, g_{2n}, b_{2n}) \\ & \ldots\ldots\ldots & & \\ (r_{m1}, g_{m1}, b_{m1}), & (r_{m2}, g_{m2}, b_{m2}), & \ldots\ldots, & (r_{mn}, g_{mn}, b_{mn}) \end{bmatrix} \quad (1)$$

For color processing and analysis, a color image is often represented as a composition of three component color images or image planes: $I = [I_r, I_g, I_b]$:

$$I_r = \begin{bmatrix} r_{11}, r_{12}, \ldots\ldots, r_{1n} \\ r_{21}, r_{22}, \ldots\ldots, r_{2n} \\ \ldots\ldots\ldots \\ r_{m1}, r_{m2}, \ldots\ldots, r_{mn} \end{bmatrix}$$

$$I_g = \begin{bmatrix} g_{11}, g_{12}, \ldots\ldots, g_{1n} \\ g_{21}, g_{22}, \ldots\ldots, g_{2n} \\ \ldots\ldots\ldots \\ g_{m1}, g_{m2}, \ldots\ldots, g_{mn} \end{bmatrix}$$

$$I_b = \begin{bmatrix} b_{11}, b_{12}, \ldots\ldots, b_{1n} \\ b_{21}, b_{22}, \ldots\ldots, b_{2n} \\ \ldots\ldots\ldots \\ b_{m1}, b_{m2}, \ldots\ldots, b_{mn} \end{bmatrix} \quad (2)$$

To extract texture features from a color image, it is usually converted to a grey level image. A grey level image is basically a 3D function $z = g(x, y)$, where (x, y) is the pixel position and z is the intensity. By modelling an image as a mathematical function, advanced theories on mathematical analysis, algebra and statistics can be employed for image analysis.

Figure II.1 shows the 3D function for the lady image in Fig. 3.2, where the colors in the 3D space represent the intensity of the image pixels. It is observed that a grey level image is essentially a 3D terrain or a 3D surface in space, this modelling is helpful because advanced geometric theories can also be employed on texture analysis such as *fractal*.

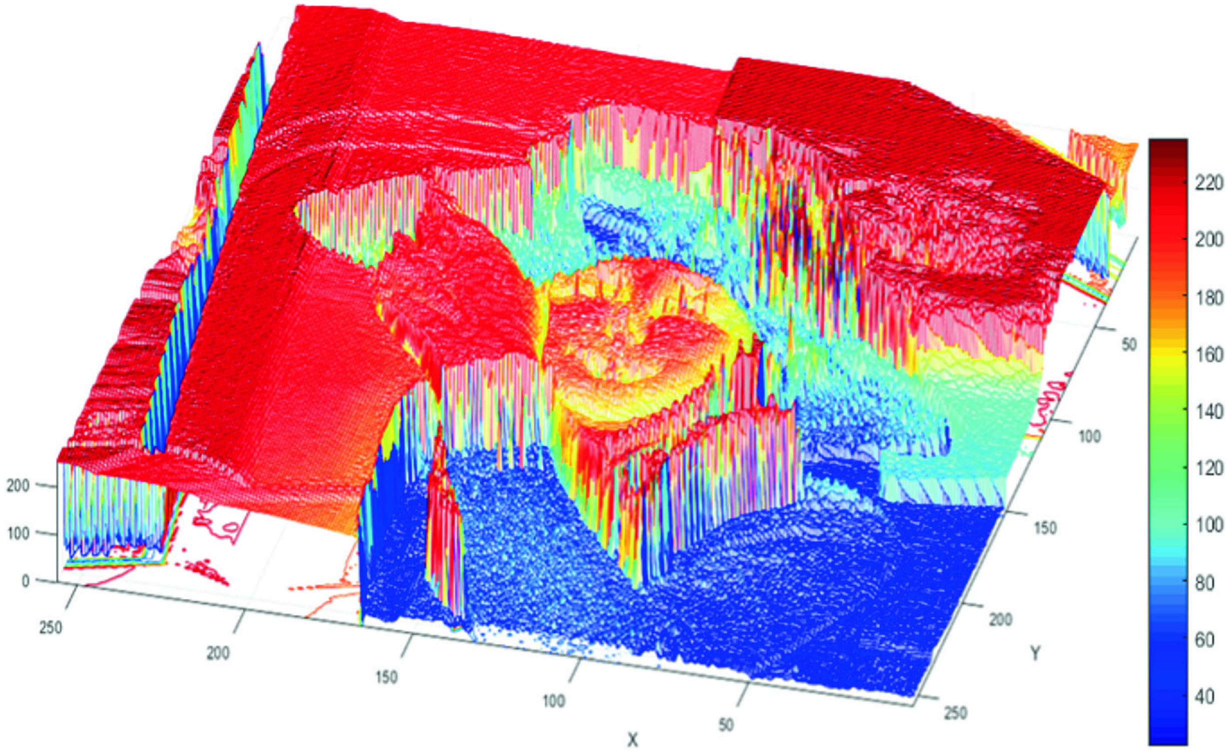

Fig. II.1 The 3D map for a 2D image

Images are a powerful media, in fact, human beings learn to understand the world visually before learning to read and write. It is widely known that a picture is worth a thousand of words. This is because people read images much more efficiently and effectively than reading text. Indeed, people nowadays get more information from TV, videos and cinema than from books.

Although images are a powerful media, it is much more difficult to mine semantic information from images than from textual documents, due to each image has a large number of image pixels and there is no visual dictionary to represent images. Image size on Internet nowadays ranges from several hundreds of thousands of pixels to several millions of pixels and it's even bigger in private storage. Image size is going to get bigger and bigger as the image capturing devices get more and more powerful and the Internet speed gets faster and faster.

To make the mining task even more complicated, an image is usually corrupted or degraded. An observed image $I(x, y)$ is typically a degraded version of an ideal image $f(x, y)$. In general, the relation between $f(x, y)$ and $I(x, y)$ is governed by $I(x, y) = T_g\ [T_d\ (f)]$, where T_d

and T_g are color and geometric *degradation operators* respectively. In practice, T_d is usually modelled as a convolution while T_g is typically modelled as a spatial transform such as affine transform or similarity transform. T_d and T_g are usually unknown. The goal is to model the unknown image $f(x, y)$ through the observed image $I(x, y)$ by the means of some a priori information or assumption.

It is known the world is consisted of objects and each object can be described with a small number of properties or features. For example, a human being can be described by his/her gender, height, weight, hair, complexion, dressing, ethnicity etc. Similar to interpreting the world, human beings tend to group image pixels into objects and describe them accordingly when reading an image.

The idea of image analysis or image data mining is to mine a small number of features from the large number of image pixels, so that images can be described effectively and similar images can be classified. Ideally, the features should be semantic so that human beings can understand them. However, to mine semantic features like water, sky, horse, tree etc. is extremely difficult for machine. Therefore, a typical image analysis mechanism starts from low level features such as color, shape, texture etc. Once low level features are extracted, higher level features can be learned through machine learning methods which will be described in Part III, and similar images can be retrieved through image retrieval methods which will be described in Part IV.

In Part II, the three types of common low level image features will be described in details.

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4. Color Feature Extraction

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Every picture tells a story, by colors.

4.1 Introduction

Arguably, color is the most important feature of an image. After all, people see this world as colors or the world presents itself to us as colors. However, color is a complex topic and difficult to understand. As a matter of fact, few people are good at painting a picture or image. There are an infinite number of colors in this world, and colors can be created from different types of palettes. Computers use a trichromatic palette to mix all the colors in this world. That means each color in computers is represented as a three-dimensional vector (c_1, c_2, c_3). These color vectors created a 3D color space. Depending on how each of the trichromatic colors is defined, different color spaces or color models have been created.

The most commonly used color space is the RGB color space, where each of the colors is defined by adding three primary colors in the visible light spectrum (red, green and blue) with various proportions. Other commonly used color spaces include LUV, HSV/HSL/HSI, YCrCb.

Color spaces are models for representation of pixel values. To compare and classify color images, however, we need to analyze and understand the *color patterns* in an image. In order to understand the color patterns in an image, we extract color features from the image and compare them with features of other images. Color features are usually based on color statistics computed from an image or regions of an image.

A number of color features have been proposed in the literatures, including color *histogram*, *color moments* (CM), *color coherence vector* (CCV), color *correlograms*, etc. MPEG-7 also standardizes a number of color features including *dominant color descriptor* (DCD), *color layout descriptor* (CLD), *color structure descriptor* (CSD) and *scalable color descriptor* (SCD).

4.2 Color Space

To process and analyze color images, we need to understand how different color models work, and their applications in image processing and analysis. Color is a complex theory, there are infinite number of colors in this world, and colors can be created using varieties of ways. There needs a standard color model so that colors can be reproduced with accuracy and colors produced in different applications by different devices can be translated interchangeably. The first step is to find a way of representing each color numerically and identify the space or gamut of all visible colors.

The building of a standard color model is made possible thanking to the three scientists: *Isaac Newton*, *James Clerk Maxwell* and *Hermann Grassmann*. *Newton* laid the foundation of our understanding of colors by first splitting a light source into spectral or pure colors (rainbow colors, Fig. 4.2). This lets us to understand that a light is a mixture of pure colors and colors are just reflectance of lights of different wavelengths by objects. *Maxwell* found that by projecting and superimposing the three red, green and blue monochromatic pictures on screen, other colors in the scene such as orange, yellow and purples also showed up, suggesting other colors can be created by mixing red, green and blue colors. *Grassmann* found that colors are additive. That means any color can be matched by a linear combination of three other colors (primaries), provided that none of those three can be matched by a combination of the other two; a mixture of any two colors can be matched by linearly adding together their primary components.

4.2.1 CIE XYZ, *xyY* Color Spaces

Modern color models are all based on XYZ color space created by CIE (International Commission on Illumination) in 1931. The CIE XYZ color space was created using Maxwell's *tristimulus* theory, which is based on the theory of *trichromatic* color vision found by Young and Helmholtz [1], who discovered that human vision consists of three types of cones which are sensitive or responsive to three narrow bands of visible lights. Figure 4.1 shows the three color-matching functions which indicate human eyes' response to visible colors. It can be observed that three functions peak at around 600 nm, 550 nm and 450 nm, respectively. It demonstrates that human vision is most sensitive to three bands of lights which are perceived as red, green and blue.

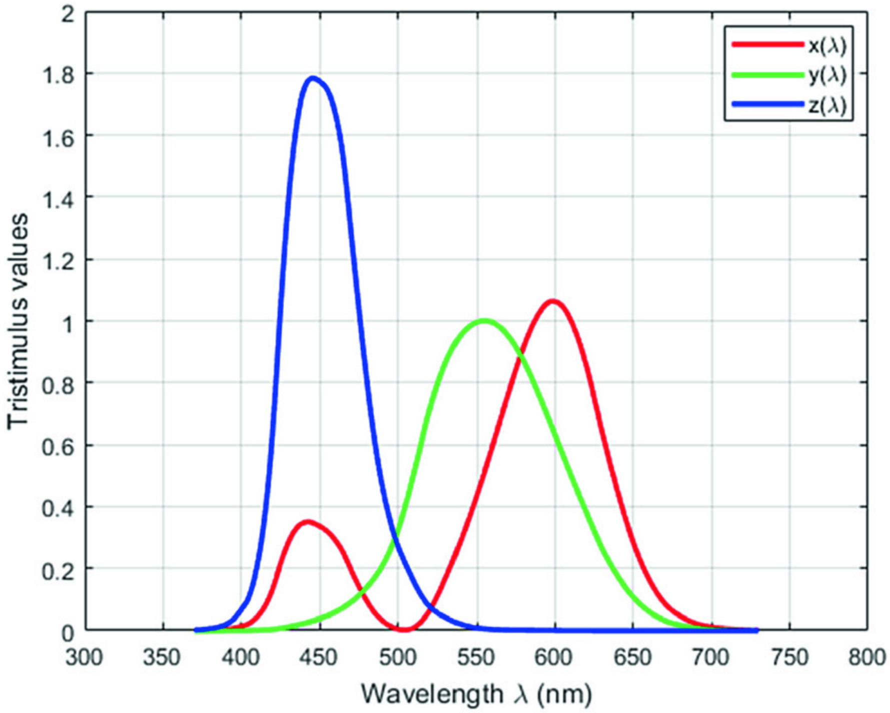


Fig. 4.1 CIE XYZ color-matching functions of human vision

Based on this discovery, CIE uses three *primary colors* to match out all the *spectral colors*, i.e., pure colors or colors with a single wavelength (Fig. 4.1) [2]. The three primary colors are all pure colors, and they are *R* (700 nm), *G* (546.1 nm) and *B* (435.8 nm), respectively, which are shown on the visible color spectrum in Fig. 4.2. The choice of the three particular primaries was due to practical reason at that time. The primaries *G* (546.1nm) and *B* (435.8nm) were chosen because they could easily be reproduced using mercury excitation lines. The 700 nm primary color was chosen because the hue near that wavelength is homogenous and nearly constant; therefore, slight inaccuracy in production of the wavelength of this spectral primary would introduce no error at all.

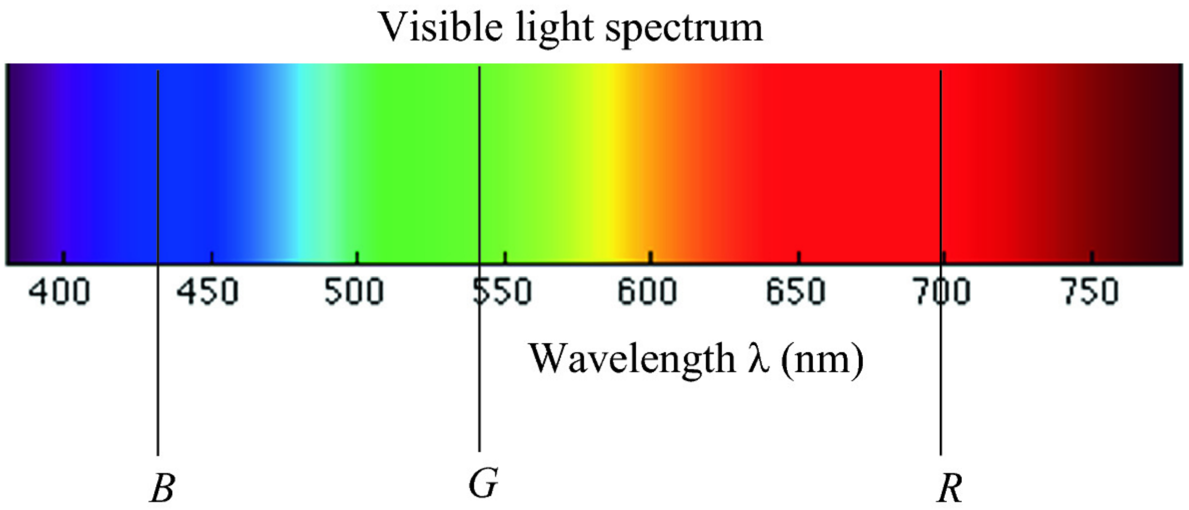
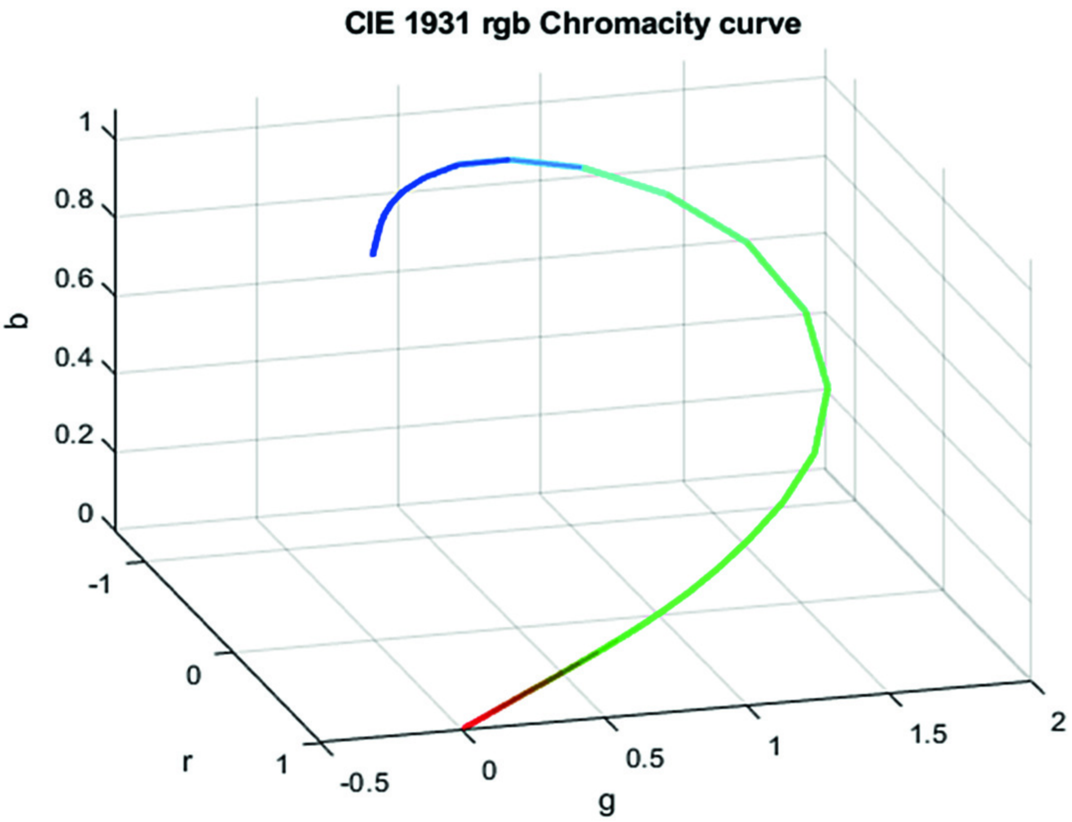


Fig. 4.2 Visible light spectrum and the tristimulus

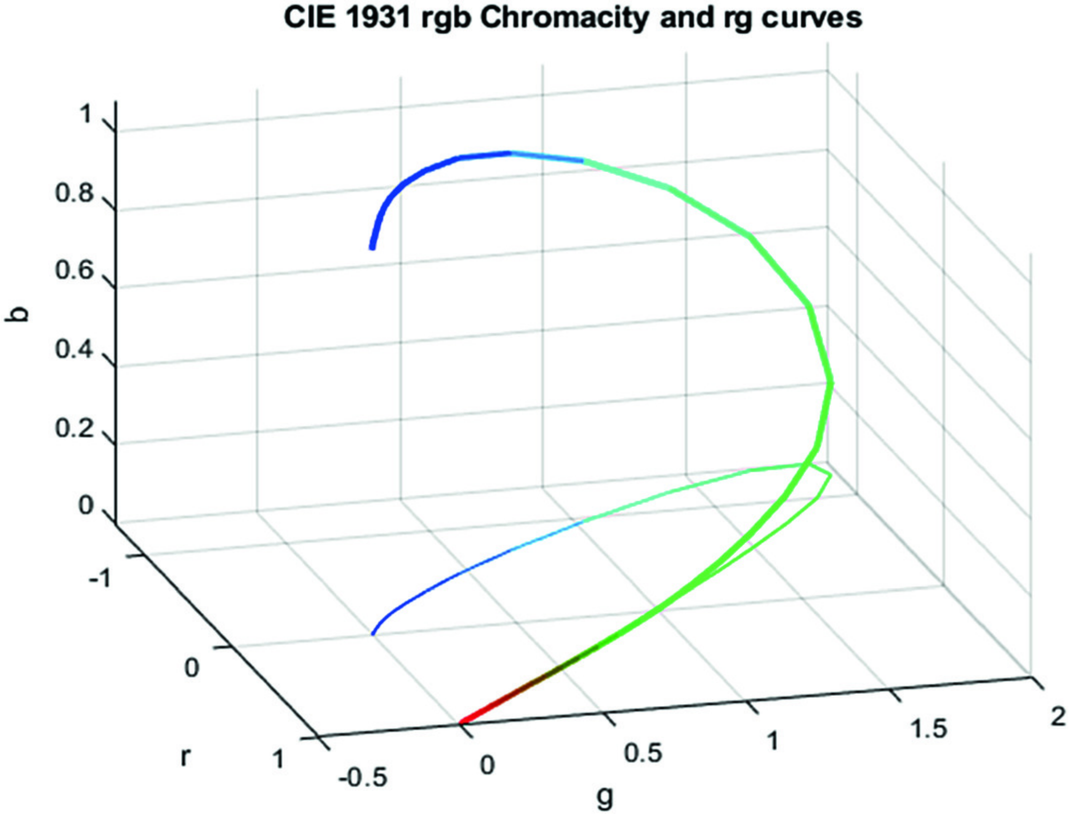
The three primary stimuli are projected on a screen with relative power and are mixed/added by various proportions to match out each of the *spectral colors* in the visible color spectrum using Grassmann's laws. Each color can now be represented as a three-value tuple (R, G, B). The R, G, B values are then normalized using the formulas in (4.1) to remove the intensity from the color representation. The normalized r, g, b values are purely chromatic values. This creates three color-matching functions (CMFs) $r(\lambda)$, $g(\lambda)$ and $b(\lambda)$, where λ is the wavelength. The color space created based on the three CMFs is called CIE RGB color space.

$$\left.\begin{aligned} r &= \frac{R}{R+G+B} \\ g &= \frac{G}{R+G+B} \\ b &= \frac{B}{R+G+B} \end{aligned}\right\} \tag{4.1}$$

Now if we plot the (r, g, b) coordinates of all the spectral colors in 3D space, it forms a curve (Fig. 4.3a) [3]. It is easy to see from (4.1) that $r + g + b = 1$ or $b = 1 - r - g$, which means b is a dependent function of r and g, so there is no need to keep the information b. Therefore, by projecting the *rgb* curve into the 2D *rg* plane, we get the horseshoe-shaped 2D *rg* curve which is shown at the bottom plane in Fig. 4.3b.


CIE 1931 rgb Chromacity curve

(a)


CIE 1931 rgb Chromacity and rg curves

(b)

Fig. 4.3 Color-matching function of spectral colors. **a** *rgb* curve of spectral colors; **b** projection of the *rgb* curve onto the 2D *rg* plane

This *rg* curve is then transformed to the CIE *xy* curve by aligning the $g(\lambda)$ with the CIE luminosity function $V(\lambda)$ and removing the negative values in $r(\lambda)$. The color space created based on the *xy* curve is called CIE XYZ color space.

The colors on the 2D *xy* curve are all *spectral colors*; to obtain *non-spectral colors*, i.e., mixed colors or colors with multiple wavelengths, we draw a straight line between any two points on the *xy* curve. Then each point on the straight line represents a non-spectral color mixed by the two colors at both ends of the line according to Grassmann's second law. For example, by connecting the two primary colors *R* (700 nm) and *B* (435.8 nm) on the *xy* curve, purple colors are created. By this way, all possible *non-spectral colors* can be created. In practice, a white color or white point is first defined, such as D65 which represents the midday sunlight, and lines are drawn from the white point to each of the spectral colors on the *xy* curve. Then colors of different purities are created by mixing the white color with each of the pure colors on the curve. Figure 4.4 shows the color gamut of CIE XYZ color space or CIE *xy* gamut [2]. The color gamut created in this way is a *hue* and *saturation* gamut.

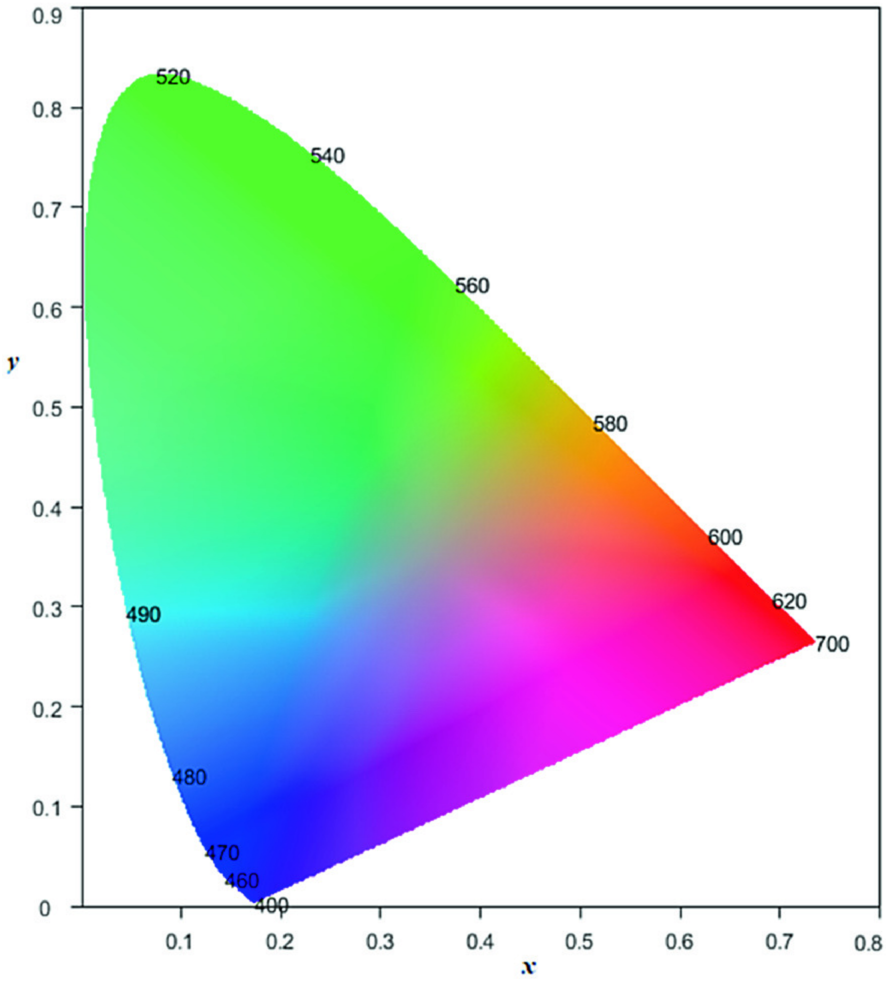


Fig. 4.4 CIE *xy* color gamut

CIE *xy* gamut is a chromaticity domain, and it doesn't specify luminance or brightness of colors. To create object colors, the luminance/brightness must be given as the third dimension, named as *Y*. Therefore, CIE *xyY* color space is created and is called the *object color space*, where *x* and *y* are chromaticity values, and *Y* is the luminance value.

CIE XYZ color space is a cornerstone for modern color modeling. The significance of CIE XYZ color space can be summarized in the following:

- Provides a color gamut with all possible colors;
- Specifies each color with a three-value tuple or a 3D vector (x, y, z);
- Provides a reference for all other color models;
- It is a device-independent color space.

4.2.2 RGB Color Space

Digital images are generated using RGB colors. RGB colors are device dependent, which means that each type of digital devices typically uses a different set of RGB primaries to generate colors. For example, computers use a standard RGB color model or sRGB, which is based on the following three primaries chosen from the CIE XYZ color gamut.

Chromaticity	x	y	Y
R	0.6400	0.3300	0.2126
G	0.3000	0.6000	0.7125
B	0.1500	0.0600	0.0722
W(hite)	0.3127	0.3290	1.0000

The three primaries of sRGB color model are shown in Fig. 4.5 [4]. The gamut of sRGB color space is a triangle inside the CIE XYZ gamut.

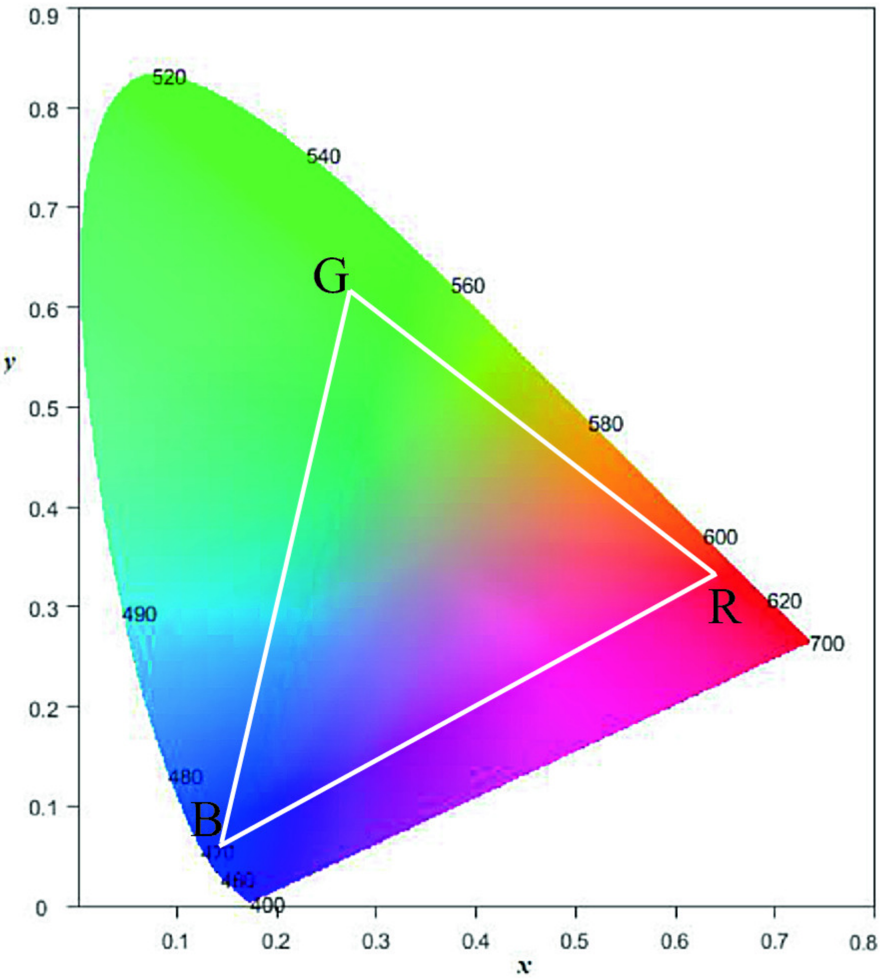


Fig. 4.5 sRGB triangle gamut shown inside the CIE XYZ gamut

The RGB color gamut can be regarded as a color palette. All possible colors created by the RGB palette can be visualized in a 3D cube, called RGB color space as shown in Fig. 4.6. The colors in the RGB color cube are usually quantized for the convenience of viewing. Given the pixel values (r, g, b) from a color image, a color c can be defined in the RGB color space and reproduced by mixing the three primaries using $c = rR + gG + bB$.

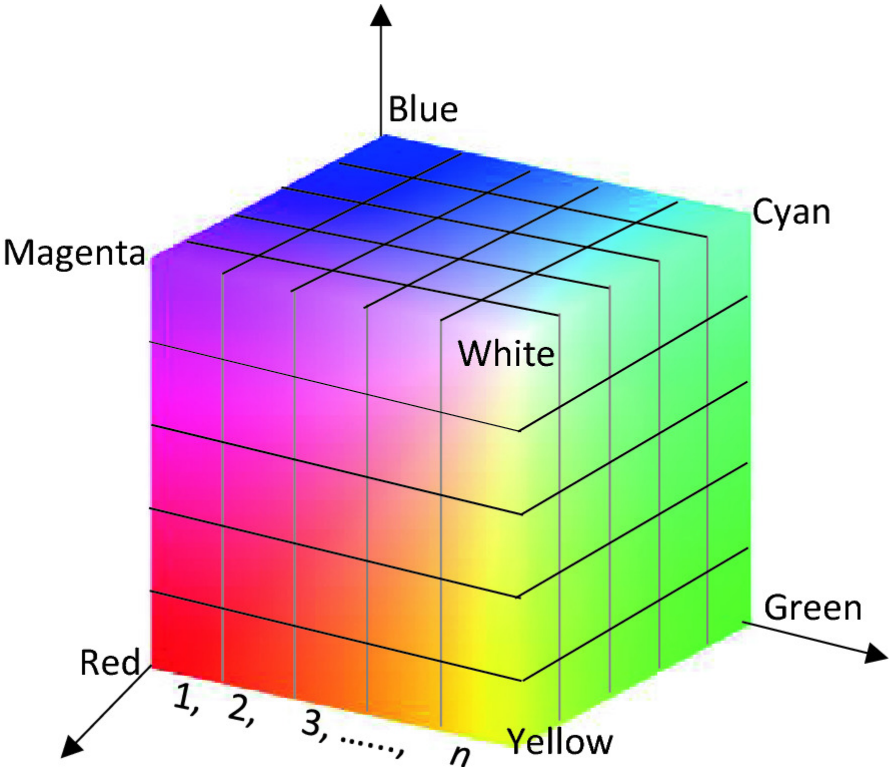


Fig. 4.6 RGB color space in 3D

It is clear that the gamut of any RGB color model is a triangle inside the CIE XYZ color gamut, and consequently, a RGB color space cannot represent all visible colors. In case of a color out of the RGB color gamut, an approximation has to be made. For a color C out of the RGB gamut, the approximation of C is given by the color C_A at the intersection of the RGB triangle and line CW which is the connection between color C and white point W. The approximation is usually acceptable because C_A is just a desaturated color from C.

RGB module is useful for color display and printing; however, it is not desirable for image processing and analysis. This is because the three channels are dependent on each other and there is high correlation between the three channels, which means, changing any one of the color channels will change the other two color channels. Furthermore, RGB color space is not perceptually uniform, meaning that the same amount of numerical change in color values does not correspond to about the same amount of visually perceived change. This leads to color spaces with separation of luminance from chromaticity and color spaces with uniform color distance.

4.2.3 HSV, HSL and HSI Color Spaces

RGB color model is efficient because it just uses three primaries to create all required colors. However, RGB color model is not intuitive because it does not conform to how human beings understand and make colors. For example, artists and painters do not use RGB mixture to make colors; instead, they use pigments to mix with either white or black or both (gray) to make required colors. The pigments are equivalent to pure colors or spectral colors; when they are mixed with white or black, lighter or darker colors are created; when they are mixed with gray, colors with a different purity or saturation are created. Figure 4.7a shows how different tints, shades and tones of reddish colors are created by artists.

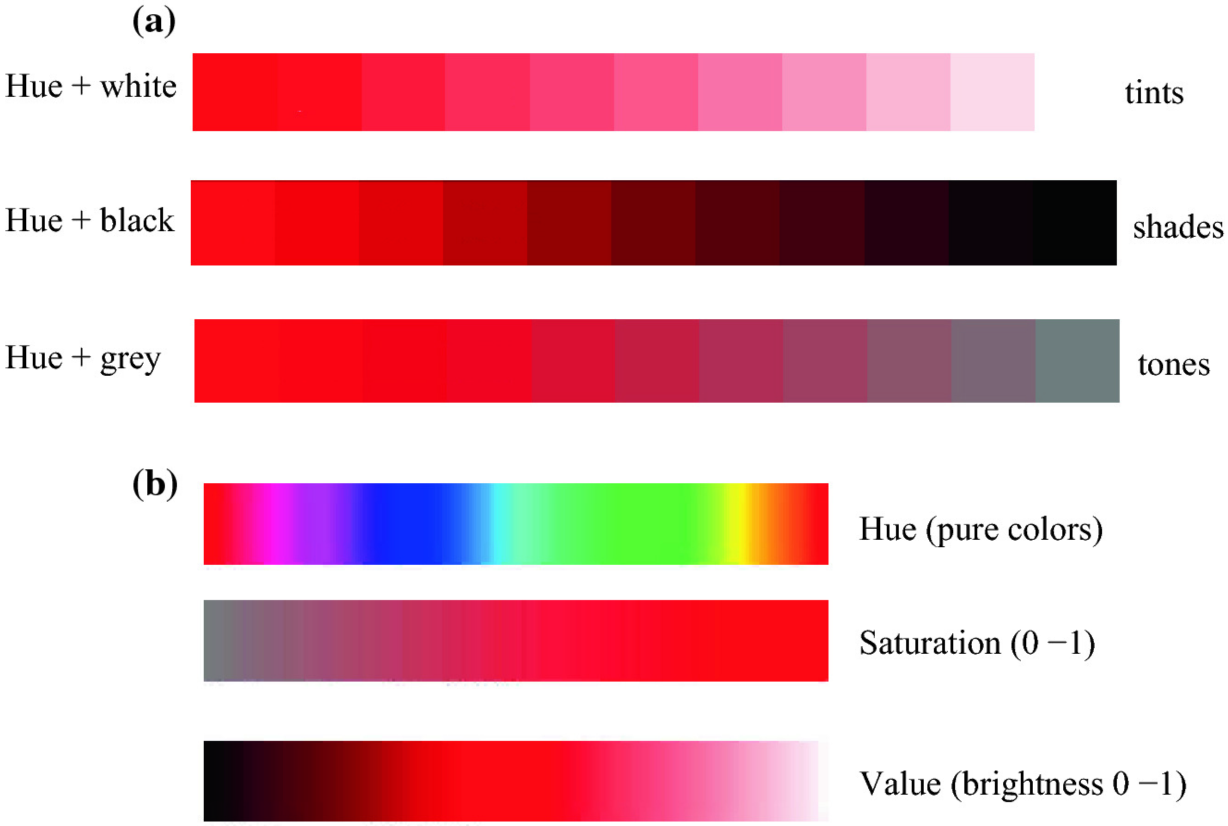


Fig. 4.7 **a** Artists' way of making reddish colors. **b** Components of HSV

The way artists and painters making colors is the idea behind the HSV color model. It demonstrates that a color can be specified by three components/properties: hue, saturation and value or (H, S, V), where hue is a pure color and value = brightness. The *hue* tells what color it is, and it is determined by the dominant wavelength on the visible color spectrum (Fig. 4.2). The *saturation* tells how much or how colorful is the color, and the more saturated the color, the more vibrant or vivid the color is. The *value* tells how bright or dark is the color, colors become disappearing when they are too dark or too bright. Therefore, a color specified by the (h, s, v) values makes a lot more sense than that given by the (r, g, b) values. Multimedia editors and image processing software nowadays all provide intuitive HSV color picker simply because users have better chance to make the desirable colors using HSV model than using other color models.

Figure 4.7b demonstrates the HSV color making using red colors as an example. The first bar shows all the pure colors or hues; the second bar shows red colors with a different purity or saturation (but with the same brightness); the third bar shows red colors with a different brightness.

To create the HSV color model, pure colors (spectral colors) are first collected and put on a circle or a ring (Fig. 4.8, left), and colors with different a saturation are created along the radii of the circle to create a hue–saturation disk/wheel (Fig. 4.8, right). Hue–saturation disks with a different brightness are then generated and stacked on top of each other to make a color cylinder which is the HSV color space, shown in Fig. 4.9a. For HSV, the most saturated colors are on the top of the cylinder and the top of the cylinder has a V value of 1. For HSL, the most saturated colors are in the middle of the cylinder and the top of the cylinder is the white color ($L = 1$); this is shown in Fig. 4.9b.

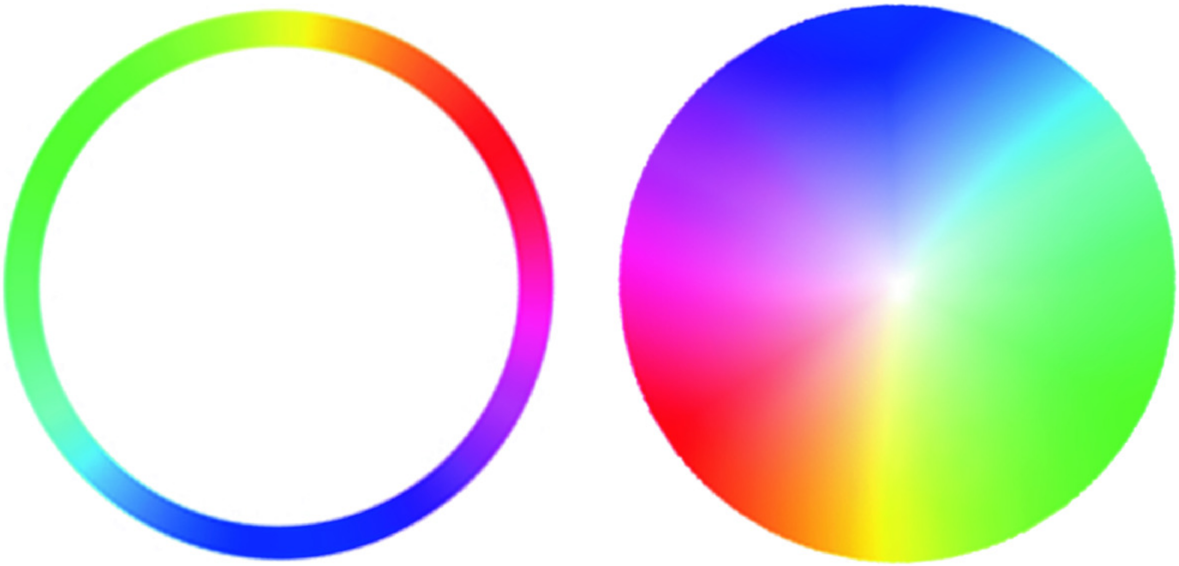


Fig. 4.8 Hue and saturation. Left: pure colors on a ring; right: hue–saturation wheel

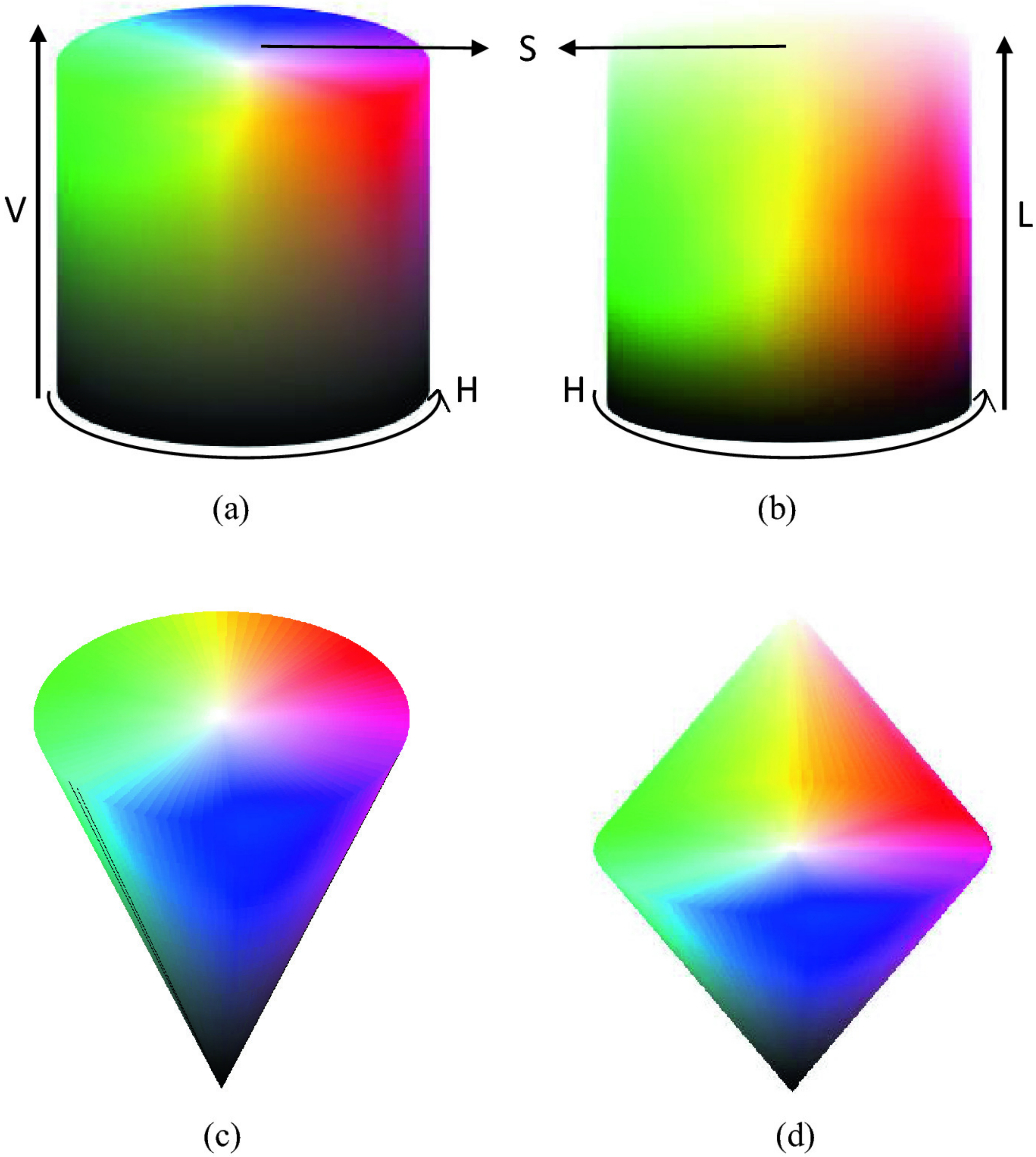


Fig. 4.9 HSV and HSL color spaces. **a** HSV cylinder; **b** HSL cylinder; **c** HSV cone; **d** HSL double cone

It is observed from the value strip of Fig. 4.7b that as colors become darker or brighter, they become less colored; consequently, as shown in Fig. 4.9a, b, colors on the HSV and HSL cylinders become more and more redundant as they go down the cylinders and as they go up the HSL cylinder. Therefore, the actual HSV color space is often shown as a single cone (Fig. 4.9c) while HSL color spaces are often shown as a double cone (Fig. 4.9d). Because every slice of the HSV/HSL cone is colorful, the radiuses of the cone are called *chroma* instead of *saturation*.

Digital images are represented using RGB colors. To derive HSV, HSL and HSI color values, RGB values are normalized into 0–1. Given a (R, G, B) color, the H, S, V values are computed using the following guidelines.

- The hue values are organized into 0° to 360° around a pure color circle, with red color at 0°/360°, green at 120° and blue at 240°.
- To determine the H value of a (R, G, B) color, the maximum of the three values is used to determine the *dominant hue* on the pure color circle and the difference of the other two values tells what side is the RGB color located at the *dominant hue*.
- The value/intensity/lightness of the (R, G, B) color is determined by either the maximum of the three RGB values or the average or in between.
- The saturation of a color is determined by how far the color is from the pure color circle (hue) which has a color saturation of 1. Saturation is given in percentage, e.g., 40%.

Let

$$\begin{aligned} M &= \max(R, G, B) \\ m &= \min(R, G, B) \\ C &= M - m \end{aligned}$$

The maximum of the three RGB values M dominants the *hue* and *brightness* of a color. The C value, called *chroma*, is proportional to *saturation* of a color. With these in mind, HSV values can be computed using the following formulas:

$$H = \begin{cases} 0^\circ & \text{if } M = m \\ 60^\circ \times \frac{G-B}{C} + 0^\circ, & \text{if } M = R \text{ and } G \geq B \\ 60^\circ \times \frac{G-B}{C} + 360^\circ, & \text{if } M = R \text{ and } G < B \\ 60^\circ \times \frac{B-R}{C} + 120^\circ, & \text{if } M = G \\ 60^\circ \times \frac{R-G}{C} + 240^\circ, & \text{if } M = B \end{cases} \tag{4.2}$$

$$S = \begin{cases} 0 & \text{if } M = 0 \\ \frac{C}{M} = 1 - \frac{m}{M}, & \text{otherwise} \end{cases} \tag{4.3}$$

$$V = M \tag{4.4}$$

For *HSL* model:
H is the same as (4.2)

$$L = \frac{1}{2}(M + m) \tag{4.5}$$

$$S = \begin{cases} 0 & \text{if } M = m \\ \frac{C}{2L}, & \text{if } L \leq \frac{1}{2} \\ \frac{C}{2-2L}, & \text{if } L > \frac{1}{2} \end{cases} \tag{4.6}$$

For *HSI* model:
H is the same as (4.2)

$$I = \frac{1}{3}(R + G + B) \tag{4.7}$$

$$S = \begin{cases} 0 & \text{if } I = 0 \\ \frac{I-m}{I} = 1 - \frac{m}{I}, & \text{otherwise} \end{cases} \tag{4.8}$$

HSV values can also be derived using the following formulas:

$$H = \arctan\left(\frac{\beta}{\alpha}\right) \tag{4.9}$$

$$S = \sqrt{\alpha^2 + \beta^2} \tag{4.10}$$

$$V = \max(R, G, B) \tag{4.11}$$

where

$$\alpha = R - \frac{1}{2}(G + B), \quad \beta = \frac{\sqrt{3}}{2}(G - B) \tag{4.12}$$

The H and S components are invariant to lighting variations or intensity changes. Intensity changes are only reflected in the V component, which can be corrected by a linear scaling.

Figure 4.10 shows a color image and its H, S, V channels. In the H image, white and black are starting and arrival points on the color wheel, and they represent red color and yellow color. Gray intermediate levels are corresponding to intermediate hues on the wheel. Both the S and V channels are in the 0 to 1 range. For S channel, white is pure color and black is minimum saturation. For V channel, white is very bright and black otherwise.

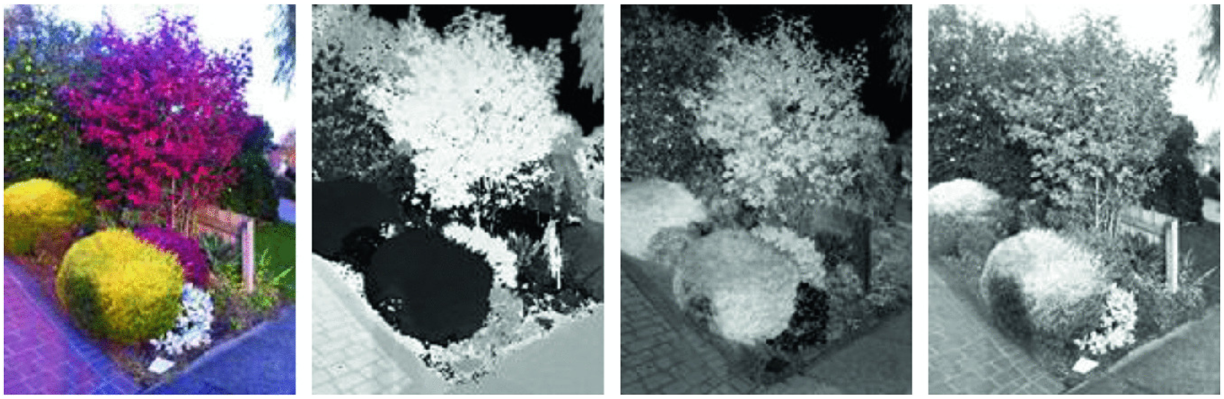


Fig. 4.10 A color image on the left and its H, S, V channels on the right columns

It can be observed from the S and V channels that both the yellow plants at the bottom left of the image are highly saturated and also very bright, while the red leaf tree is highly saturated but with moderate brightness. Notice the shadow at the bottom left of the color image has no to little effect on the H and S channels, and it only affects the V channel.

4.2.4 CIE LUV Color Space

The CIE XYZ color space is non-uniform in terms of color differences, so is RGB color space. Non-uniform means that the calculated difference between two colors is not proportional to their perceived color difference. This phenomenon is shown as MacAdam ellipses in the CIE *xy* gamut in Fig. 4.11. Each ellipse shown in the figure represents colors within the just noticeable difference (JND) threshold. In other words, colors within each ellipse are perceivably the same. As can be seen, the sizes of the ellipses in different areas of the gamut vary significantly. This implicates that colors within certain distance may be perceived as same colors in one area but as different colors in another areas. This causes confusions for many color applications including displaying, image processing and image analysis, which rely on computing color differences.

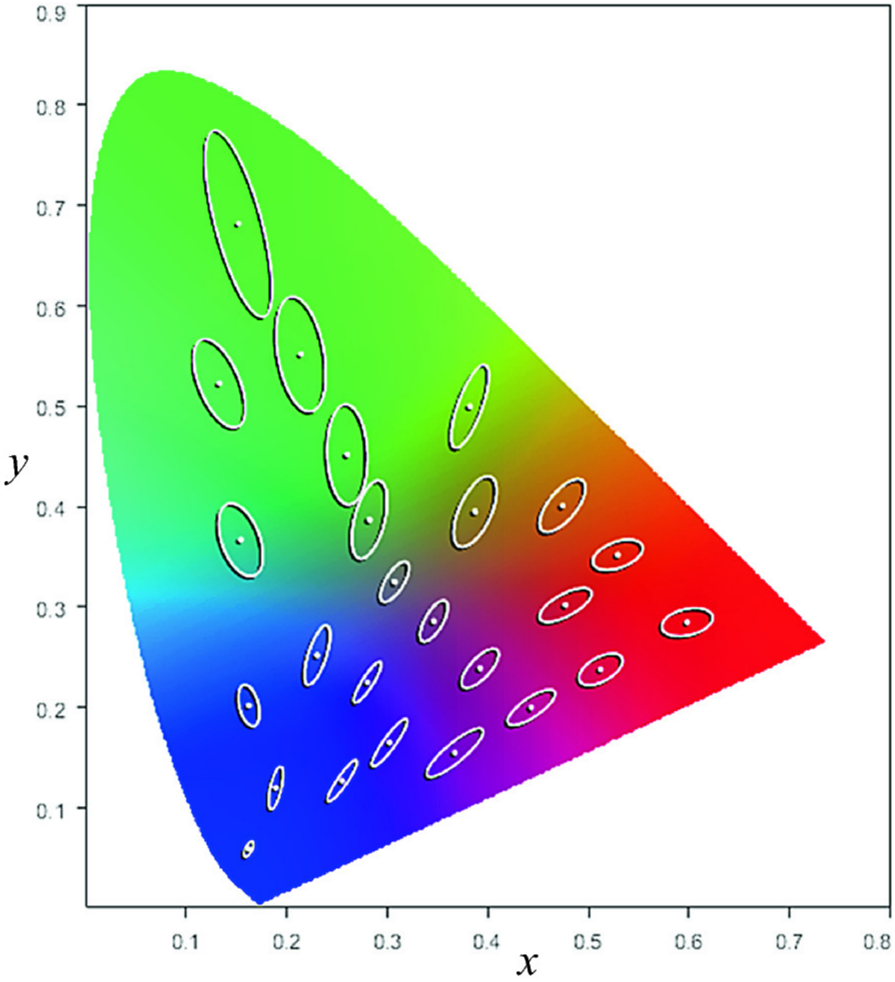


Fig. 4.11 MacAdam ellipses (magnified 10 times) on the CIE *xy* gamut

To overcome the non-uniform color spread problem, CIE *Luv* (1960) and CIE *Lu′v′* (1976) color spaces have been created. Both *Luv* and *Lu′v′* spaces are transformed from CIE XYZ space, and the two color spaces are only different at the *v* component. The idea is to stretch or squeeze the CIE *xy* gamut at certain directions so that the MacAdam ellipses are made to equal size.

$$L^* = \begin{cases} 116\left(\frac{Y}{Y_n}\right)^{\frac{1}{3}} - 16 & \text{if } \frac{Y}{Y_n} > 0.008856 \\ 903.3\left(\frac{Y}{Y_n}\right) & \text{if } \frac{Y}{Y_n} \leq 0.008856 \end{cases} \tag{4.13}$$

$$u = \frac{4X}{X + 15Y + 3Z} = \frac{4x}{3 - 2x + 12y} \tag{4.14}$$

$$v = \frac{6Y}{X + 15Y + 3Z} = \frac{6y}{3 - 2x + 12y} \tag{4.15}$$

$$u' = u, \quad v' = 1.5v \tag{4.16}$$

where Y_n is the luminance of the white point and

$$\left.\begin{aligned} x &= \tfrac{X}{X+Y+Z} \\ y &= \tfrac{Y}{X+Y+Z} \end{aligned}\right\} \tag{4.17}$$

L^* scales from 0 to 100 due to the relative luminance (Y/Y_n) scales from 0 to 1. The cubic root function of L^* is nonlinear and is intended to mimic the *logarithmic response* of human eyes to lightness. The transformed *uv* and *u′v′* gamuts marked with the MacAdam ellipses are shown in Fig. 4.12. It can be seen that the differences between the sizes of the ellipses are considerably reduced (refer to Fig. 4.11).

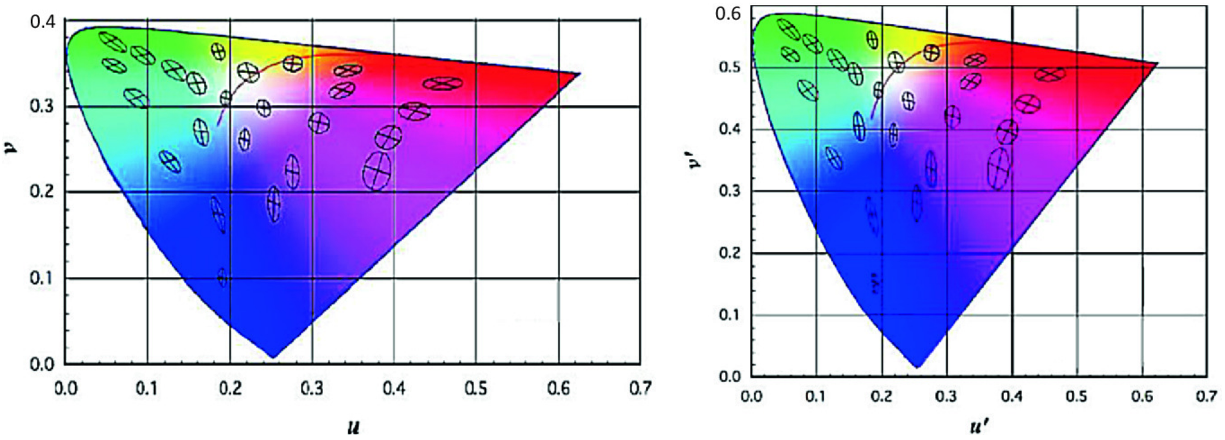


Fig. 4.12 CIE *Luv* and *Lu′v′*. Left: MacAdam ellipses on CIE *uv* gamut; right: MacAdam ellipses on CIE *u′v′* gamut

The non-uniformity can be further reduced by using the $u^* v^*$ chromaticity:

$$u^* = 13L^* (u' - u'_n) \tag{4.18}$$

$$v^* = 13L^* (v' - v'_n) \tag{4.19}$$

where (u'_n, v'_n) are the coordinates of the white point on the (u', v') gamut.

To derive LUV from RGB color space, RGB values are first transformed into XYZ values using the following matrix, where RGB values have been normalized to 0–1.

$$\begin{bmatrix} X \\ Y \\ Z \end{bmatrix} = \begin{bmatrix} 0.4124 & 0.3576 & 0.1804 \\ 0.2126 & 0.7152 & 0.0722 \\ 0.0193 & 0.1192 & 0.9503 \end{bmatrix} \begin{bmatrix} R \\ G \\ B \end{bmatrix} \tag{4.20}$$

Although CIE LUV color spaces are close to uniform color spaces, the source RGB primaries are assumed to be known, so that a specific transform matrix of (4.20) can be used. This can be an issue for image applications, because the source (device) RGB primaries are usually unknown.

4.2.5 Y′CbCr Color Space

Both HSV and LUV color spaces are based on the same idea, i.e., the separation of luminance from chromaticity. This idea has been found ideal and desirable for most of color applications including image processing and feature extraction. Y′CbCr is another such kind of color space which is often used for image compression and representation. The transformation from RGB space to Y′CbCr space is given by the following equation:

$$\begin{bmatrix} Y' \\ \mathrm{Cb} \\ \mathrm{Cr} \end{bmatrix} = \begin{bmatrix} 0 \\ 128 \\ 128 \end{bmatrix} + \begin{bmatrix} 0.299 & 0.587 & 0.114 \\ -0.169 & -0.331 & 0.500 \\ 0.500 & -0.419 & -0.081 \end{bmatrix} \begin{bmatrix} R \\ G \\ B \end{bmatrix} \qquad (4.21)$$

where Y' is the luminance, Cb is the blue component and Cr is the red component. Both RGB values and Y′CbCr values are in the range of [0, 255].

By separating the luminance Y' from the chromaticity Cb and Cr, most of the image information has been concentrated onto Y'. This is ideal for image communication and representation, because each channel can now be treated independently instead of treating all the three channels equally as in the RGB space. For example, more importance can be given to Y' as in many situations. This makes the communication more efficient (e.g., fewer bits for color channels) and representation more compact.

Figure 4.13 shows an example of Y′CbCr channels from a flower image. It can be seen that the Y' channel is basically the gray-level version of the original image, while the Cb and Cr channels are just for the color information, and both Cb and Cr channels contain very little information compared with the Y' channel. In TV broadcast, the Y' channel can be sent out independently to be compatible with the old non-color TVs.

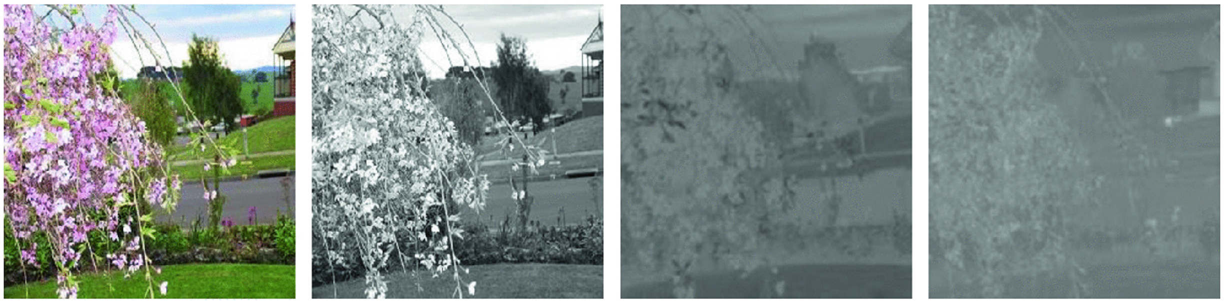


Fig. 4.13 Flower image on the left most and its Y', Cb and Cr channels on the right

4.3 Image Clustering and Segmentation

Digital images are complex data. Unlike textual documents which are made of words from a dictionary of a small vocabulary, there is no visual dictionary or vocabulary for images. Each image consists of thousands to millions of pixels which represent color values, and the possibilities of the pixel colors are almost infinite. Therefore, the first step to analyze an image is usually to group the image pixels into a small number of regions or objects so that further analysis can be carried out, and this is called *image clustering or segmentation*. There are many segmentation and clustering algorithms in the literature; in the next, we discuss two widely used algorithms in image feature extraction.

4.3.1 *K*-means Clustering

One of the simplest segmentation methods is the *K-means* clustering. *K*-means clustering attempts to divide a dataset into *K* clusters with each data point belonging to the cluster with the closest mean, which serves as the centroid of the cluster. The *K*-means clustering algorithm is given as follows.

```
K-means ($K$) {

Input: X = {$\mathbf{x}_1, \mathbf{x}_2, ......, \mathbf{x}_n$}, a set of data points

Output: $C = \{c_1, c_2, ......, c_K\}$, a set of clusters

1. Randomly select $K$ cluster centers or seeds.

2. Calculate the distance between each data point and all the $K$ cluster
   means $\mathbf{m}_k$.

3. Assign the data point to the cluster with the nearest cluster mean.

4. Recalculate the new means for each cluster.
```

5. Repeat from step 2 until no data point needs to be reassigned.

}

K-means clustering algorithm aims at minimizing an objective function known as *sum of squared error* or SSE function, which is given by:

$$J(C) = \sum_{k=1}^{K} J_k \tag{4.22}$$

and J_k is the SSE of the *k*th cluster:

$$J_k = \sum_{i=1}^{|c_k|} (\|\mathbf{x}_i - \mathbf{m}_k\|)^2 \tag{4.23}$$

where $\mathbf{m}_k$ is the mean of cluster c_k and $|c_k|$ is the number of instances in cluster c_k.

K-means is one of the most commonly used clustering algorithms in image processing and analysis. It is especially useful for many color-based clustering such as *color quantization*, which aims to group similar colors and reduce the number of colors in an image. The key issue with a *K*-means clustering algorithm is the parameter *K*. The performance of the clustering depends on a good guess of *K*; however, there is no easy solution. This leads to other more sophisticated algorithms to improve the method.

4.3.2 JSEG Segmentation

JSEG method is based on the believe or assumption that color regions and textures agree each other in an image, which means that a region with similar colors also has similar texture. Based on this idea, the method attempts to find the agreement between the two types of features. The procedure of JSEG is summarized as follows [5]:

- **Color quantization**. At first, pixel colors of the image are quantized into a number of classes using a clustering algorithm such as *K*-means clustering.

- **Color map**. Pixels in the image are then replaced with the color class labels, such as 1, 2, 3, ... A class map is then formed, and region growing is followed on the class map (Fig. 4.14b).

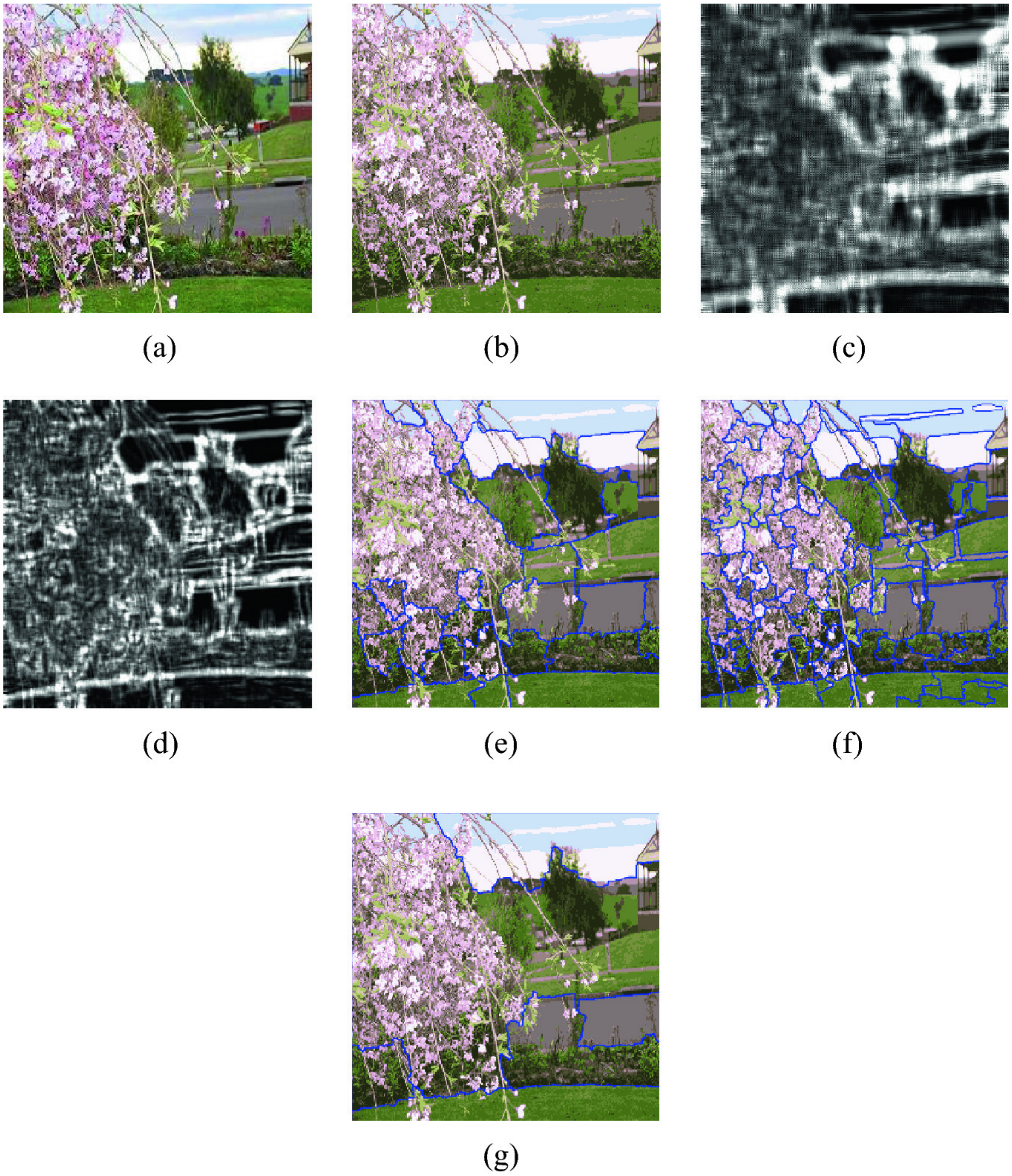


Fig. 4.14 An image segmentation using JSEG. **a** An original color image; **b** result of color quantization with 13 colors; **c** *J*-image at scale 3; **d** *J*-image at scale 2; **e** segmentation result at scale 3; **f** segmentation result at scale 2; **g** final result of segmentation after merging

- **J-image**. The key to JSEG method is the computing of a *J-image* which is computed by moving a local window through each pixel and calculating the SSE over the window (4.23). The SSE is related to the variance over a local neighborhood, and neighborhoods with relatively uniform colors (or little to no texture) tend to have small J values, while neighborhoods with high J values correspond to region boundaries or edges. The window size determines the sharpness of the J-image and the size of the regions that can be detected. The J-image computed using larger local window is more blurred than that computed using smaller window (Fig. 4.14c, d).
- **Region growing**. Based the J-image, a region growing method is carried out starting from areas with the lowest J values. After each region growing, the total J values of each region k (J_k of (4.23)) and the average J values ($\overline{J}$) of all the J_k are computed. The region growing is then repeated using a J-image with smaller scale until the $\overline{J}$ value stops decreasing (Fig. 4.14e).
- **Merging**. The region growing can result in oversegmentation due to texture variations (Fig. 4.14f). Therefore, a merging process is followed by merging J-segmented regions with similar colors (Fig. 4.14g).

Due to the use of both color and texture features and a merging process, JSEG gives a less fragmented segmentation than K-means clustering. However, the performance of JSEG segmentation depends on several parameters, such as the numbers of quantized colors, the seed selection threshold during the region growing and the threshold of color similarity during the region merging. The computation is also very expensive, and the segmentation of a 512 × 512 image can take about 4 min on a PC.

4.4 Color Feature Extraction

4.4.1 Color Histogram

The simplest feature of a color image is its histogram, which describes the color distribution within an image. To create a histogram for an

image, a number of bins (*N*) are first created, and each bin represents a group of similar colors. Each pixel in the image is then examined and put into a bin with similar colors to the pixel. After all pixels in the image are checked, the pixels in each bin are counted and each bin is represented as a value which is the number of pixels in the bin. A bar chart consists of all the *N* bin values created, and it's called a color histogram, which is a sequence of (*c*, *n*) pairs shown in a graph, where *c* is the color of the bin and *n* is the number of pixels in the bin.
Figure 4.15 shows the three color histograms of the R, G, B channels of the Lena image in one graph.

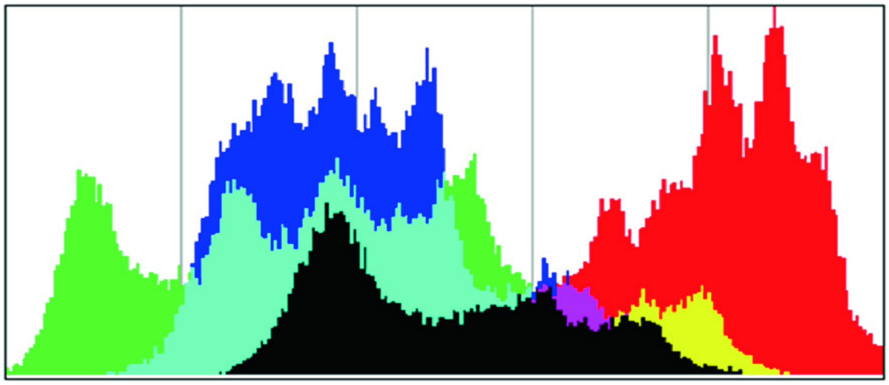


Fig. 4.15 RGB histograms of the Lena color image. Non-RGB colors are the areas of overlap between the R, G, B channels. Each channel is quantized into 256 colors or bins which are on the horizontal axis, and vertical axis shows the number of pixels in each bin or color

In terms of histogram feature extraction, there are three ways to create a histogram for a color image: *component histogram*, *indexed color histogram* and *dominant color histogram*.

4.4.1.1 Component Histogram

The first way is to split a color image into individual R, G, B channels (Fig. 4.16, top row), and each individual channel is equivalent to a gray-level image (Fig. 4.16, bottom row). A contrast with Fig. 4.13 tells that there is a lot of redundancy or correlation between R, G and B channels. A histogram is first created for each individual channel. The three individual channel histograms can then be concatenated into a single histogram. If each individual color channel is represented by l, m and n bins, respectively, the final histogram will have $N = l + m + n$ bins.

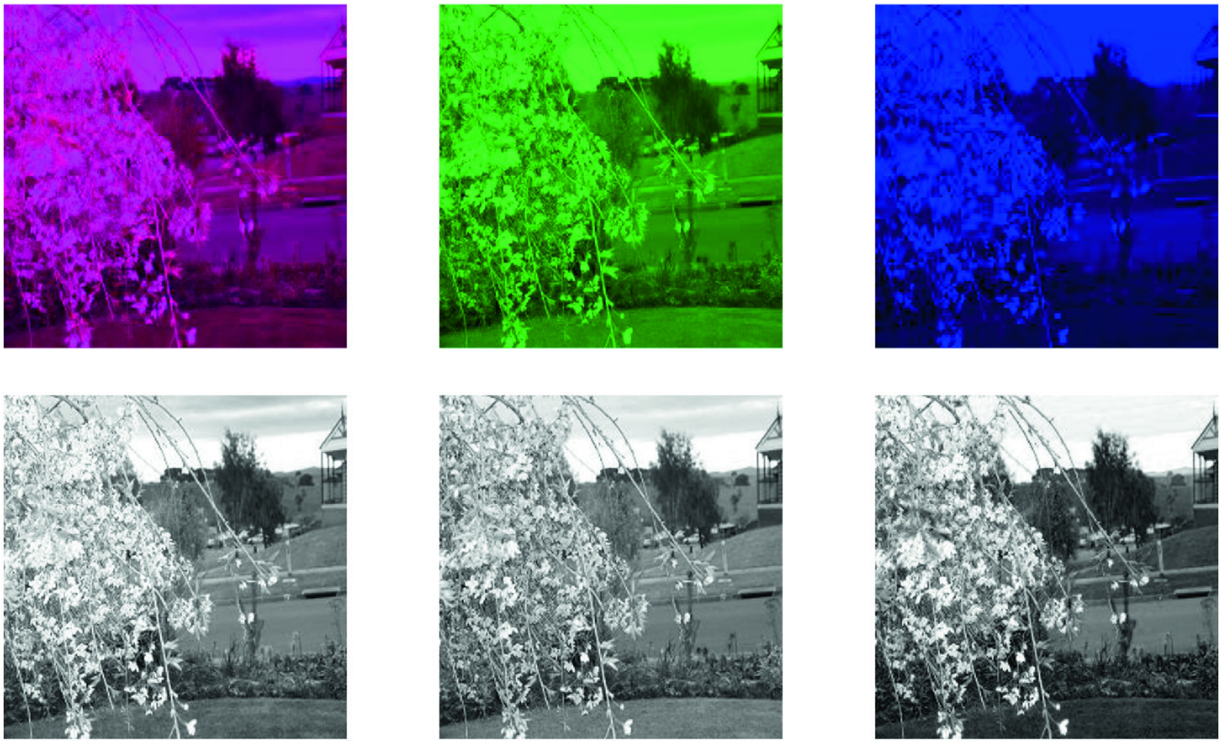


Fig. 4.16 RGB channels of a color image. Top row: R, G, B channels of the flower image; bottom row: corresponding gray-level images of the R, G, B channels at the top row

For example, for Lena image in Fig. 4.15, each R, G, B channel is represented by 8 bits and a total of 256 colors/bins. By concatenating the three histograms, the final histogram would have $N = 3 \times 256 = 768$ bins. This is, however, too long for image representation; therefore, colors of each individual R, G, B channel are usually quantized to reduce the number of colors.

To quantize the color channels, colors in each channel are divided into equal intervals and each interval is used as a bin. For example, to create a 4-bin histogram for R channel, the 256 colors in R channel are divided into the 4 intervals: (0, 63), (64, 127), (128, 191) and (191, 255). Figure 4.17 shows a 216-bin histogram by quantizing each of the R, G, B histograms in Fig. 4.15 into 72 bins. This is less than one-third of the length of the histogram without color quantization.

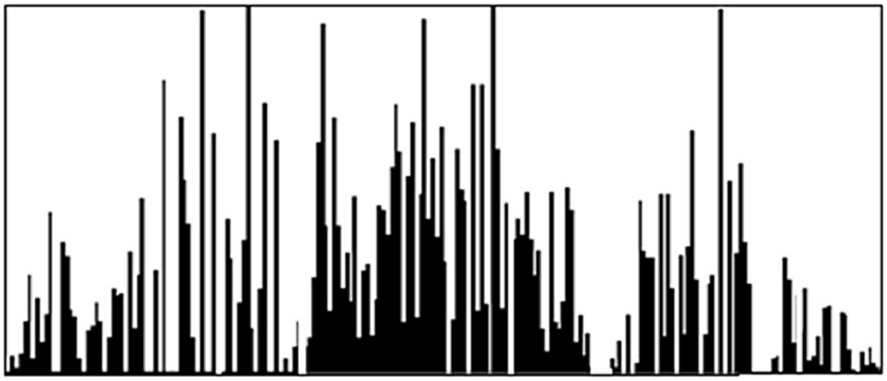


Fig. 4.17 Concatenation of histograms of individual R, G, B channels into a single histogram (216 bins, 72 bins for each channel)

4.4.1.2 Indexed Color Histogram

Another way to create a color histogram is to quantize the RGB color space (instead of each color plane) into N colors and use the N colors as bins to create a color histogram. This is equivalent to indexed colors, and the N colors are equivalent to a global color palette, i.e., a palette representing all image colors or a palette for all the images in the world.

To quantize the RGB color space, the R, G, B planes are divided into l, m, n intervals respectively using the same way as in the first method, the RGB color space (a big cube) is then divided into $N = l \times m \times n$ small color cubes (Fig. 4.6). Each small cube represents a group of similar colors and is used as a histogram bin.

To create a histogram for a color image using the indexed colors, each pixel in the image is examined and put into a bin with similar colors to the pixel. A histogram is then created by counting the number of pixels in each of the bins. Figure 4.18a shows the flower image with 216 quantized or indexed colors, and the 216-bin histogram for the quantized color image is shown in Fig. 4.18b.

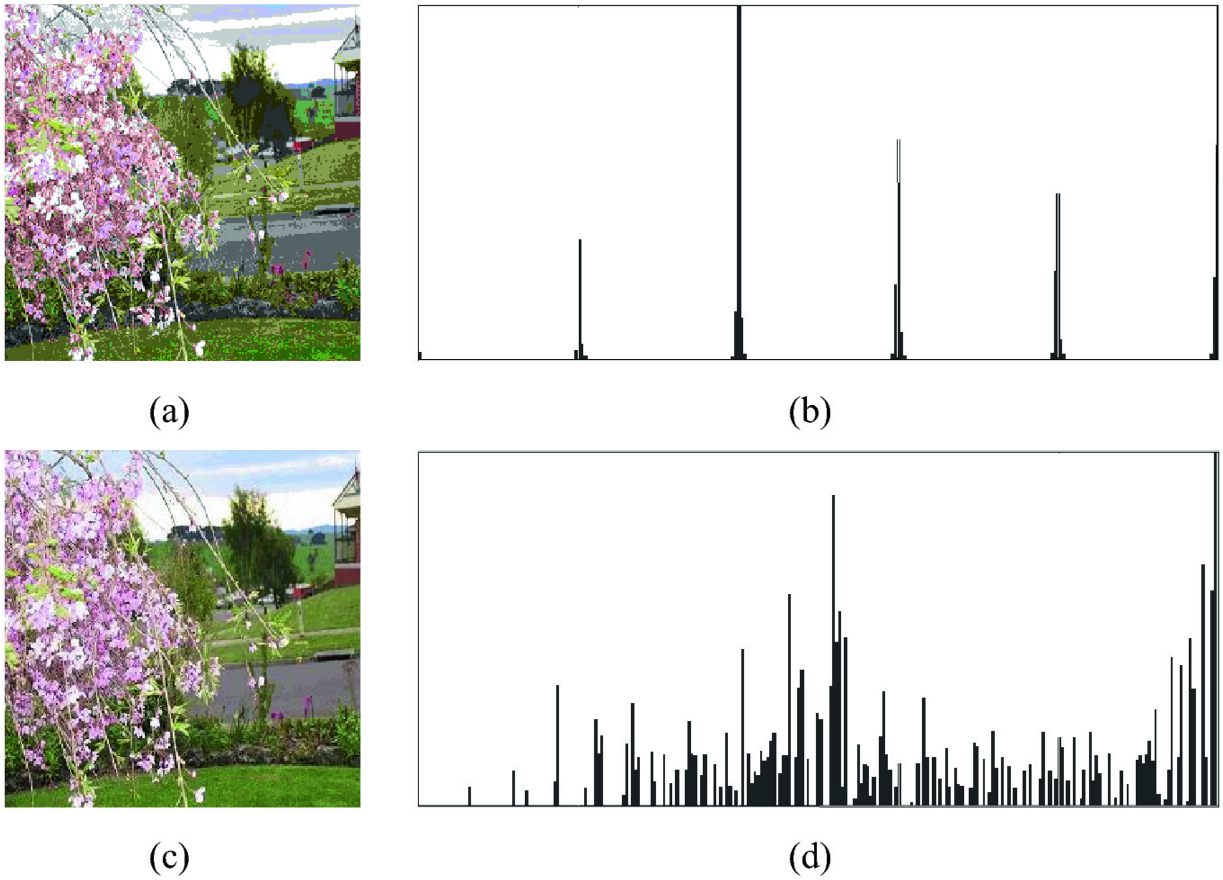

(a) (b)
(c) (d)

Fig. 4.18 Indexed color histograms of a color image. **a** The flower image quantized with a global palette of 216 indexed colors (notice the visible distortion on the sky and grass); **b** indexed color histogram of **a** (216 bins); **c** the flower image quantized with an adaptive palette of 216 indexed colors; **d** dominant color histogram of **c**

4.4.1.3 Dominant Color Histogram

A histogram created from a global palette (a single fixed palette for all images) is usually sparse (Fig. 4.18b), this is because when a global palette is used, most of the colors in an image are often missing from the color representation, and this effect is shown up in both the quantized image and the color histogram (Fig. 4.18a, b). In practice, an adaptive or native palette created from the image itself can be used, and a histogram created from *adaptive indexed colors* is essentially a *dominant color histogram*. Figure 4.18c, d shows the flower image quantized with an adaptive palette of 216 colors and its histogram. Dominant colors can be obtained by either using a histogram thresholding or using a *K*-means clustering.

A histogram is invariant to translation and rotation changes, and scale invariance can be achieved by normalizing each bin value with the total number of pixels in the image. The key issue with a histogram is the difficulty to determine the number of bins. If the number of bins is too small, the colors in a bin can vary so much that it causes too much confusions during the matching. On the other hand, if the number of bins is too large, it causes overfitting, means there are too few pixels in a bin, and this too can cause confusions during the matching. In practice, there is always a compromise on the number of bins. Regardless, features based on color histograms usually have very high dimensions; e.g., 512 and 1024 dimensions are common.

Another issue with the histogram method is that a color histogram does not tell pixels' spatial information. Therefore, visually different images can have similar color histograms. This is undesirable for image representation. A number of other color feature extraction methods have been designed to address these two issues, and they are discussed in the next.

4.4.2 Color Structure Descriptor

One of the key drawbacks of a histogram is the absence of spatial information of pixel colors in an image. The spatial information of pixel colors tells the patterns of colors, or how colors are spread out inside an image. Without the spatial information of pixel colors, perceptually different images can have the same histogram and this can lead to incorrect image retrieval or classification. For example, Fig. 4.19 shows two perceptually different binary images with the same size and the same number of red pixels. The image on the left is visually structured, and the red color is perceived as a regular shape; in contrast, the image on the right is visually unstructured and the red color is perceived as being cluttered. However, the two images have exactly the same color histogram.

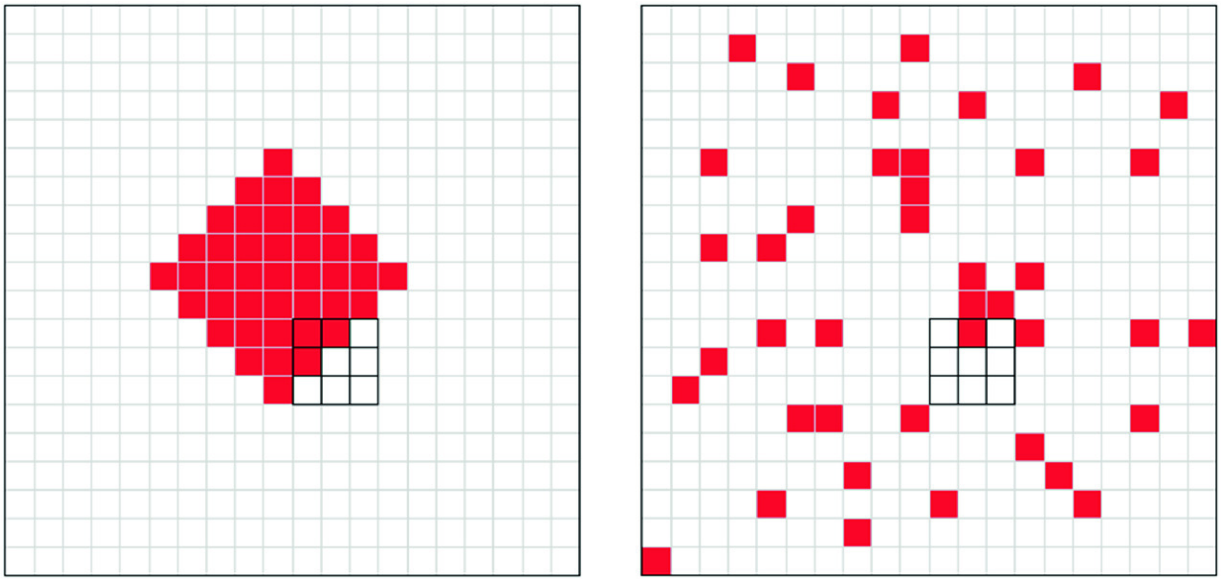


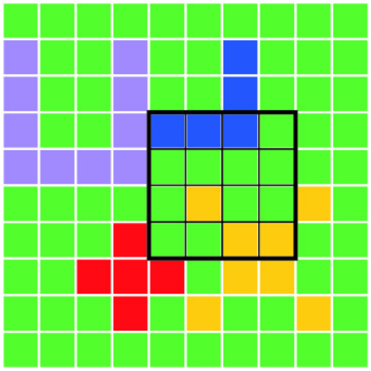
Fig. 4.19 Computation of color structure descriptor. Left: a color image with a 3 × 3 structure moving through the image. The structure captures the red color 56 times; right: a color image with a 3 × 3 structure moving through the image. The structure captures the red color 218 times

One solution to detect color patterns inside an image is to use a structure element or window as the color picker instead of the pixel color picker/counter used in the ordinary histogram computation. When the window moves throughout an image, only the *colors* (e.g., white, red, gray, brown, etc.) inside the window are counted instead of counting the *pixels* of each color inside the window. The histogram created in this way is called color structure (CS) histogram. A CS histogram has a *multiplying* effect on the counting of isolated or scattered colors; the larger the structure window is used, the more the counting is multiplied. On the oher hand, the CS histogram only has a mild over-counting of grouped or clumped colors.

For example, in Fig. 4.19, both images have 41 red pixels; however, by moving a 3 × 3 structure window throughout the images, the red color in the right image is counted for 218 times, while the red color in the left image is only counted for 56 times. The large difference of the two figures accurately reflects the sharp difference of the two red patterns.

To create a CS histogram for an image, the image is first converted to HSV color space and is quantized into a smaller number of colors, e.g., 256, 128, 64 or 32 colors. A structuring element (e.g., square) is then moved throughout the image. Bin *i* of the histogram records how many times the structuring element captures at least one pixel with color *i*. If the window is of size 1 pixel, the CS histogram is just an ordinary histogram. In this sense, the ordinary histogram is just a special case of a CS histogram.

For example, the left-hand side of Fig. 4.20 shows a color image with 5 colors and the 4 × 4 window (black) capturing three types of colors: blue, green and brown [6]. The right-hand side shows how the CS histogram accumulates the three colors (green, blue and brown) captured by the window into corresponding histogram bins (1, 2 and 4). The CS histogram is then normalized with total number of counts of the histogram, and the normalized CS histogram is the CSD.



(a)

Colour	Bin Count
Colour$_1$ 🟩	h (1) +1
Colour$_2$ 🟦	h (2) + 1
Colour$_3$ 🟪	h (3)
Colour$_4$ 🟨	h (4) + 1
Colour$_5$ 🟥	h (5)

(b)

Fig. 4.20 Accumulation of color structure descriptor. **a** A 5-color image and a 4 × 4 structuring element. **b** The accumulation of color structure histogram at a particular position of the structuring element in the image

It can be expected that the CSD is more robust than an ordinary histogram, because it captures the information about local spatial structure as well as the color distribution of an image. The spatial information makes the CS histogram sensitive to certain color patterns to which an ordinary histogram is blind.

Furthermore, a CSD uses a window of size greater than 1 pixel, and it is less susceptible to noise. However, the performance of CSD depends on the size and structure of the window. Scale invariance can only be achieved by varying the size of the structure element and doing a best match between two images. Rotation invariance can be achieved by using a circular element instead of a squared one.

4.4.3 Dominant Color Descriptor

It is understood that an image is visually interpreted based on a few dominant colors. Those other colors are either noise or just for details, and they are not important and can be ignored. Therefore, a dominant color histogram will better describe an image than a common histogram. The *dominant color descriptor* (DCD) is just based on this idea, and it's a variation of a common histogram.

To derive a DCD, a histogram h of all colors (without quantization) in an input image I is first created. A thresholding is then applied to h to eliminate those bins whose values are less than a threshold τ. The remaining n colors are called dominant colors. Each dominant color is represented as $(\mathbf{c}_i, p_i)$, $i = 1, 2, \ldots, n$, where $\mathbf{c}_i$ is a 3D color vector and p_i is the percentage of pixels in the image having color $\mathbf{c}_i$. A DCD is just the n dominant colors in a sequence:

$$\mathrm{DCD} = \{(\mathbf{c}_i, p_i),\ i = 1, 2, \ldots, n\} \tag{4.24}$$

The DCD significantly reduces the dimensions of a color histogram, but it still does not address the absence of spatial information from the colors. Therefore, an image is usually segmented into regions and a DCD is extracted from each region of the image.

The number of selected dominant colors in a region depends on the threshold τ. However, statistics based on more than 36,000 image regions show that over 98% of image regions can be described by no more than 4 DCDs (Fig. 4.21) [6–8]. MPEG-7 recommends 1–8 DCDs for each image region.

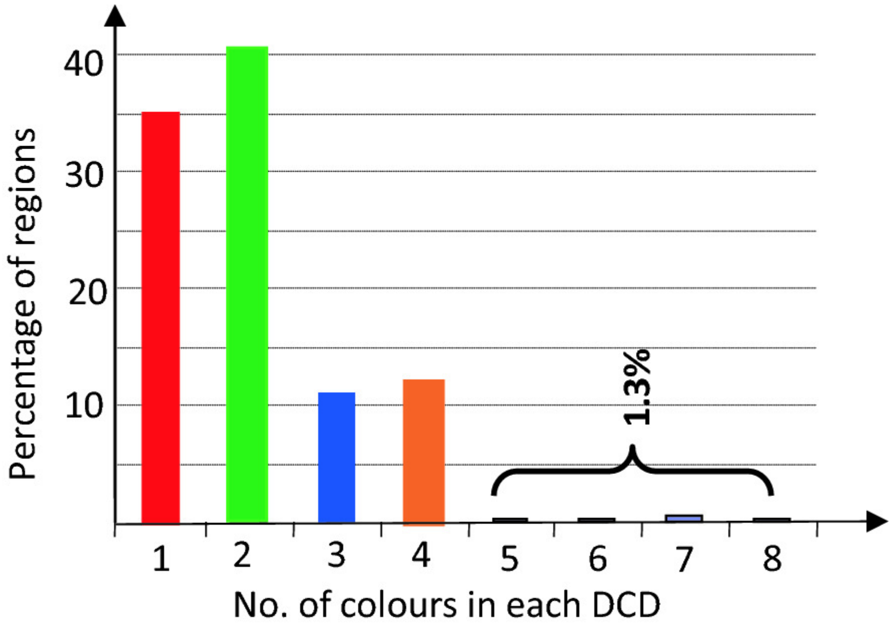


Fig. 4.21 Statistics of DCD numbers from 36,692 regions

Figure 4.22 shows some examples of the segmented image regions and their corresponding DCDs [6–8].

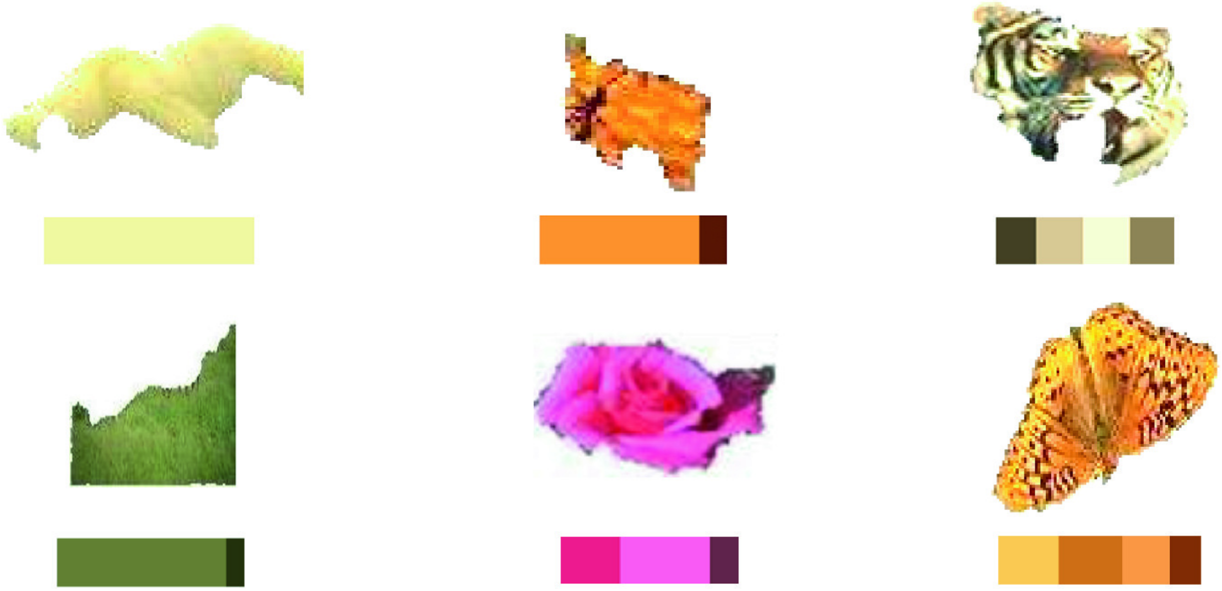


Fig. 4.22 Segmented regions and their dominant colors underneath. The dominant colors are shown according to their percentages in the region

Small proportions of colors in a DCD are usually due to segmentation errors or region boundary, and they can be discarded without affecting performance. Figure 4.23 shows a few segmented regions and their corresponding DCDs after discarding insignificant colors [6–8].

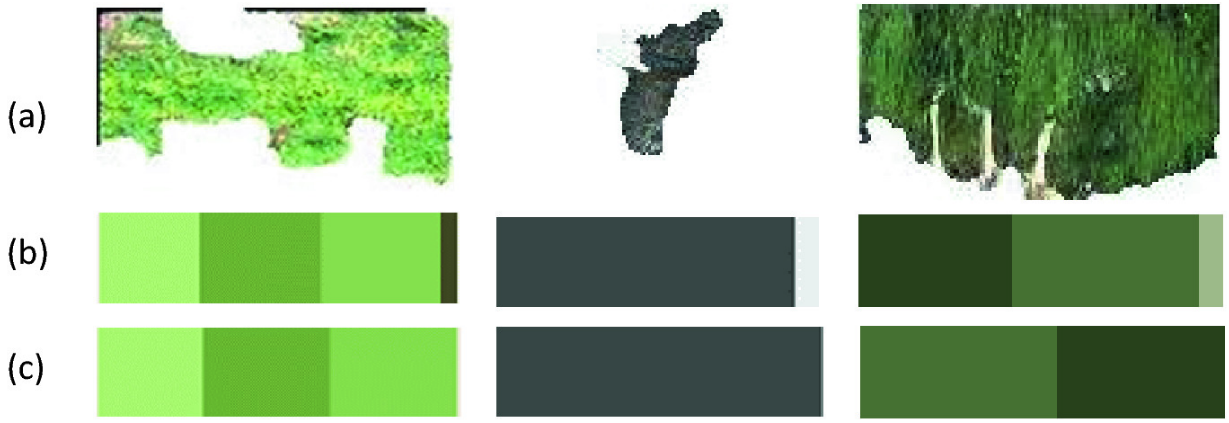


Fig. 4.23 Removal of noisy colors from segmented regions. **a** Three sample regions; **b** dominant colors of corresponding regions above; **c** DCDs after discarding insignificant colors from **b**

Region-based DCDs are not only compact but also reflect spatial information in an image, and they are a desirable representation for color images. However, unlike conventional color histogram, the order of colors and the number of colors in two DCDs are usually not the same, and the matching of two DCDs needs to use many-to-many quadratic matching (12.18).

DCDs can be easily translated into color names which can be used to describe color images. Human beings tend to describe the visual world using color names, and we can only describe a few hundreds of colors. It is possible to annotate an image with color names based on DCDs [9].

4.4.4 Color Coherence Vector

An ordinary histogram does not tell spatial information about the colors in a bin. The *color coherence vector* (CCV) is a method to incorporate spatial information into a conventional histogram. The idea is to divide each histogram bin into two components: coherent (C) and non-coherent (N). The coherent component includes those pixels which are spatially connected, while the non-coherent component includes those pixels that are isolated. A CCV can be computed by using the following procedure:

1. Create a conventional histogram H of k bins for image I using a method in Sect. 4.4.1.

```
2. For each of the histogram bins $B_i$ in $H$
    2.1. Create a binary image $I_i$ from $I$ by marking all pixels with color $B_i$ as 1 (white) and others as 0 (black).
    2.2. Set $j = 0$.
    2.3. For each white pixel $p$ in $I_i$
        2.3.1. If $p$'s west, northwest, north and northeast are all black.
            2.3.1.1. Create a new region $R_j$.
            2.3.1.2. $R_j = R_j + p$.
            2.3.1.3. $j = j + 1$.
        2.3.2. Otherwise, $R_j = R_j + p$.
    2.4. For each region $R_j$
        2.4.1. Count the total number of pixels $n$ in $R_j$.
        2.4.2. If $n \geq \tau$, $C_i = C_i + n$                // $\tau$ is a threshold.
        2.4.3. Otherwise, $N_i = N_i + n$.
3. The normalized sequence $\{(\frac{C_i}{|I|}, \frac{N_i}{|I|}), i = 1, 2, \ldots, k\}$ is the CCV.
```

By dividing each histogram bin into coherent colors and incoherent colors, CCV captures spatial information in an image, and it usually performs better than a color histogram. However, the dimension of a CCV is twice of that of a conventional histogram.

4.4.5 Color Correlogram

A color *correlogram* is the color version of *gray-level co-occurrence matrix* (Sect. 5.2.2) which is used for texture feature extraction. It characterizes the distribution of color pairs in an image. A color correlogram can be viewed as a 3D histogram where the first two dimensions represent the colors of any pixel pair and the third dimension is their spatial distance. Thus, in a correlogram, each bin (i, j, k) represents the number of color pairs (i, j) at a distance k.

An input image I is first quantized into m colors $\{c_1, c_2, \ldots, c_m\}$. The computation of a color correlogram is then to find the probability of pixel pairs (p_1, p_2) which meet the following two conditions:

(a) $C(p_1) = c_i$ and $C(p_2) = c_j$

(b) $|p_1 - p_2| = k$

where $C(p_i) = c_i$ means the color of p_i is c_i.

Mathematically, each element of a correlogram is given by

$$\gamma^{k}_{c_i,c_j}(I) = Pr\{(p_1, p_2)\,|C(p_1) = c_i, C(p_2) = c_j \text{ and } |p_1 - p_2| = k\} \tag{4.25}$$

If $c_i = c_j$, (4.25) becomes an autocorrelogram which is the probability of finding identical colors at distance k:

$$\alpha^{k}_{c} = r^{k}_{c,c}(I) \tag{4.26}$$

Figure 4.24 shows an example of computing a color correlogram [6]. The color correlogram in Fig. 4.24 is calculated for $k = 1$. Correlograms for other distance $k \in \{1, 2, \ldots, d\}$ can be calculated in similar way.

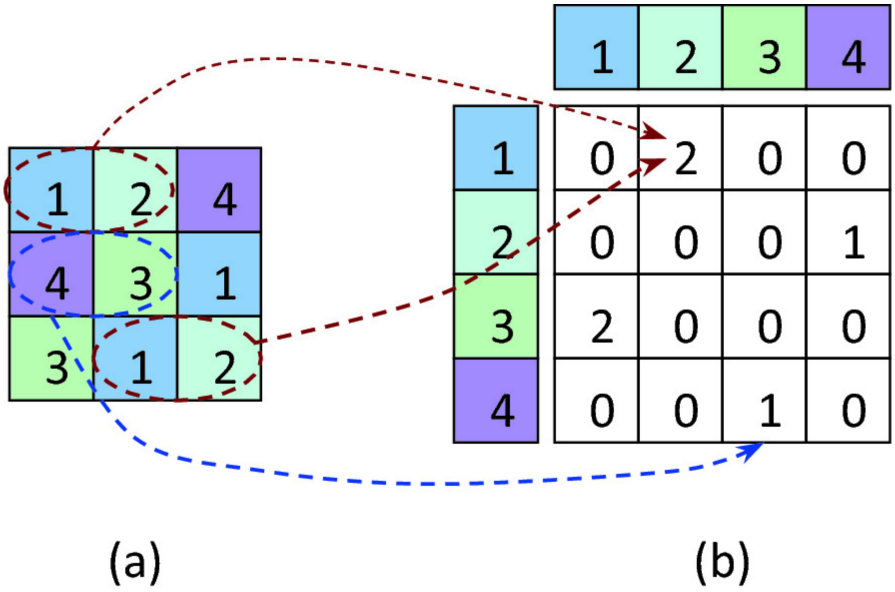


Fig. 4.24 Computation of color correlogram. **a** A 4-color image; **b** the color correlogram of **a** for horizontal distance $k = 1$

In total, d correlograms (matrices) can be computed from an image. If the colors are globally quantized, i.e., colors of all images are quantized using a single global palette, two corresponding correlograms from two images can be matched element by element. However, if a local (adaptive) palette is used to quantize each image, either a many-to-many matching is needed or the matching is done through statistics computed from the correlogram matrices (Sect. 5.2.2).

Matching between two color correlograms involves matrix matching which is expensive. In practice, however, only autocorrelograms are used because they are sufficient to produce a good result. Autocorrelograms of each color form a d-dimensional vector, which can be matched using a conventional distance such as L_1 [10].

The performance of the color correlogram is better than the CCV because it captures not only the special information but also the patterns of the spatial information.

4.4.6 Color Layout Descriptor

It is well know that a spectral transform can capture the frequency of texture changes in an image, and the frequency information is used for identifying most important information from the image. This idea can also be used to capture the frequency of color changes in an image. The *color layout descriptor* (CLD) is just based on this idea.

The computation of CLD consists of four stages: image partitioning, color quantization, DCT transform and zigzag scanning.

- **Image partitioning**. In the first stage, an input image I is divided into an 8 × 8 grid of 64 blocks. If the size of the input image is $M \times N$, then the size of each block of the grid will be $(M/8) \times (N/8)$. The reason to divide all images into equal number of blocks is to ensure resolution or scale invariance.
- **Color quantization**. In the second stage, a single dominant color is computed from each block. The DCD method in Sect. 4.4.2 can be used for the dominant color extraction, but the simplest method is to use the *average* of pixel colors as the representative color. Once the color of each block is quantized, the input image I is converted into an 8 × 8 color image I_q.
- **DCT transform**. In the third stage, the RGB colors of I_q are converted to Y′CbCr colors (4.21). Then, each of the three Y′CbCr channels of I_q is transformed by an 8 × 8 discrete cosine transform or DCT, so three sets of 64 DCT coefficients are obtained.
- **Zigzag scanning**. In the final stage, three sets of 64 DCT coefficients are zigzag scanned, respectively, and the first few coefficients of each set, e.g., 4–8, are chosen. The selected coefficients are then organized into (DY′, DCb, DCr) which is used as the CLD. The reason of only choosing the first few coefficients is because they represent the low-frequency information of the image and they are the most significant coefficients; the remaining coefficients are too small and can be neglected.

CLD allows scalable representation of an image by controlling the number of selected coefficients. MPEG-7 recommends to use a total of 12 coefficients, 6 for luminance and 3 for each chrominance, for most of the images. CLD is both compact and scalable; however, it is not robust to rotation change.

4.4.7 Scalable Color Descriptor

As can be seen from the CLD above, a spectral transform like DCT can dramatically reduce the data dimension. This idea can also be used to reduce histogram dimension. A histogram can be regarded as a 1D time series with fluctuations in vertical direction. Each histogram has a unique pattern of fluctuations or changes along the horizontal direction. This pattern can be effectively captured by using efficient 1D wavelet transform. Because coefficients from a wavelet transform are scalable, i.e., the number of selected coefficients depends on requirement or applications, the result of the wavelet transform is a *scalable color descriptor* or SCD. A SCD is derived using the following procedure.

- **RGB to HSV**. An input image is first converted from RGB color space to HSV color space.
- **Color quantization**. The HSV color space is quantized into 256 colors by dividing the H, S and V channels into 16, 4 and 4 intervals, respectively. A 256-bin color histogram is then created for the image.
- **Bin value quantization**. Each bin value is then nonlinearly quantized into a 4-bit integer to give high significance to small values.
- **Haar wavelet transform**. The histogram is then applied with Haar wavelet transform. Each round of Haar wavelet is a two-pass transform, i.e., low pass and high pass. The low pass of Haar wavelet transform takes two neighboring bins and calculates their sum, while the high pass calculates their difference. Therefore, after the first round, two histograms with half of the original histogram length are obtained: a summed histogram and a differenced histogram. Repeat the transform on the summed histogram for a number of rounds until the two histograms are shortened to the desired length, e.g., 64, 32 or 16 bins.
- **SCD formation**. The final results from the wavelet transform are two short histograms: a summed histogram and a differenced histogram. The two histograms are concatenated to be used as the SCD. However, due to the values of the differenced histogram bins are so small, the magnitudes of the bin values are discarded and only the signs of the bins are kept. The sign patterns are sufficient to retain the finer details of the original histogram.

SCD is useful for applications which need short or compact histogram features; however, it does not include spatial information as other color descriptors such as CLD; therefore, it’s performance is generally lower.

4.4.8 Color Moments

It is well known in data analysis community that descriptive statistics provide a good summary of a dataset and provide a quick understanding of the characteristics or distribution of the dataset such as central tendency, variability and skewness. An image is just a set of color pixel data; therefore, it can also be described by the mean, variance, skewness, etc., which are called *color moments* (CM).

To compute color moments, an input image I is decomposed into individual channels, such as R, G, B channels or H, S, V channels. The moments are then computed from each channel using the following equations.

$$M_1 = \frac{1}{N}\sum_{i=1}^{N} p_i \tag{4.27}$$

$$M_r = \left(\frac{1}{N}\sum_{i=1}^{N} (p_i - M_1)^r\right)^{\frac{1}{r}} \tag{4.28}$$

where

- N is the total number of pixels in image I;
- r is the order of a color moment, $r = 2, 3, \ldots$;
- p_i is the ith pixel value in the color channel;
- M_1 is the first-order color moment or the mean color of the color channel;
- M_2 is the second-order color moment or the variance of the color channel;
- M_3 is the third-order color moment or the skewness of the color channel.

Color moments can also be computed from a color histogram h using the following equations.

$$M_1 = \sum_{k=1}^{K} h_k C_k \tag{4.29}$$

$$M_r = \left(\sum_{k=1}^{K} h_k \left(C_k - M_1 \right)^r \right)^{\frac{1}{r}} \tag{4.30}$$

where

- h_k is the value of the kth bin of histogram h;
- C_k is the color of kth bin of histogram h;
- K is the number of bins of h_q;
- r is the order of a color moment: 2, 3, …

Typically, only the first three order color moments are computed for a color channel or an image. If three color moments are computed for each color channel, the moments from each of the three channels are concatenated to form a 9-dimensional feature vector which is used to describe the image.

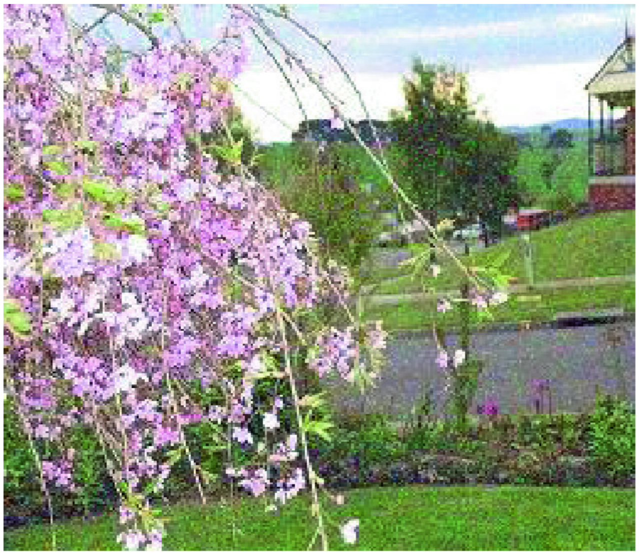
Color moments are a very concise description of an image; however, it can be very inaccurate; e.g., the mean or average color of an image is usually a very coarse description of the image color. Furthermore, color moments do not tell the spatial information of the colors. Therefore, color moments are usually calculated for image regions.

4.5 Image Enhancement

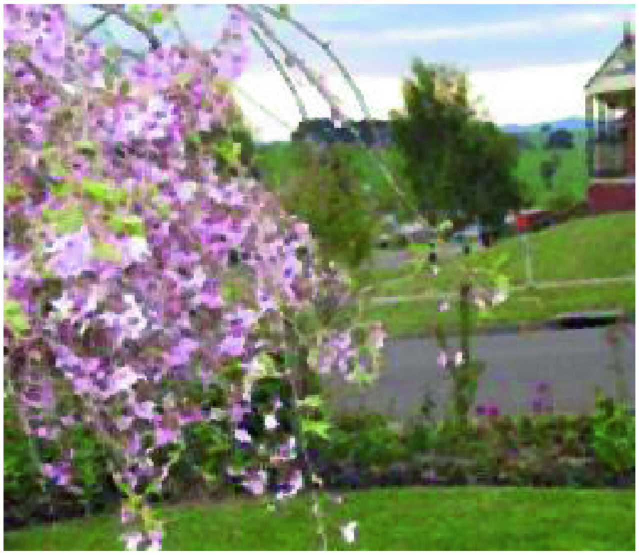
Images are often corrupted with noise due to poor capturing devices and lighting conditions. The noise affects both image segmentation and feature extraction results. Many images are also either too dark or too bright due to poor lighting conditions during the capturing. The poor lighting can have significant effect on accurate feature extraction. Both noise and poor lighting issues need to be addressed before segmentation and feature extraction.

4.5.1 Noise Removal

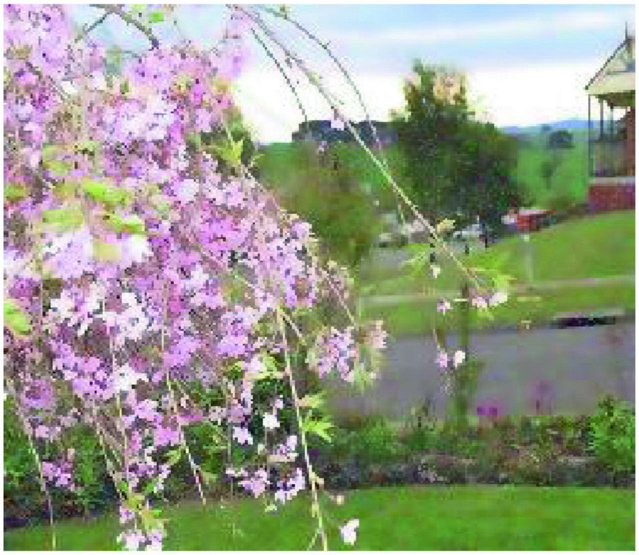
Filtering is commonly used to improve the quality of noisy images. An image corrupted with noise can be corrected or improved by using either a *median filter* or a *Gaussian filter*. Figure 4.25a shows a flower image corrupted with noise, Fig. 4.25b shows the image corrected with a 3 × 3 median filter and Fig. 4.25c shows the image corrected by a Gaussian filter with $\sigma = 2$. It can be observed that the Gaussian filter gives a better result than the median filter. However, both the filtered images can improve the image segmentation and feature extraction.



(a)



(b)



(c)

Fig. 4.25 **a** An image corrupted with noise; **b** the image after a median filter; **c** the image after a Gaussian filter

4.5.2 Contrast Enhancement

Contrast enhancement is a technique to correct images taken under poor lighting conditions, e.g., either too dark or too bright. A traditional approach to enhance the contrast of an image under poor lighting condition is to threshold an image histogram using a binary thresholding function (a 0–1 or step function), which is shown as black in Fig. 4.26. While a binary thresholding can enhance contrast of a poorly captured image, it however also removes the colors and most of the texture information from the image. A much better solution in this case is to first normalize an image histogram to a distribution function by dividing the total number of pixels into the image and then use the cumulative distribution function (*cdf*) as the thresholding function to scale each level of pixel values. Compared with the 0–1 function, the *cdf* is a continuous and incremental function (shown as a blue curve in Fig. 4.26) which is ideal to keep both the colors and texture information after the thresholding. This is because both the colors and texture information are captured by the intermediate levels of image values, which are well kept in the continuous *cdf*.

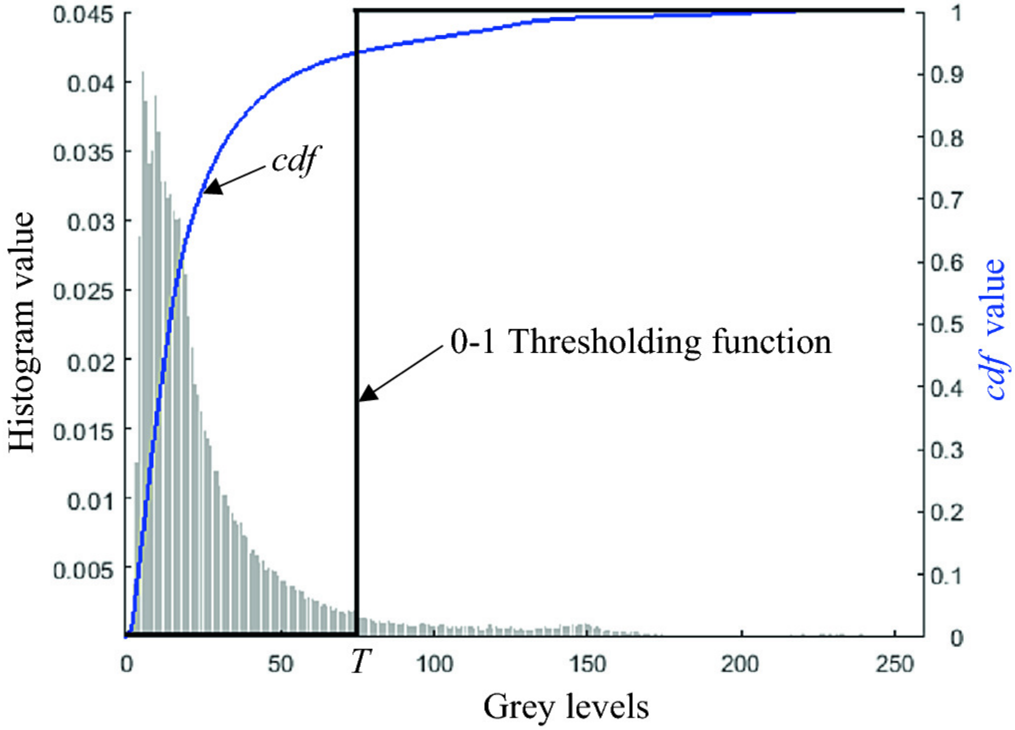


Fig. 4.26 Binary thresholding (black) and *cdf* thresholding (blue) of an image histogram

For example, Fig. 4.26 shows the histogram of a dark image, the *cdf* climbs rapidly at lower gray levels, and in other words, the rate of vertical increase is several times higher than that of horizontal increase. Therefore, by using *cdf* values to scale the gray levels (horizontal), the lower gray levels (dark pixels) are raised significantly and spread to medium gray levels. For example, in Fig. 4.26, pixels with a gray-level value of 5 will be scaled to 0.1 × 255 = 25.5 and pixels with a gray-level value of 6.5 will be scaled to 0.2 × 255 = 55. Other pixel values are similarly raised and spread to the higher gray levels. For images with too many bright pixel values, pixel values are lowered and spread to the left by *cdf* scaling. The result of this *cdf* scaling is that the pixel values after scaling are more evenly spread across all the gray levels rather than squeezing into a small range of gray levels. In the literature, this is called *histogram equalization*. For a color image, the *cdf* scaling is done to each of the three channels.

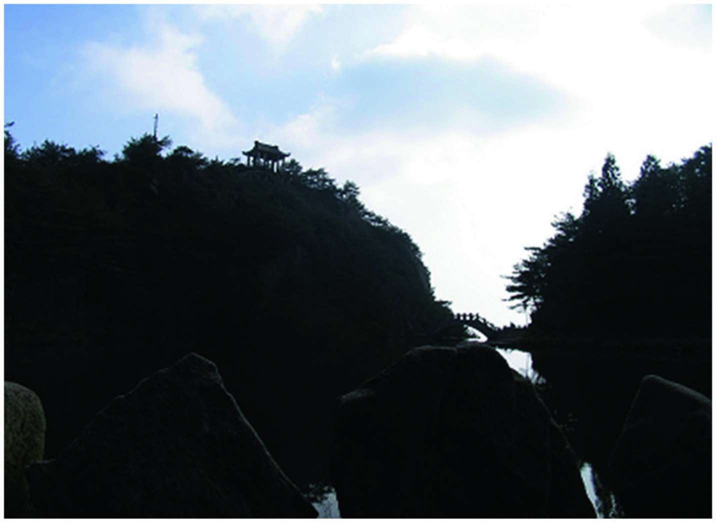
In case of an image having significant number of black pixels, the *cdf* of the image is greater than 0. This implicates the normalized image would not have black pixels if the *cdf* were to be used for pixel value normalization. To include the black level and further increase the contrast of the *cdf* normalized image, the following formula is used in an actual *cdf* thresholding:

$$h(l) = \mathrm{round}\left(\frac{cdf(l) - cdf_{\min}}{cdf_{\max} - cdf_{\min}} \times 255\right) \tag{4.31}$$

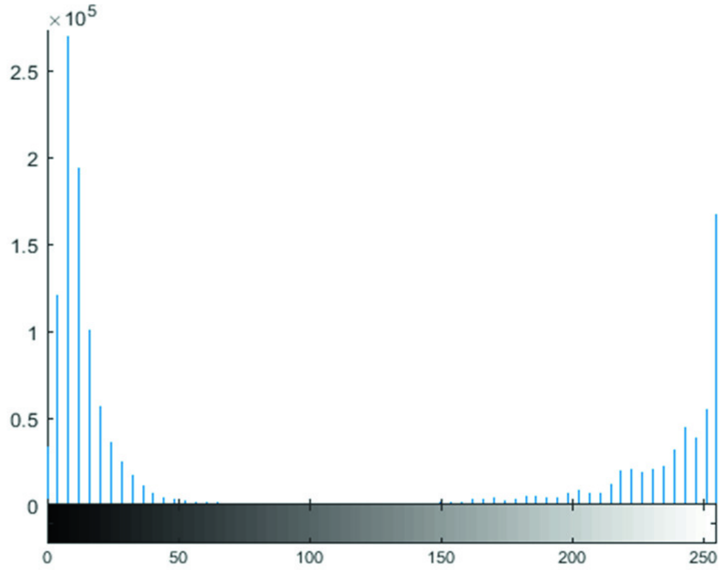
where

- h is the histogram after *cdf* thresholding or normalization;
- $0 \le l \le 255$ is the gray level to be normalized;
- $cdf_{\min}$ is the minimum of the *cdf* function;
- $cdf_{\max}$ is the maximum of the *cdf* function and $cdf_{\max} = 1$.

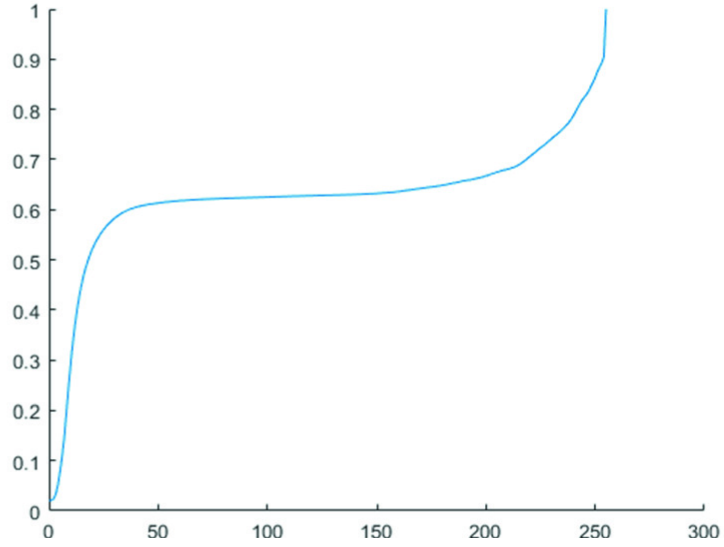
Figure 4.27a shows a picture captured with backlight, and the color and texture in the dark area are almost completely unseen. The gray-level histogram of the image and its *cdf* are shown in Fig. 4.27b, c, respectively. The histogram is a bimodal one with two dominant bands of colors: dark and bright. The *cdf* climbs sharply before gray level 30; this means the pixels with values less than 30 will be brighter and have a chance to show up in the *cdf* normalized image. Figure 4.27d shows the image after the *cdf* thresholding, and it can be seen that most of the colors and texture information of the original color image have been restored. Figure 4.27e shows the gray-level histogram of the *cdf* normalized image. As expected, the histogram of the *cdf* normalized image is well spread across all the gray levels.



(a)


×10^5
2.5
2
1.5
1
0.5
0
0
50
100
150
200
250

(b)


1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
50
100
150
200
250
300

(c)

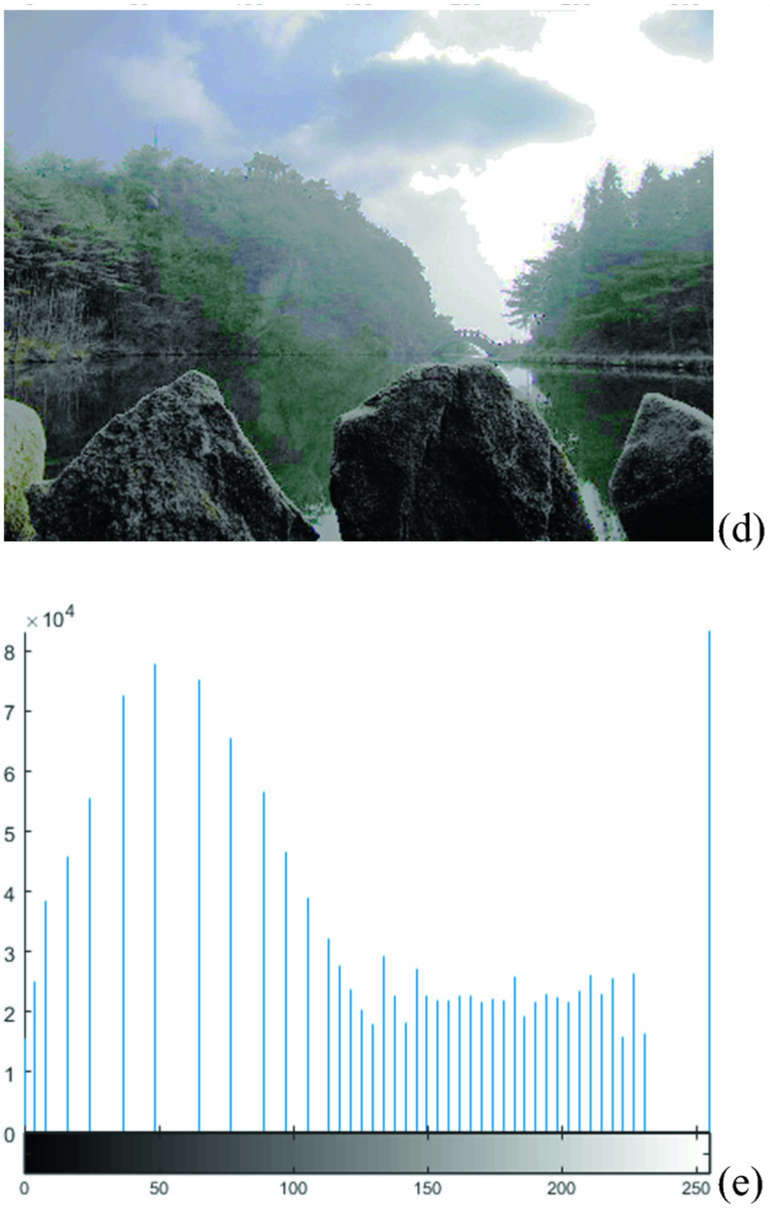
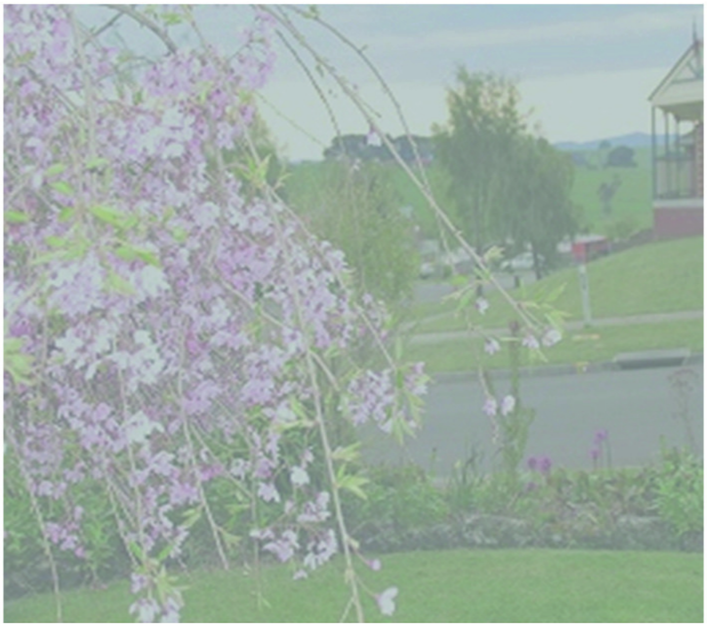
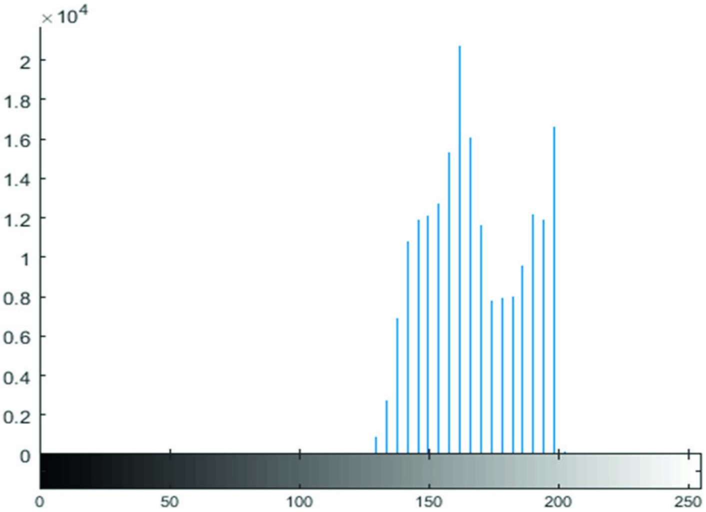


Fig. 4.27 Dark image correction using *cdf* thresholding. **a** A original color image; **b** the gray-level histogram of the original color image; **c** the *cdf* of the original gray-level histogram; **d** the corrected image after *cdf* thresholding; **e** the gray-level histogram of the *cdf* normalized image

Figure 4.28a shows a picture captured in a misty condition, and it has disproportional bright colors, which results in very poor contrast. The gray-level histogram of the image and its *cdf* are shown in Fig. 4.28b, c, respectively. It can be observed that the pixel values are concentrated in a narrow range of 130–200. The *cdf* of the histogram is almost an *S* curve which is a canonical thresholding function. By using (4.31), those bins between 130 and 160 will be pushed to the left most, which makes the image darker. Figure 4.28d shows the image after the *cdf* thresholding, and it can be seen that the colors, texture and contrast are all improved significantly after normalization. Figure 4.28e shows the gray-level histogram of the *cdf* normalized image. Compared with Fig. 4.28b, the histogram bins of Fig. 4.28e are much more evenly distributed across all the gray levels.

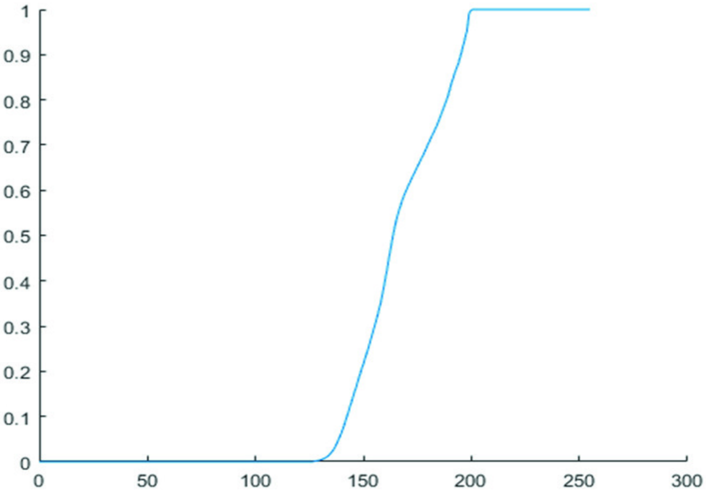


(a)



×10^4
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0
50
100
150
200
250

(b)



1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
50
100
150
200
250
300

(c)

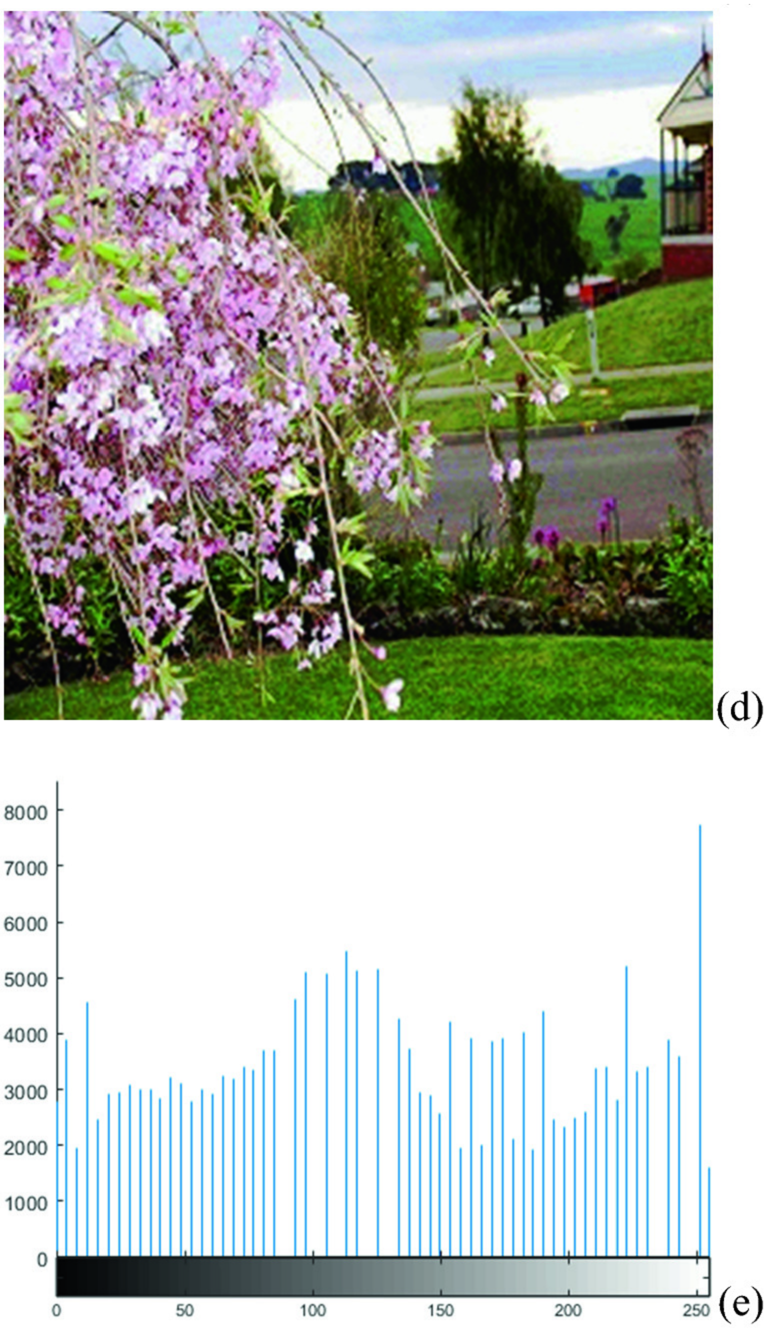


Fig. 4.28 Bright image correction using *cdf* thresholding. **a** A original color image; **b** the gray-level histogram of the original color image; **c** the *cdf* of the original gray-level histogram; **d** the normalized image after *cdf* thresholding; **e** the gray-level histogram of the *cdf* normalized image

4.6 Summary

Color is often the first feature to consider during image processing and analysis. A number of preprocessing or preparation are usually performed before the actual color feature extraction, such as color space conversion, noise reduction, contrast enhancement, image scaling, clustering and segmentation.

A good understanding and choice of color space can make a significant difference on the performance of the extracted color features. Usually, HSV, LUV and Y′CbCr color spaces are preferred to RGB color space. This is because unlike RGB color space, channels of HSV, LUV and Y′CbCr color spaces are independent of each other. The independence of color channels leads to less confusions in image classification and retrieval.

Color feature extraction typically starts with color quantization which aims to remove insignificant colors from an image and increase the robustness of the extracted color features. Colors of an image can be further quantized by image segmentation which merges similar colors into regions. The difficulty of image segmentation is to determine the granularity or region size of the segmentation. This can be determined by the ratio of region size to image size. Before the image segmentation, an image is typically preprocessed by noise removal and contrast enhancement as shown in Sect. 4.5.

Histogram plays a key role in color feature extraction, and most of the color features are histogram-based or histogram-related. These methods usually aim at either reducing the dimensions of a histogram, e.g., SCD, CM, or incorporating spatial information into a histogram, e.g., CCV, CSD, correlogram or both, e.g., DCD.

A histogram itself is a scalable descriptor, because as shown in SCD, neighboring bins can be merged to shorten a histogram to a desirable length. Histograms are usually invariant to rotation and translation, and they can also be normalized to scale invariance using the total number of pixels in an image or a region.

Histograms created from color channels and indexed colors can be matched using a simple distance measure such as L_p. However, histograms created from dominant colors need to be matched using a many-to-many matching such as quadratic distance. This is because colors of corresponding bins of two dominant color histograms are different.

The computation cost of color descriptors ranges from low such as histogram, CM, to moderate such as DCD, SCD, CSD, to high such as correlograms, CCV, CLD.

4.7 Exercises

1. Find a gray-level image, use the Matlab code from the following Web page to generate the histogram of the image: https://au.mathworks.com/help/images/ref/imhist.html. Explain the values on both the horizontal and vertical axes.

2. Normalize the above histogram values to between 0 and 1 to convert the histogram into a feature vector.

3. Apply logarithm transform to the histogram in problem 1, and compare the log-transformed histogram with the original histogram. Explain the similarity and difference between the two histograms, and tell how useful is the log-transformed histogram in image data mining.

4. Generate histograms for similar images with a different brightness, images with different patterns, and tell the pros and cons of using image histograms as image features.

5. Find a color image, open Gimp image processing software (free software from gimp.org), and use command:
   Colors → Components → Decompose (uncheck 'Decompose to layers') to decompose the color image into RGB, HSV, Lab and YCbCr channels. Write a short report to contrast the difference between the 4 color spaces, and tell the applications of the 4 color spaces.

6. Download the Matlab code of JSEG from https://sse.tongji.edu.cn/zhaoqinpei/Software/ (or https://au.mathworks.com/matlabcentral/fileexchange/64123-jseg-unsupervised-segmentation-of-color-texture-regions-in-images, run JSEG function). Find a color image and run the 'script.m' file in Matlab editor (change the path to your image file, e.g., filename = ['..\images\flower.jpg']). Analyze the segmentation results. Try more images and explain how well it can be used for color feature extraction.

7. Find a color image X with noise, and run the following Matlab code to remove the noise from the image:

```
A=imread('X.jpg');
R = A(:,:,1);
G = A(:,:,2);
B = A(:,:,3);
C(:,:,1) = medfilt2(R);
C(:,:,2) = medfilt2(G);
C(:,:,3) = medfilt2(B);
imshow(C)
```

8. Find a color image X with too bright or too dark colors, and run the following Matlab code to show the *cdf* curve, the *cdf* normalized image, the original image histogram and the normalized image histogram:

```
A=imread('X.jpg');
[counts, location]=imhist(A);
x=linspace(0, 255, 256);
pdf=counts/sum(counts);
plot(x, cumsum(pdf), 'b', 'LineWidth', 1);
set(gca,'box','off')

B=histeq(A);
figure;
imshow(B);
figure;
imhist(A, 64);
ylim([0,max(counts)*2.8])
set(gca,'box','off');
figure;
imhist(B, 64);
set(gca,'box','off')
```

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5. Texture Feature Extraction

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The devil is in the detail.

5.1 Introduction

Texture is a general pattern that can be attributed to almost everything in nature. For a human, texture patterns relate to specific and spatially repetitive structure of surfaces formed by repeating a particular element or several elements in different spatial positions. Generally, the repetition involves local variations of scale, orientation or other geometric and optical features of the elements.

Texture is a inherent feature of an object. For example, we can easily tell if an object surface is fine or rough, regular or natural, quiet or busy, etc. It is found that human beings tent to recognize texture by its structure or how often it changes. As the result, the texture methods designed in the last few decades are along two directions: spectral methods and spatial methods. Spatial texture methods attempt to capture the primitive patterns of objects and compute the structural features, while spectral texture methods attempt to capture the change patterns of objects and compute the frequency of changes. Spatial methods are generally more intuitive, while spectral methods are generally more efficient and robust. In this chapter, we discuss those important texture methods for image representation.

5.2 Spatial Texture Feature Extraction Methods

In spatial approach, texture features are extracted by computing the pixel statistics or finding the local pixel structures in original image. These methods include the Tamura textures, co-occurrence matrix method, Markov random field (MRF) method and fractal dimension (FD) method. Tamura et al. are among the earliest researchers to formally define texture features [1]. The mostly cited Tamura texture features in literature consist of six perceptual characteristics of images such as the degree of contrast, coarseness, directionality, linearity, roughness and regularity. In most of the cases, only the first three Tamura features are used as the other three features are defined based on the combinations of the first three features. Tamura features are nice because they are high-level perceptual features and suitable for texture browsing. However, it is difficult to define more such types of high-level features. Therefore, Tamura features are not enough to distinguish all the textures in the world.

5.2.1 Tamura Textures

Tamura et al. [1] introduce six statistical features. These include *coarseness*, *contrast*, *directionality*, *line-likeness*, *regularity* and *roughness*. The last three features are defined based on the first three features. Therefore, most of the image retrieval systems only use the first three Tamura features.

Coarseness relates to the size of the primitive elements (textons) forming the texture; it measures the image granularity. It is calculated as the average of the largest window sizes needed to identify texture elements centered at different pixel positions. Formally, it is defined as

$$f_{crs} = \frac{1}{n^2} \sum_{x=1}^{n} \sum_{y=1}^{n} 2^k I(x, y) \tag{5.1}$$

where $n \times n$ denotes the image size of $I(x, y)$, and k is obtained as the value which maximizes the differences of the moving averages of

$A_k = \frac{1}{2^{2k}} \sum_{x=1}^{n} \sum_{y=1}^{n} I(x, y)$, taken over a $2^k \times 2^k$ neighborhood along the horizontal and vertical directions. The specific procedure is to compute the differences between the average signals for the non-overlapping windows of different sizes:

(1) At each pixel (x, y), compute six averages for the windows of size $2^k \times 2^k$, $k = 0, 1, \ldots, 5$, around the pixel.

(2) At each pixel, compute absolute differences $E_k(x, y)$ between the pairs of non-overlapping averages A_k in the horizontal and vertical directions.

(3) At each pixel, find the value of k that maximises the difference $E_k(x, y)$ in either direction and set the best size $S_{\text{best}}(x, y) = 2^k$.

(4) Compute the coarseness feature f_{crs} by averaging $S_{\text{best}}(x, y)$ over the entire image. Textures with multiple coarseness can be computed from the histogram of $S_{\text{best}}(x, y)$.

Contrast tells how well an object is distinguishable from other objects or background. It measures how gray levels q vary in the image I and to what extent their distribution is biased to black or white. The second-order σ^2 and normalized fourth-order central moments μ_4 of the gray-level histogram (empirical probability distribution P) are used to define the contrast feature:

$$f_{\text{con}} = \frac{\sigma}{\left(\frac{\mu_4}{\sigma^4}\right)^{\frac{1}{4}}} \tag{5.2}$$

where $\mu_4 = \sum_{q=0}^{q\max} (q - m)^4 P(q|I)$ is the *kurtosis*; $\sigma^2 = \sum_{q=0}^{q\max} (q - m)^2 P(q|I)$ is the *variance* and m is the *mean* gray level.

Directionality tells if there exists any directional pattern in an image, like vertical, horizontal or diagonal, etc., the degree of directionality is measured using the frequency distribution of oriented local edges against their directional angles. The edge strength $e(x, y)$ and the directional angle $a(x, y)$ are computed to approximate the pixelwise x and y derivatives of the image:

$$e(x, y) = \left(|\Delta_x(x, y)| + \left|\Delta_y(x, y)\right|\right)/2 \tag{5.3}$$

$$\phi(x, y) = \arctan\left(\Delta_y(x, y)/\Delta_x(x, y)\right) \tag{5.4}$$

where $\Delta_x(x, y)$ and $\Delta_y(x, y)$ are the horizontal and vertical grey-level differences between the neighboring pixels, respectively. They are computed by using Prewitt edge detectors

$$\begin{array}{ccc} & \Delta_x & \\ -1 & 0 & 1 \\ -1 & 0 & 1 \\ -1 & 0 & 1 \end{array} \qquad \begin{array}{ccc} & \Delta_y & \\ 1 & 1 & 1 \\ 0 & 0 & 0 \\ -1 & -1 & -1 \end{array}$$

A histogram $h_{dir}(\phi)$ of quantised direction values ϕ is constructed by counting numbers of the edge pixels with the corresponding directional angles and the edge strength greater than a pre-defined threshold. The histogram is relatively uniform for images without strong orientation and exhibits peaks for highly directional images. The directionality feature is defined as the *sharpness* of the histogram:

$$f_{dir} = 1 - r n_p \sum_{p=1}^{n_p} \sum_{\phi \in w_p} \left(\phi - \phi_p\right)^2 h_{dir}(\phi) \tag{5.5}$$

where n_p is the number of peaks, ϕ_p is the position of the pth peak, w_p is the range of the angles attributed to the pth peak (i.e., the range between valleys around the peak), r denotes a normalising factor related to quantising levels of the angles ϕ, and ϕ is the quantised directional angle.

Figure 5.1b shows the edge map of an original image in Fig. 5.1a. To compute f_{dir}, h_{dir} is first computed by quantizing ϕ and counting the number of edge pixels with $e(x, y)$ greater than a threshold, and the edge histogram of angles is shown in Fig. 5.1c. The angles ϕ in the horizontal axis are in the range of −90° to +90° and are quantized into 12 intervals, and the quantized angles are −75°, −60°, −45°,..., +90°. The vertical axis shows the percentage of edge pixels at different angles [2].

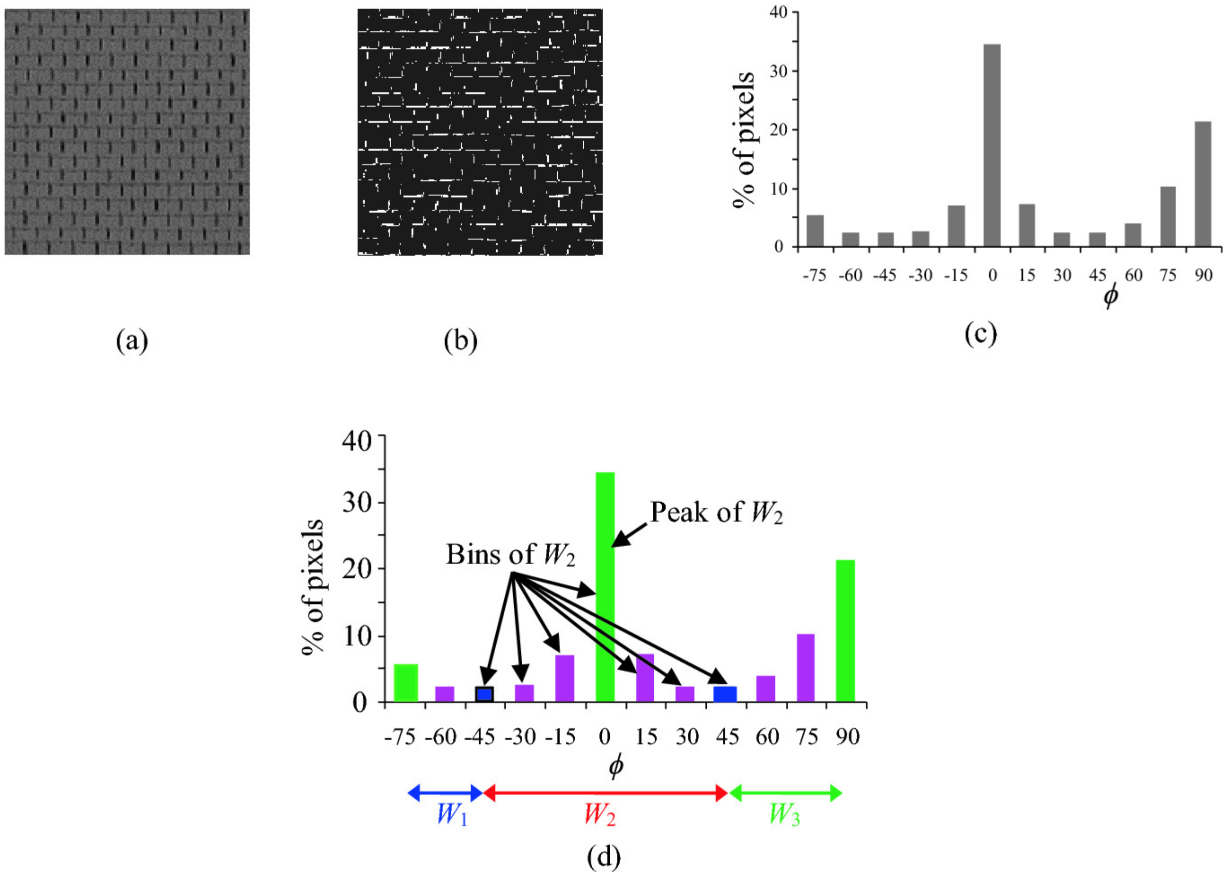


Fig. 5.1 Example of computing directionality

After computing the h_{dir}, all peaks and valleys in h_{dir} are detected. Figure 5.1d shows the peaks and valleys in green and blue, respectively. Suppose, there are n_p peaks in the histogram. For each peak p, let w_p be the window of bins from the previous valley to the next valley (a window contains a peak in it), and ϕ_p be the angular position of the peak in w_p. Based on the definition of f_{dir}, the more directional an image, the higher the directionality the image. However, f_{dir} is not invariant to rotation; rotation of an image causes circular shift of the h_{dir} histogram; this can cause false peak detection. For example, the first peak in Fig. 5.1d is actually part of the hill defined by the last peak of the histogram. Therefore, in practice, several rounds of circular shift are needed to find out the real peaks of the histogram.

Tamura textures are intuitive in terms of definitions; however, the computation processes are complex. This affects the robustness and the overall performance of the computed features.

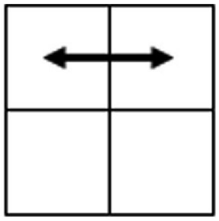
5.2.2 Gray-Level Co-Occurrence Matrices

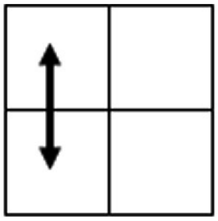
Many statistical texture features are based on gray-level co-occurrence matrices (GLCM) or its color counterpart color correlogram. A GLCM represents how frequent is every particular pair of gray levels in an image, separated by a certain distance *d* along a certain direction *a*.

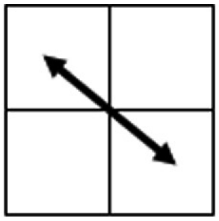
Formally, given an $n \times m$ image $I(x, y)$, a cell in a GLCM is defined as

$$C_{\Delta x, \Delta y}(i, j) = \sum_{x=1}^{n} \sum_{y=1}^{m} \begin{cases} 1, & \text{if } I(x, y) = i \text{ and } I(x + \Delta x, y + \Delta y) = j \\ 0, & \text{otherwise} \end{cases} \tag{5.6}$$

For an image with 256 gray-level values, a GLCM is a 256 × 256 matrix. With the combination of Δx and Δy, a large number of GLCMs can be created. In practice, only four GLCMs are created by capturing the following four structures: horizontal, vertical, left lean diagonal and right lean diagonal.







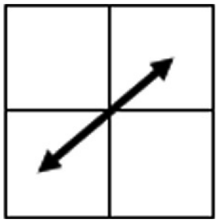


Figure 5.2 shows an example GLCM of an image $I(x, y)$ with eight gray-level values. In this case, the structure to be captured by the GLCM is the *horizontal* structure. The arrows in the figure link the pixel pairs in the image with their corresponding entries in the GLCM.

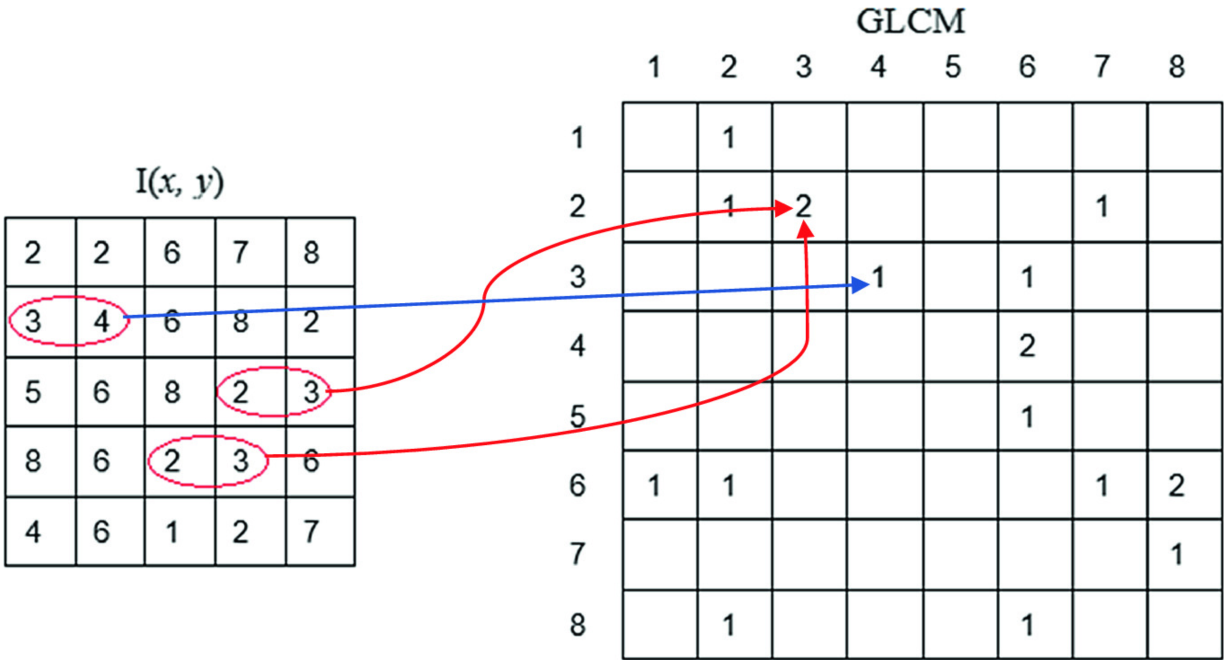


Fig. 5.2 Computation of a GLCM. An eight gray levels image $I(x, y)$ on the left and its GLCM on the right

A GLCM itself is a gray-level image; therefore, a number of statistical features called Haralick features can be computed from each GLCM image, such as the homogeneity, contrast, correlation, energy, entropy, variance [3].

Suppose $p(i,j)$ is the normalized value of a GLCM entry; it is equivalent to the probability of a particular structural distribution in the image; N_g is the number of gray levels in the quantized image. The three major texture features *angular second moment*, *contrast* and *correlation* are given in the following.

Angular second moment:

$$f_1 = \sum_i \sum_j \{p\,(i, j)\}^2 \tag{5.7}$$

Contrast:

$$f_2 = \sum_{n=0}^{N_g-1} n^2 \left\{ \sum_i \sum_j [p\,(i, j)\,|\,|i - j| = n] \right\} \tag{5.8}$$

Correlation:

$$f_3 = \frac{\sum_i \sum_j (ij)\, p(i,j) - \mu_x \mu_y}{\sigma_x \sigma_y} \tag{5.9}$$

where μ_x, μ_y, σ_x, σ_y are the means and standard deviations of the marginal probabilities p_x and p_y, respectively. f_1 is a measure of homogeneity of the image, and f_3 is a measure of gray tone linear dependencies in the image.

Because a GLCM is usually a large matrix and there needs a number of GLCMs to capture different texture structures, GLCM features are expensive to compute.

5.2.3 Markov Random Field

MRF texture methods model image pixel location as a random variable; as a result, an image is a random field. Each type of textures is characterized by a joint probability distribution of signals that accounts for spatial inter-dependence or interaction among the signals. The interacting pixel pairs are usually called neighbors, and a random field texture model is characterized by geometric structure and quantitative strength of interactions among the neighbors.

Among the many MRF texture methods, the simultaneous auto-regressive (SAR) model is the most widely used, as it uses fewer parameters. In SAR, the intensity $I(x, y)$ at pixel (x, y) is estimated as a linear combination of the neighboring pixel values $I(s, t)$ and an additive Gaussian noise $\varepsilon(x, y)$.

$$I(x, y) = \mu + \sum_{(s,t)\in N} \theta(s,t)\, I(s,t) + \varepsilon(x,y) \tag{5.10}$$

where

- μ is the mean of the image.
- N is the neighborhood of (x, y), e.g., a 3 × 3 window.
- $\theta(s, t)$ are the weights or coefficients associated with each of the neighborhood pixels,
- and $\varepsilon(x, y)$ is a Gaussian error with zero mean and standard deviation of σ.

The set of parameters θ and σ are the measurement of the texture; they can be estimated using either the least square error (LSE) technique or the maximum likelihood estimation (MLE). Both LSE and MLE involve complex optimization which are computationally expensive. A higher σ value indicates finer granularity or less coarseness; a higher $\theta(x, y + 1)$ and $\theta(x, y - 1)$ values indicate the texture is vertically oriented and so on so forth.

Rotation-invariant SAR model (RISAR) can be created by replacing N with a circular neighborhood. In order to make SAR more robust, multiresolution MRF (MRMRF) can also be created, where an image is represented by a multiresolution Gaussian pyramid before applying the MRF model.

The number of parameters or the feature dimensions of a SAR depends on the size of the neighborhood, e.g., a 3 × 3 neighborhood results in 9 parameters, while a 4 × 4 neighborhood results in 16 parameters. To be scale invariant, SARs with multiple window size are needed; this makes the computation of MRF features prohibitively expensive.

5.2.4 Fractal Dimension

The fractal dimension (FD) method [4] is based on the theory of fractal geometry which characterises shapes or patterns of self-similarity. The idea of fractal is to find the smallest structure which replicates the whole pattern. According to fractal theory, a bounded set S in Euclidean space R^n is self-similar if S is the union of $N(r)$ distinct (non-overlapping) copies of itself scaled up or down by a ratio r, and the relationship between $N(r)$ and r is given by:

$$N(r) \approx C\left(\frac{1}{r}\right)^d \tag{5.11}$$

where d is the fractal dimension or FD.

In image applications, FD method models a gray-level image as a 3D terrain surface, and a differential box counting is done under the surface to measure how rough the surface is. In logarithm term, the above relationship means the number of boxes under the surface is inversely proportional to the size of the boxes, which is expected. *d* is given by the following approximation

$$d = \lim_{r \to 0} \frac{\log N(r)}{\log \frac{1}{r}} \tag{5.12}$$

or

$$d \approx \frac{\log N(r)}{\log \frac{1}{r}} \tag{5.13}$$

From (5.13), the log $N(r)$ and log $(1/r)$ have an approximately *linear* relationship; therefore, FD can be estimated from a least square fitting of the two variables. By fitting a straight line for the log $N(r)$ versus log $(1/r)$ curve, the *slope* of the straight line is taken as the approximation of FD.

Since FD only models the roughness feature, other features like directionality and contrast are missed from FD. Therefore, in [4], six FDs have to be computed from a number of modified images derived from the original image, such as the original image, low gray-valued image, high gray-valued image, horizontally smoothed image, vertically smoothed image and the second moment of the original image. Despite of these additional FD features, FD can be very sensitive due to the triple approximation during the box counting, linear fitting and image modification.

5.2.5 Discussions

Spatial texture methods are based on the ideas of capturing the elemental or microstructures of a textured image. The definitions of the structures are based on how humans describe a textured image, such as rough vs fine, regular vs natural, directional vs random. The advantage of these methods is that they are intuitive and semantically meaningful. However, there are infinite types of textural structures in the nature; human beings can only define or describe a small number of them. This can limit the application of spatial texture methods.

The other major issue with spatial approach is that spatial features are sensitive to noise. Furthermore, spatial texture methods are usually complex to compute, and they often involve complex optimization which is very expensive to compute. These issues affect the robustness and the overall performance of spatial texture methods.

5.3 Spectral Texture Feature Extraction Methods

Instead of defining and describing specific structures in an image, which is difficult, spectral texture methods attempt to capture how frequent the patterns change in a textured image. Spectral texture methods are based on Fourier transform (FT), discrete cosine transform (DCT), discrete wavelet transform (DWT), Gabor filters and curvelet transform, etc.

Global power spectra computed from the DFT are not effective in texture classification and retrieval, compared with local features computed from small windows such as DCT. At present, the most promising features for texture retrieval are based on multiresolution features obtained with orthogonal wavelet transforms or Gabor filters. These features describe spatial distributions of oriented edges in the image at multiple scales.

5.3.1 DCT-Based Texture Feature

Compared with the traditional spatial texture methods, DCT is a simple yet robust method to capture local textures of an image. The idea is equivalent to STFT, or applying FT on a small window. However, due to the use of 1D cosine transform on both rows and columns, the computation is very efficient.

For a color image *I*, it is first converted to Y′CbCr or YBR colors. The image is then divided into a set of overlapping 8 × 8 regions or blocks, which are obtained by a sliding window that moves by two pixels between consecutive samples. At each location of the three YBR color channels, apply the DCT on the local 8 × 8 window. Each block is then represented by:

$$\mathbf{x} = \left[\mathbf{x}^{Y}, \mathbf{x}^{B}, \mathbf{x}^{R}\right] \tag{5.14}$$

where $[\mathbf{x}^{Y}, \mathbf{x}^{B}, \mathbf{x}^{R}]$ is the concatenation of the DCT vectors extracted from each of the YBR color channels by a zigzag scanning. For efficient computation, the 192-dimensional YBR-DCT vector is usually shortened by only retaining the first few coefficients from each of the YBR channels. This is because the well-known energy compaction properties of the DCT.

To compute the texture features of the image *I*, a Gaussian mixture model of eight components is computed using the EM algorithm. This produces the following conditional distribution for each image:

$$P(\mathbf{x}|I) = \sum_{k=1}^{8} \pi_I^k G(\mathbf{x}, \mu_I^k, \sigma_I^k) \tag{5.15}$$

where π_I^k is the weight and μ_I^k and σ_I^k are the maximum likelihood parameters of mixture component *k*. The (μ_I^k, σ_I^k) pair are then organized into a feature vector which is used for texture representation. For a gray-level image, the DCT method just needs to replace the three color channels with a single gray channel.

DCT computation is efficient due to the use of FFT; however, the EM is an optimization method which incurs significant computation cost.

5.3.2 Texture Features Based on Gabor Filters

5.3.2.1 Gabor Filters

Although DCT is efficient to compute locally, the image-level texture features are complex to compute due to the use of EM algorithm. An alternative is to use Gabor filters. Gabor filters are based on traditional filter-based image processing approach, which computes one filtered value at each pixel as opposing to computing multiple transformed values at each location as in the DCT. Different from traditional filters, by combining both Gaussian and FT, Gabor filters simulate the powerful properties of perceptual vision of mammals. Furthermore, they can be tuned to different orientations and scales.

Gabor transform creates a filter bank consisting Gabor filters with various scales and orientations. For a given image $I(x, y)$ with size $P \times Q$, its discrete Gabor transform is given by a convolution:

$$G_{mn}(x, y) = \sum_{s=0}^{K} \sum_{t=0}^{K} I(x - s, y - t) g^*_{mn}(s, t) \tag{5.16}$$

where K is the filter mask size, and g^*_{mn} is the complex conjugate of g_{mn} which is a class of self-similar wavelets generated from dilation and rotation of the following mother wavelet:

$$g(x, y) = \frac{1}{2\pi\sigma_x\sigma_y} \exp\left[-\frac{1}{2}\left(\frac{x^2}{\sigma_x^2} + \frac{y^2}{\sigma_y^2}\right)\right] \cdot \exp(j2\pi Wx) \tag{5.17}$$

where W is called the modulation frequency. The self-similar Gabor wavelets are obtained through the generating function:

$$g_{mn}(x, y) = a^{-m} g(\tilde{x}, \tilde{y}) \tag{5.18}$$

where m and n specify the *scale* and *orientation* of the wavelet, respectively, with $m = 0, 1, \ldots M\text{-}1$, $n = 0, 1, \ldots, N\text{-}1$ and

$$\left.\begin{aligned} \tilde{x} &= a^{-m}(x \cos\theta + y \sin\theta) \\ \tilde{y} &= a^{-m}(-x \sin\theta + y \cos\theta) \end{aligned}\right\} \tag{5.19}$$

where $a > 1$ and $\theta = n\pi/N$.

In order to decide the bank of Gabor filters, the parameters in (5.17) to (5.19) have to be determined. The Gabor wavelets generated using (5.17) through (5.19) are complete but not orthogonal wavelets; it implies there is redundancy in the filters. Therefore, we may design a bank of Gabor filters so that redundancy will be significantly reduced while image texture will be well represented by the set of individual filter response. Due to the same functional form of Gabor wavelet function $g(x, y)$ and its frequency response $\Psi(u, v)$ (i.e., its 2-D Fourier transform):

$$\Psi(u, v) = \exp\left\{-\frac{1}{2}\left[\frac{(u - W)^2}{\sigma_u^2} + \frac{v^2}{\sigma_v^2}\right]\right\} \tag{5.20}$$

where $\sigma_u = (2\pi\sigma_x)^{-1}$ and $\sigma_v = (2\pi\sigma_y)^{-1}$, an optimal representation of an image in spatial domain can be achieved by finding an optimal representation of the image in frequency domain. The idea of achieving so is to use the full width at half maximum (FWHM) of the Gabor spectral functions to form a complete coverage of the frequency plane within the modulation frequency bandwidth (Sect. 2.2). Specifically, the design follows three principles [5]: (*i*) *uniform sampling* of orientation angles; (*ii*) *exponential sampling* of modulation bandwidth W; (*iii*) continuous coverage of the frequency space. This strategy is illustrated in Fig. 5.3.

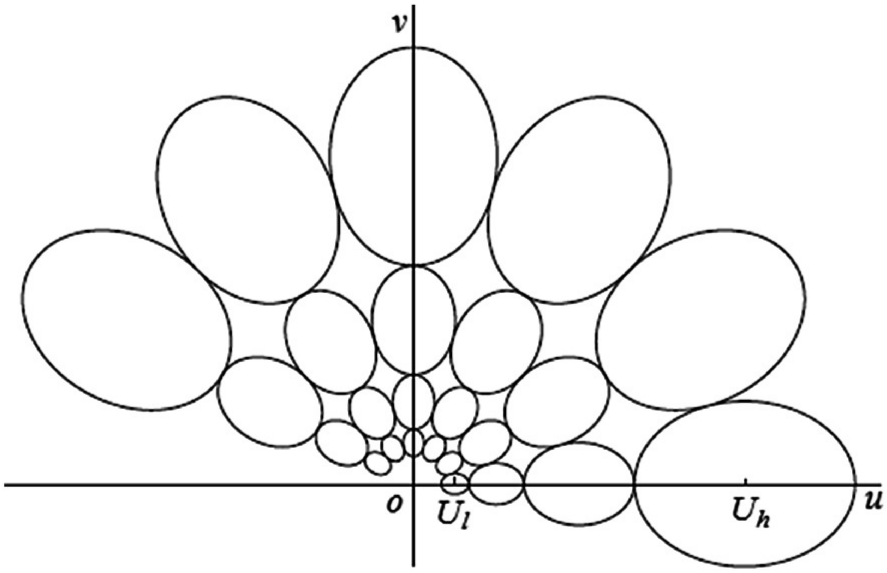


Fig. 5.3 FWHM sampling of spectral responses of Gabor filters in frequency plane

Let U_l and U_h be the lowest and highest frequencies of interest, such that the coarsest scale filter and the finest-scale filter are cantered in the frequency domain at distances U_l and U_h from the origin, respectively. By the above strategy of redundancy reduction, the parameters of Gabor filters in spatial domain can be determined as following:

$$a = (U_h/U_l)^{\frac{1}{M-1}} \tag{5.21}$$

$$\sigma_{x,m,n} = \frac{(a+1)\sqrt{2\ln 2}}{2\pi\, a^m (a-1) U_l} \tag{5.22}$$

$$\sigma_{y,m,n} = \frac{1}{2\pi \tan\left(\frac{\pi}{2N}\right) \sqrt{\frac{U_h^2}{2\ln 2} \left(\frac{1}{2\pi\sigma_{x,m,n}}\right)^2}} \tag{5.23}$$

The parameters are independent of orientations (n); in other words, the parameters repeat in every orientation. In practice, the following parameter values are used:

$$U_l = 0.05,\ U_h = 0.4,\ K = 60$$

5.3.2.2 *Gabor Spectrum*

Figure 5.4 shows the Gabor-filtered subband images from the lady image of Fig. 3.2. It shows how different image features are captured by Gabor filters from different scales and orientations. It can be observed that low-frequency information are captured at lower scales, and as scale increases (*in spectral domain*), more fine details can be seen.

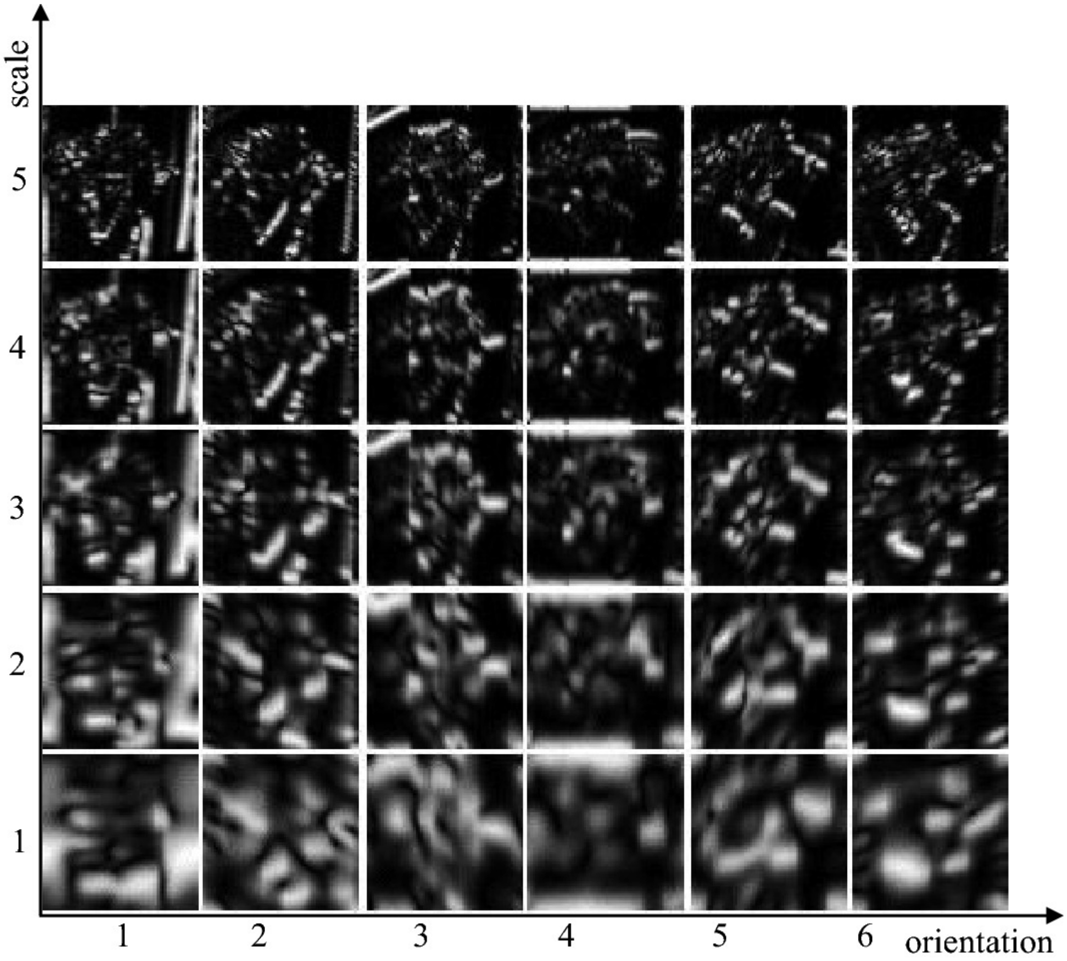


Fig. 5.4 Gabor-filtered subbands for the lady image

5.3.2.3 Texture Representation

After applying Gabor filters on the image with different orientations at different scales, a set of magnitudes is obtained:

$$E(m,n) = \sum_{x=0}^{P} \sum_{y=0}^{Q} |G_{mn}(x,y)|,\ m = 0, 1, \ldots,\ M-1; n = 0, 1, \ldots,\ N-1 \quad (5.24)$$

where

- *m* is the scale.
- *n* is the orientation.
- *M* is the maximal scale.
- *N* is the maximal orientation.
- *P*x*Q* is the size of the size of the input image.

The magnitudes represent the energy map at different scales and orientations of the image under transform (Fig. 5.5 right) [6].

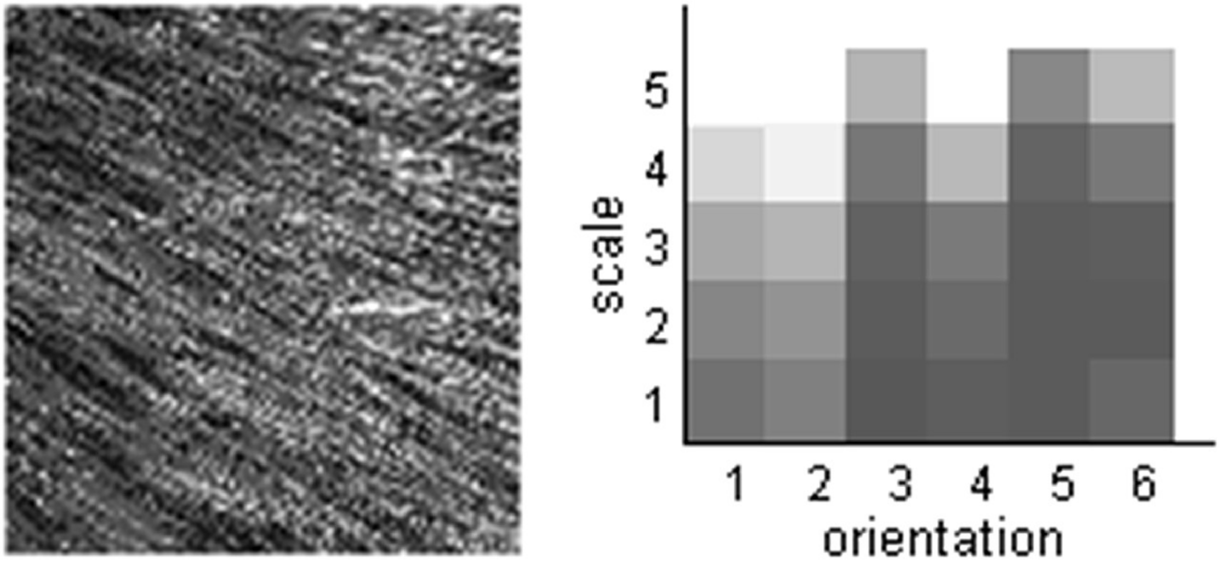


Fig. 5.5 Computation of Gabor texture descriptor. A straw image on the left and its energy map on the right. The higher the energy the brighter the block

The main purpose of texture-based retrieval is to find images or regions with similar texture. It is assumed that we are interested in images or regions that have homogenous texture; therefore, the following mean μ_{mn} and standard deviation σ_{mn} of the magnitude of the transformed coefficients are used to represent the homogenous texture feature of the image or region:

$$\begin{aligned}\mu_{mn} &= \frac{E(m,n)}{P \times Q} \\ \sigma_{mn} &= \frac{\sqrt{\sum_x \sum_y (|G_{mn}(x,y)| - \mu_{mn})^2}}{P \times Q}\end{aligned} \tag{5.25}$$

A feature vector **f** (texture representation) is created using μ_{mn} and σ_{mn} as the feature components. Five scales and six orientations are used in common implementation, and the Gabor texture feature vector is thus given by:

$$\mathbf{f} = (\mu_{00}, \sigma_{00}, \mu_{01}, \sigma_{01}, \ldots, \mu_{45}, \sigma_{45}) \tag{5.26}$$

In order to remove the influence of various lighting issues of camera, the features μ_{mn} and σ_{mn} can be normalized to [0, 1] using the maximum of the respective components. The similarity between two texture patterns is measured by the city block or Euclidean distance between their Gabor feature vectors.

5.3.2.4 Rotation Invariant Gabor Features

The above acquired texture feature is not invariant to rotation; similar texture images with different direction may be missed out from the retrieval or get a low rank. A simple circular shift on the feature map can be used to solve the rotation variant problem. Specifically, the orientation with the highest energy is detected as the dominant direction of the image and the feature elements in the dominant direction are moved to the first elements in **f**. The other elements are then circularly shifted accordingly. For example, if the original feature vector is '*abcdef*' and '*c*' is at the dominant direction, then the normalized feature vector will be '*cdefab*' [7].

This circular shift approach is based on the theory that image rotation in spatial domain is equivalent to circular shift in spectral domain. Assume the original image is $I(x, y)$ and $I_\phi(x, y)$ is the result of $I(x, y)$ after rotation of angle ϕ; by using (1.40), we have the following:

$$I_\phi(x, y) = I(x, y) \times \mathrm{e}^{-j\phi} \tag{5.27}$$

For notation convenience, the Gabor transform of $I(x, y)$ and $I_\phi(x, y)$ at scale s and angle θ is denoted as $G(I, s, \theta)$ and $G(I_\phi, s, \theta)$, respectively. Then according to (5.16), we have:

$$G(I, s, \theta) = I(x, y) * g_{s\theta}(x, y) \tag{5.28}$$

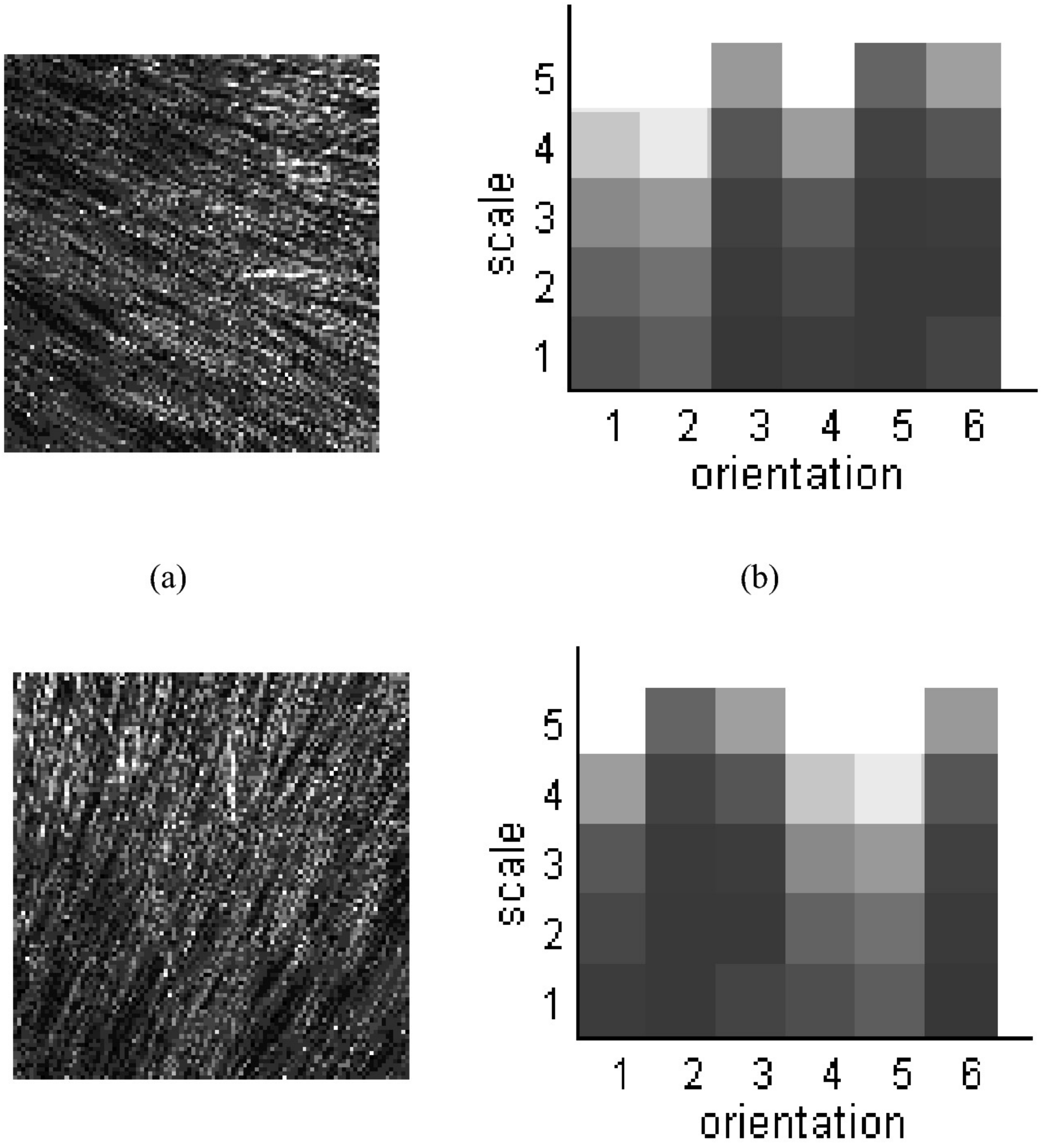
and by the commutability of convolution, we have

$$\begin{aligned} G(I_\phi, s, \theta) &= I_\phi(x, y) * g_{s\theta}(x, y) \\ &= \left[I(x, y) \cdot \mathrm{e}^{-j\phi}\right] * g_{s\theta}(x, y) \\ &= I(x, y) * \left[g_{s\theta}(x, y) \cdot \mathrm{e}^{-j\phi}\right] \end{aligned} \tag{5.29}$$

(5.29) indicates that applying a Gabor filter on a rotated image is equivalent to applying a rotated Gabor filter on the original image. Since $g_{s\theta}(x, y) \cdot e^{-j\phi} = g_{s,\theta+\phi}(x, y)$, we have

$$\begin{aligned} G(I_\phi, s, \theta) &= I(x, y) * \left[g_{s\theta}(x, y)\,\mathrm{e}^{-j\phi}\right] \\ &= I(x, y) * g_{s,\theta+\phi}(x, y) \\ &= G(I, s, \theta + \phi) \end{aligned} \tag{5.30}$$

(5.30) indicates that a rotation of the input image $I(x, y)$ by an angle ϕ is equivalent to a translation of the output energy $G(I, s, \theta)$ by the same amount ϕ along the orientation axis. Figure 5.6 demonstrates this fact. It shows two texture patterns and their feature maps; pattern (c) is a rotation of 90° of pattern (a). Form feature map (b), it can be seen that pattern (a) has a dominant direction feature in orientation 2 (60°), while in feature map (d), this dominant direction feature has moved to orientation 5 (150°) and features in other directions are circularly shifted accordingly. In other words, the spectrum (d) is the circularly shifted version of spectrum (b) [6].



(a) (b)

(c) (d)

Fig. 5.6 Computation of rotation invariant Gabor texture descriptor. **a** A straw image; **b** energy map of (**a**); **c** a rotated image of (**a**); **d** energy map of (**c**). The higher the energy, the brighter the block

If a texture pattern has directional features, it will show dominant energy at certain direction on the energy map. If the direction of the highest energy is circularly shifted to zero degree, the resulting **f** is a rotation invariant feature. If a texture pattern does not have dominant direction feature, the matching between rotated patterns can be made at any direction, and the rotation normalization does not affect the matching in this situation.

In image analysis, there is always a compromise between spatial resolution and frequency resolution. Gabor filters achieve optimal joint localization/resolution in both space domain and frequency domain. However, due to the truncation at half-peak magnitude, the spectral cover of Gabor filters is not complete; this results in information loss in the spectral domain. For example, in Fig. 5.7, black holes are left at the FWHM in Gabor transformed spectral domain. Consequently, the high-frequency components, which are considered to be the most important in characterizing image textures, are not completely captured. Abundant redundancy also exists between transformed images at different scales, because Gabor filters use overlapped window and do not involve image down sampling. These limitations can be easily overcome by using wavelet transform.

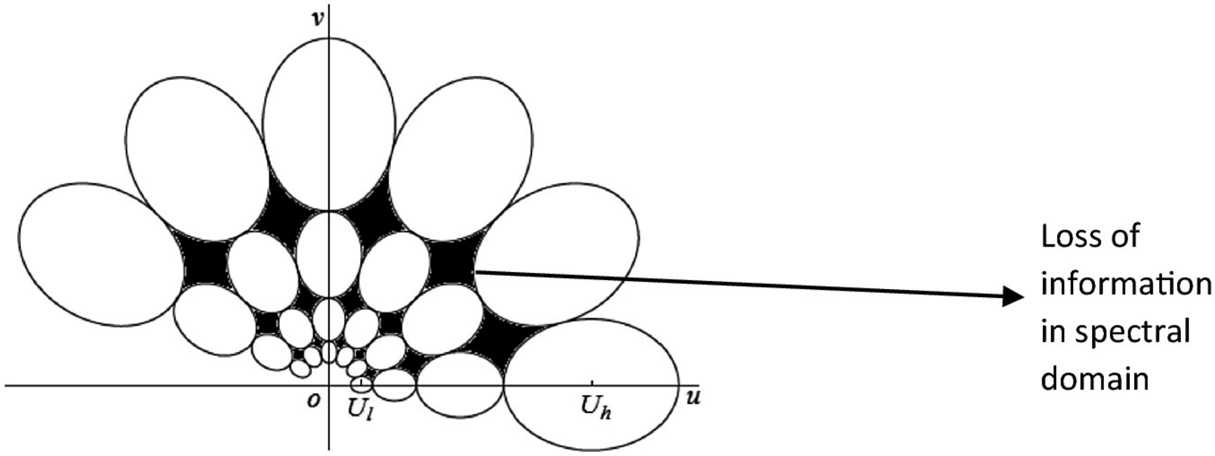


Fig. 5.7 Frequency tiling of half frequency plan by Gabor filters; the ovals are the covered spectrum while the black holes are the lost spectrum

5.3.3 Texture Features Based on Wavelet Transform

5.3.3.1 Selection and Application of Wavelets

The key idea of wavelet transform is to analyze an image using multiresolution approach by using filters of different sizes, called wavelets. This is equivalent to look at the image from different distances. The whole decomposition process provides us with an array of DWT coefficients obtained from each subbands at each scale. These coefficients can then be used to represent the texture features of an image.

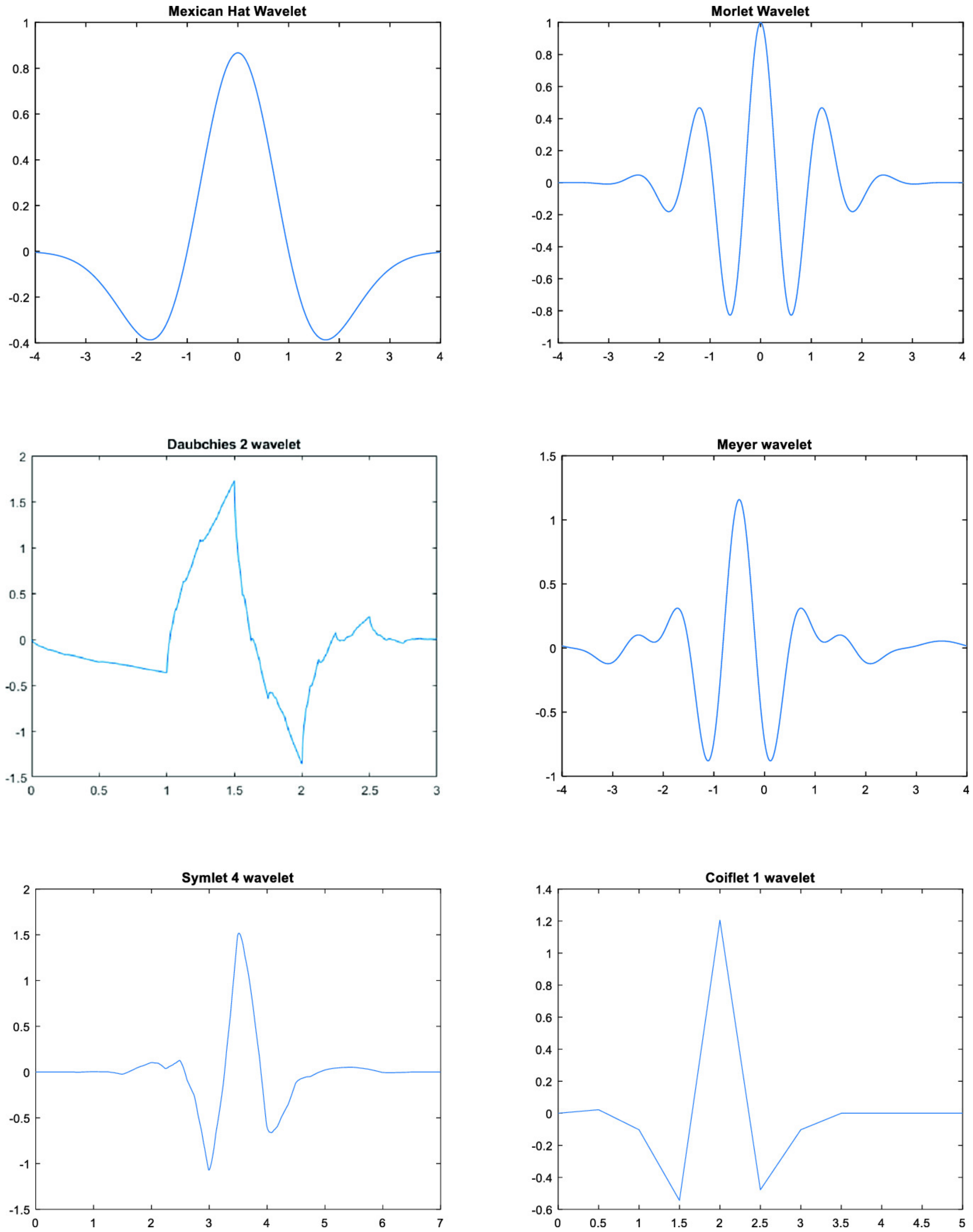
Given a 2D image $f(m, n)$, $0 \le m \le M - 1$, $0 \le n \le N - 1$, its DWT is given by (5.31):

$$W^j(k, l) = \frac{1}{2^j} \sum_{n=0}^{N-1} \sum_{m=0}^{M-1} f(m, n)\, \psi_{k,l}^j(m, n) \tag{5.31}$$

where j is the scale and (k, l) is the spatial location of the wavelet and:

$$\psi_{k,l}^j(m, n) = \psi\left(\frac{m - 2^j k}{2^j}\right) \psi\left(\frac{n - 2^j l}{2^j}\right) \tag{5.32}$$

Different wavelets have been used to capture the texture features of an image. Commonly used wavelets include *Haar*, *Mexican hat*, *Morlet*, *Daubechies*, *biorthogonal*, *symlet*, *Coiflet* and *Meyer* wavelet. Both Haar and symlet are special members of Daubechies wavelet family. Haar wavelet has been introduced earlier in Sect. 3.3.1. Figure 5.8 shows the 1D profiles six wavelets from some of the wavelet families, while Fig. 5.9 provides a 3D view for four of the wavelets.


Mexican Hat Wavelet

Morlet Wavelet

Daubchies 2 wavelet

Meyer wavelet

Symlet 4 wavelet

Coiflet 1 wavelet

Fig. 5.8 Mexican hat, morlet, daubechies, meyer, symlet 4 and coiflet wavelets

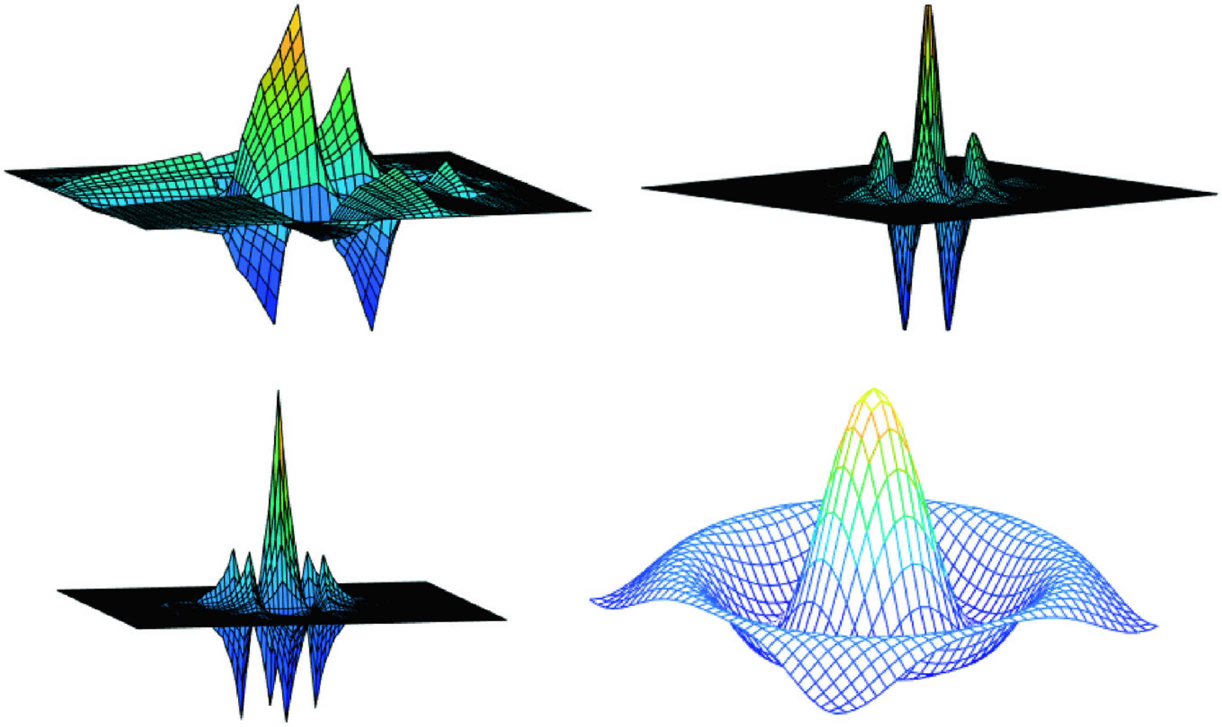
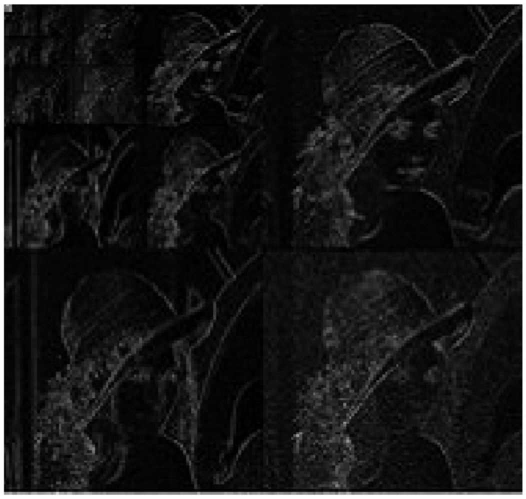
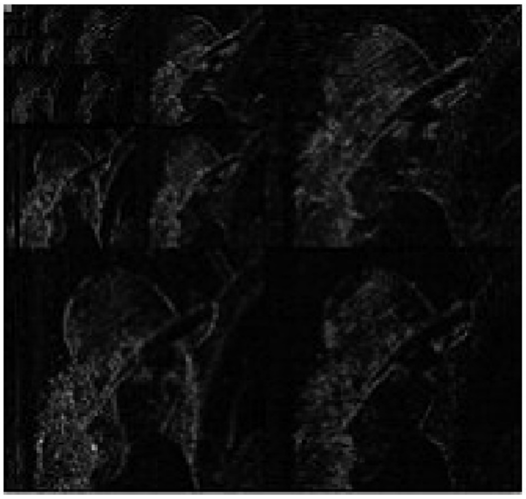


Fig. 5.9 Wavelets in 3D space. Top left: Daubechies 2; Top right: Symlet 4; Bottom left: Coiflet 1; Bottom right: Mexican hat

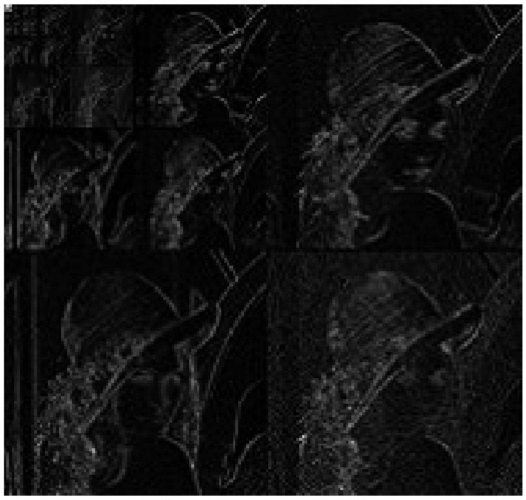
Figure 5.10 shows the spectra of the Lena image from some of the common wavelet transforms. It can be seen that the spectra images are similar but with subtle difference due to the different shapes of the wavelets. Some are more efficient due to capturing more low-frequency information while discard more high-frequency information.



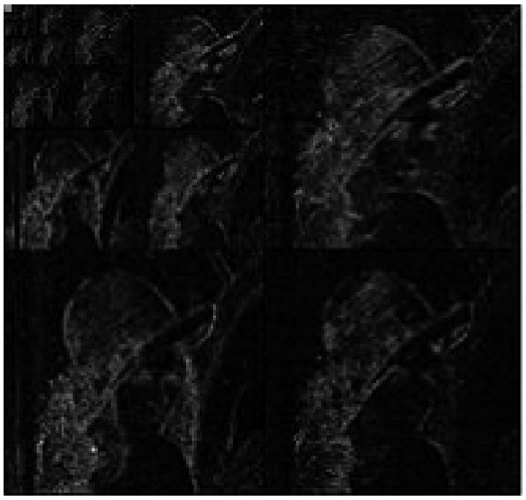
Haar



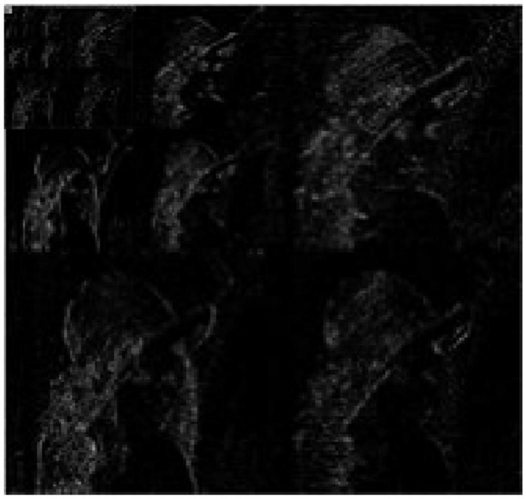
Daubechies 4



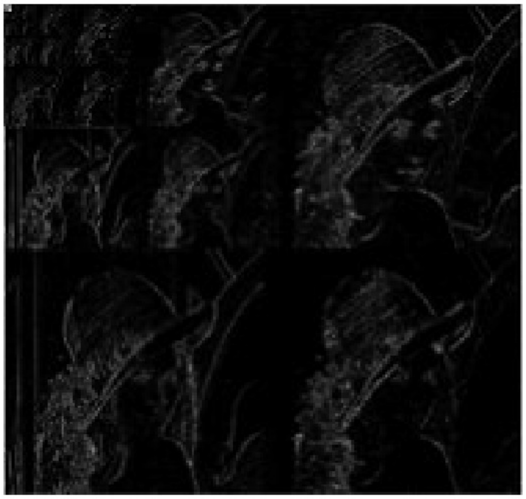
Biorthogonal



Symlet 4



Coiflets



Reverse Bior

Fig. 5.10 Wavelet spectra for the Lena image

Discrete wavelets are differentiated by their *shapes*, *orders* (vanishing moments) and *compact support*. The combination of the three factors determines the result of a wavelet transform. The choice of a wavelet usually depends on the nature of the data and applications such as image analysis, image processing or image compression. Often it requires a number of trials to determine the optimal combination of the three factors. Results of a wavelet transform also depends on if the wavelet is overlapped or not. The *maximal overlap discrete wavelet transform* (MODWT) has found popular application in image analysis.

Shape of a wavelet. The shape of a wavelet is characterized by its *symmetry* and *regularity*. A *symmetric wavelet* shows no preferred direction in time/space, while an asymmetric wavelet gives unequal weighting to different directions. *Regularity* is related to how many continuous derivatives a function has. Therefore, regularity is a measure of smoothness of a wavelet. Generally, to detect an edge in the data, a wavelet needs to be sufficiently regular. The regularity is also related to the order, the higher the order, the smoother the wavelet.

For image analysis, however, research has shown that the shape of a wavelet does not have significant influence on classification results [8].

Vanishing moments. An important property of a wavelet function is the number of *vanishing moments*, which characterize how a wavelet interacts with various signals. The names for many wavelets are derived from the number of vanishing moments. For example, db6 is the Daubechies wavelet with six vanishing moments and sym3 is the symlet with three vanishing moments. Generally, a wavelet with N vanishing moments is *orthogonal* to *polynomials* of degree N-1. For example, Daubechies 2 wavelet has 2 vanishing moments. When the Daubechies 2 wavelet is used to transform a data, both the *mean* and any *linear* trend are removed from the data. A higher number of vanishing moments imply that more moments (quadratic, cubic, etc.) will be removed from the data, which results in fewer significant wavelet coefficients. It also means higher order wavelets can capture or represent more frequency bands in the data. Higher order wavelets typically have more oscillations and require wider support. A wavelet with N vanishing moments must have a support of at least length $2N-1$.

The choice of wavelet order depends on the nature of the data; usually, it requires a number of empirical tests on the data. Theoretically, the order of the wavelet should be greater than $2H + 1$, where H is the *Hurst exponent* of a signal or data [8, 9]. H can be determined using the similar technique of finding the *fractal dimension* as described in Sect. 5.2.4.

Compact support. This value measures the effective width of the wavelet function. A narrow wavelet function such as haar, db2 or sym2 can capture closely spaced or finer features and are fast to compute, but a narrow wavelet tends to have low-frequency resolution. Conversely, a wavelet with large compact support such as the Daubechies 24 is smoother and have finer frequency resolution which is usually more efficient for denoising.

Wavelets with large support tend to result in coefficients that do not distinguish individual features. Research has shown that wavelets with wider compact support provide increased sensitivity to group differences, which leads to higher classification accuracy [8]. However, wavelet with very large compact support can decrease the localization of prominent features and more coefficients are affected by boundary conditions. In practice, wavelets with an optimal compact support can be found using an empirical test.

MODWT. MODWT is highly redundant and invariant under circular shift. This causes MODWT preserving the smooth time-varying structure in regional time series that is otherwise lost during the application of DWT [8]. MODWT is adaptive to any signal length and emphasizes on variance analysis, which is desirable for feature extraction. Research shows that MODWT has superior performance than ordinary DWT [8]. This is supported by the fact that in literature Gabor filters are usually preferred than ordinary DWTs.

5.3.3.2 Contrast of DWT and Other Spectral Transforms

If we give a comparison between wavelets, sinusoids (FT), STFT and Gabor filters, we have the following contrasts:

- **Orthogonality**. Both wavelets and sinusoids are orthogonal (1.2–1.6), while Gabor filters are not.
- **Window**. Wavelets, STFT and Gabor filters are windowed transforms, while FT is not.

- **Window attenuation**. Both wavelets and Gabor filters attenuate toward the border of a window, while STFT does not.
- **Various window size**. Wavelets vary window size, while STFT and Gabor filters do not.
- **Directionality**. Both wavelets and Gabor filters are directional transforms, while FT and STFT are not.
- **Multiresolution**. Wavelets are multiresolution transforms, while Gabor filters, FT and STFT are not.

Overall, wavelets have more advantage over FT, STFT and Gabor filters. It can observed from Fig. 5.10 that different from both FT and STFT, wavelets successfully capture the edge information of the image which is the most useful texture feature. The next is to focus on extracting texture features from the DWT spectrum.

5.3.3.3 Multiresolution Analysis

Space (time)-frequency methods attempt to find a specific frequency at a specific location, which is the main shortcoming of FT and STFT. However, it is not possible to find a specific frequency at a specific location simultaneously, just like we cannot get both a global view (zooming out) and a local view (zooming in) of a map at the same time (we lose global view when get too close to the map for details, and we lose details when we zoom out for a global view of the map). The solution is to use multiresolution or multiview to create a tradeoff between spatial resolution and frequency resolution.

Multiresolution methods are designed to obtain a good spatial resolution but less accurate frequency resolution at high frequencies or a good frequency resolution but less accurate spatial resolution at low frequencies (Fig. 3.1 left). By using multiresolution or multiview approach, both global view and local view of an image are obtained and a complete picture of an image is preserved, although not simultaneously. This approach is useful when a signal or an image contains both fine details in small areas and homogenous patches in larger areas. Usually, 2-D images follow this type of frequency patterns. The multiresolution analysis effectively overcomes the window size problem of STFT. Therefore, multiresolution approaches are more effective in image analysis, and they overcome the frequency and location dilemma found in both FT (global view) and STFT (local view).

The coefficients at each subband of a wavelet transform are usually scarce; they are not suitable for direct image representation. Statistics such as those proposed in the GLCM and Gabor filters can be computed from each subband of a wavelet transform. More robust features can be computed from each subband by using Gaussian mixture model. Since high-frequency components are more important for texture representation, features from lower scale subbands are usually given more weight.

Because digital wavelet transform (DWT) is done by two passes of 1D wavelet transform on rows and columns respectively, wavelets can only capture edge information on horizontal, vertical and diagonal directions. This gives Gabor filters an edge over wavelet on texture representation and retrieval because Gabor filters can be tuned to more directions than conventional wavelets. However, neither wavelets nor Gabor filters can effectively capture highly anisotropic elements like the curves from an image; this is the rational behind the introduction of curvelet in the next section.

5.3.4 Texture Features Based on Curvelet Transform

5.3.4.1 Curvelet Transform

Both Gabor filters and wavelets let us do space-frequency analysis of images. Gabor filter is an improvement to STFT by using a Gaussian window and multiorientations; however, it still uses a fixed window size for different frequencies. This is equivalent to looking at an image for details from a fixed distance, which is difficult. Wavelets use different window sizes for different frequencies, this creates a multiresolution view of an image and is equivalent to looking for different levels of details of an image from different distances. Therefore, wavelet is a more accurate simulation to human vision system. However, wavelet can only capture texture features from three directions, which are not sufficient for image analysis.

Curvelet [10] has been introduced in literature to take the advantages of both Gabor filters and wavelet, while overcome the limitations of both. Specifically, a curvelet is orthogonal and multiresolution like a wavelet, while it can be tuned to multiorientation like Gabor filters as well. In other words, a curvelet is a wavelet tuned to multiorientations and can capture curved or nonlinear edges in an image instead of just linear edges. Therefore, it is a more powerful tool for image analysis.

Basically, curvelet transform extends the ridgelet transform to multiple scale analysis. Given an image $f(x, y)$, the continuous curvelet transform is defined as [11, 12]:

$$\mathfrak{R}_f(a, b, \theta) = \iint \psi_{a,b,\theta}(x, y) f(x, y) \mathrm{d}x\mathrm{d}y. \tag{5.33}$$

where a ($a > 0$) is the scale, b is the translation, θ is the orientation and ψ is the curvelet which is defined as following:

$$\psi_{a,b,\theta}(x, y) = a^{-\frac{1}{2}} \psi\left(\frac{x\cos\theta + y\sin\theta - b}{a}\right) \tag{5.34}$$

where θ is the orientation and a is the scale of the curvelet. A curvelet is constant along the lines: $x\cos\theta + y\sin\theta = b$, and transverse to these ridges are wavelets. Compared with wavelet definition, the location parameters (b_1, b_2) of wavelet are replaced by the line and orientation parameters (b, θ) in a curvelet. In other words, the two transforms are related by [12]:

$$\begin{array}{ll} \text{Wavelet:} & \psi_{\text{scale, point-position}} \\ \text{Curvelet:} & \psi_{\text{scale, line-position}} \end{array}$$

In contrast, Gabor filters are Gaussian-shaped wavelets tuned to different orientations and scales.

$$g_{a,\theta,b_1,b_2}(x, y) = a^{-\frac{1}{2}} g\left(\frac{x\cos\theta + y\sin\theta - b_1}{a}, \frac{-x\sin\theta + y\cos\theta - b_2}{a}\right) \tag{5.35}$$

where the mother wavelet $g(x, y)$ is a Gaussian envelope modulated by a sinusoid wave. The shapes of the three types of wavelets are shown in Fig. 5.11 [11].

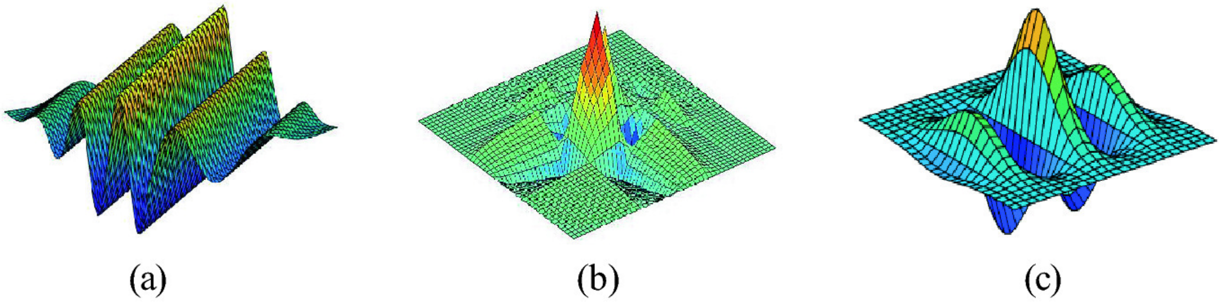

(a) (b) (c)

Fig. 5.11 Comparison of curvelet, wavelet and Gabor filter. **a** A curvelet; **b** a Daubechies wavelet and **c** a Gabor filter

It can be seen from the above figure, compared with both the wavelet and Gabor filter, a curvelet is the most sensitive to lines and edges in an image.

Similar to Gabor filters, a mother curvelet can be tuned to different orientations and different scales to create the curvelets (Fig. 5.12).

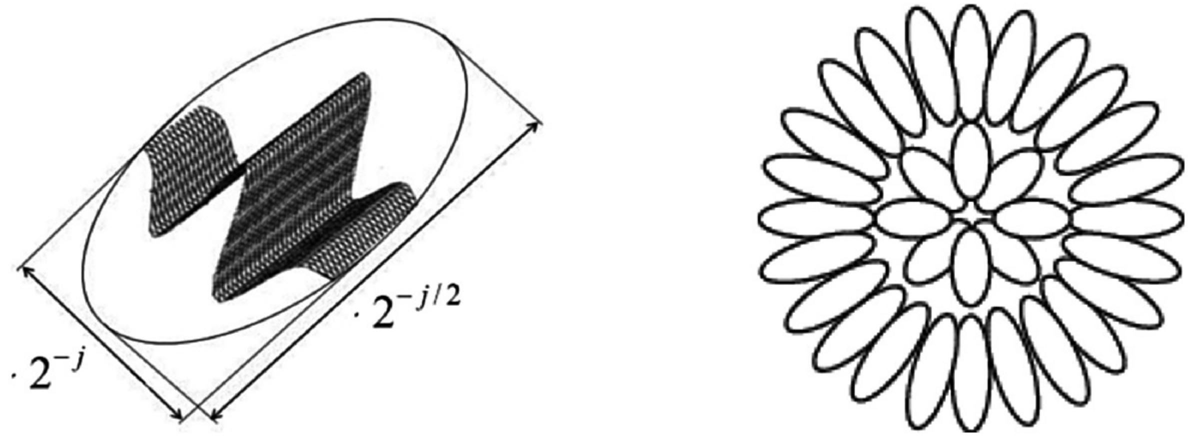


Fig. 5.12 Curvelet and curvelet tiling in spatial domain. Left: a single curvelet with width 2^{-j} and length $2^{-j/2}$; Right: curvelets tuned to 2 scales at different orientations

Curvelet takes the form of a basis element and obtains a high anisotropy. Therefore, it captures the edge information more effectively because it’s sharper than a wavelet and a Gabor filter. Although a curvelet is linear in its edge direction, due to its elongated and orientated design, it aligns with curved edges much better than conventional wavelets do. The contrast between wavelet and curvelet on capturing curved edge information is shown in Fig. 5.13 [12, 13]. It can be observed that curvelets, at higher scales, capture the edge information more accurately and tightly than wavelets.

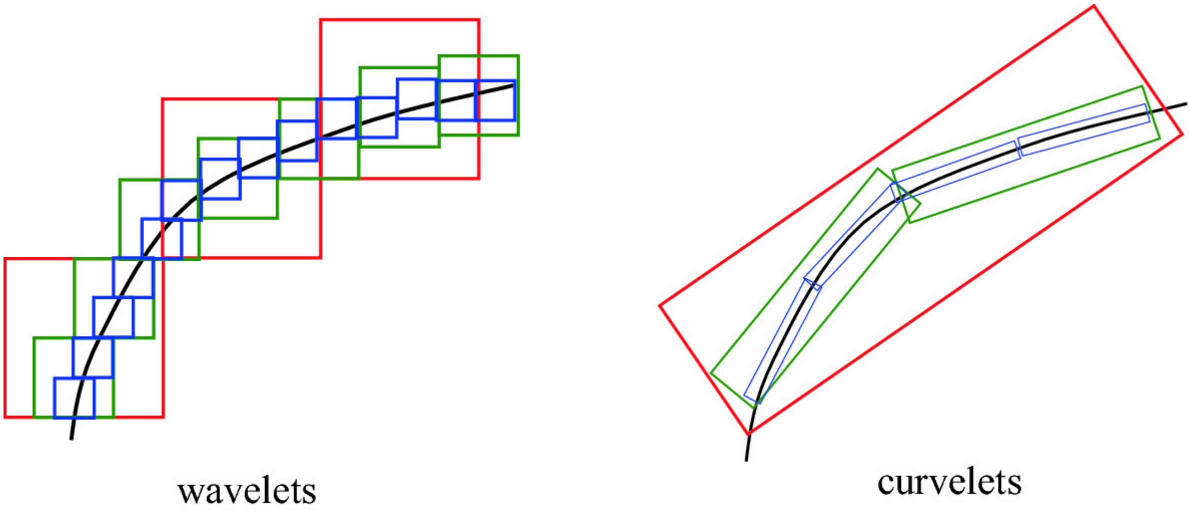


Fig. 5.13 Edge representation using wavelets and curvelets

5.3.4.2 Discrete Curvelet Transform

Given a digital image $f(m, n)$, $0 \leq m \leq M - 1$, $0 \leq n \leq N - 1$, the discrete curvelet transform is given as following:

$$C_{j,\theta}(k,l) = \sum_{n=0}^{N-1} \sum_{m=0}^{M-1} f(m,n)\,\psi_{j,\theta,k,l}(m,n) \tag{5.36}$$

where $\psi_{j,\theta,k,l}(m, n)$ is a discrete curvelet; j, θ are the scale and orientation respectively; and k, l are the spatial location parameters. The frequency response of a curvelet is a wedge, and the curvelet tiling of frequency plane is shown in Fig. 5.14.

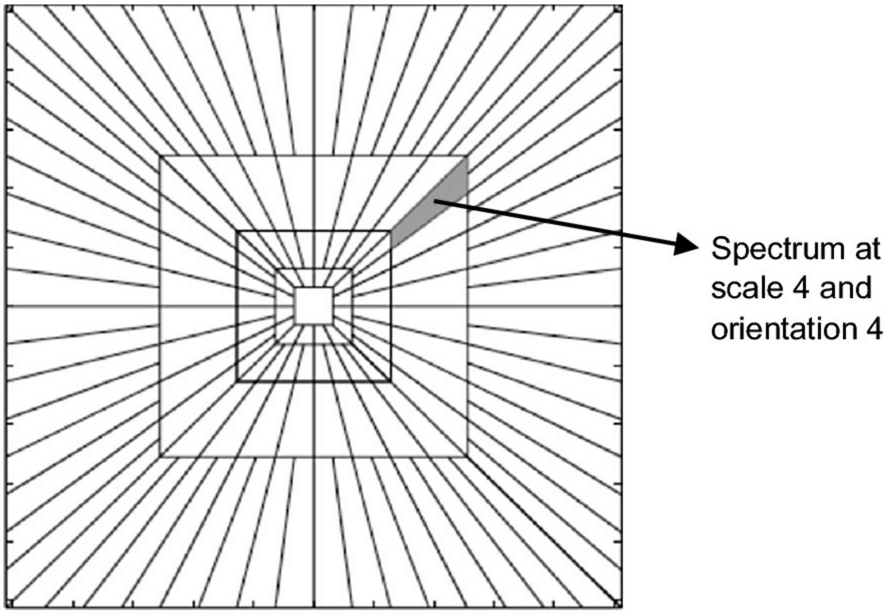
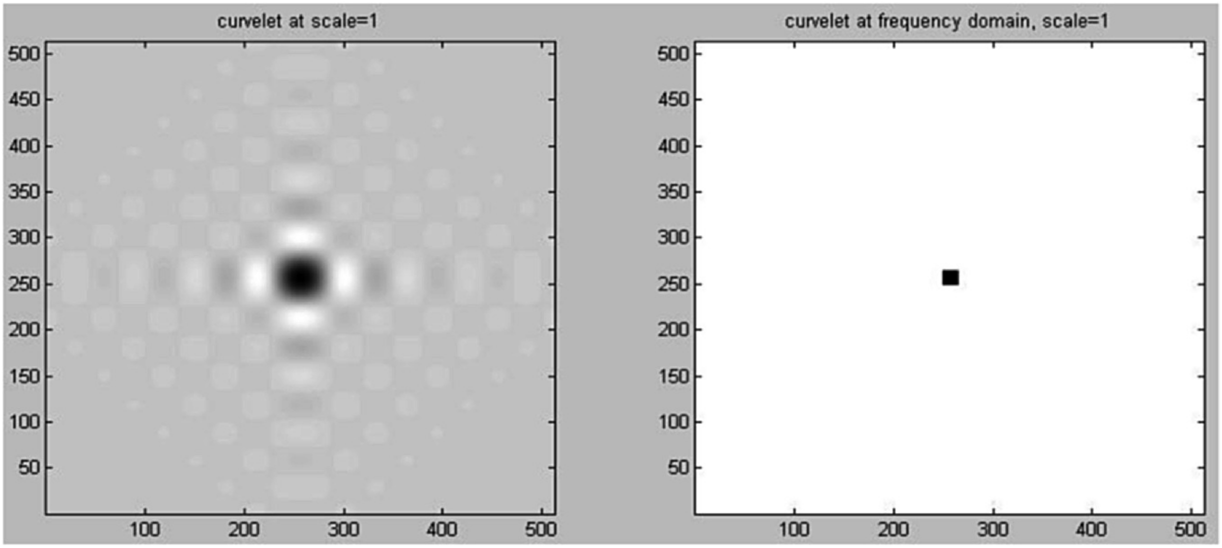
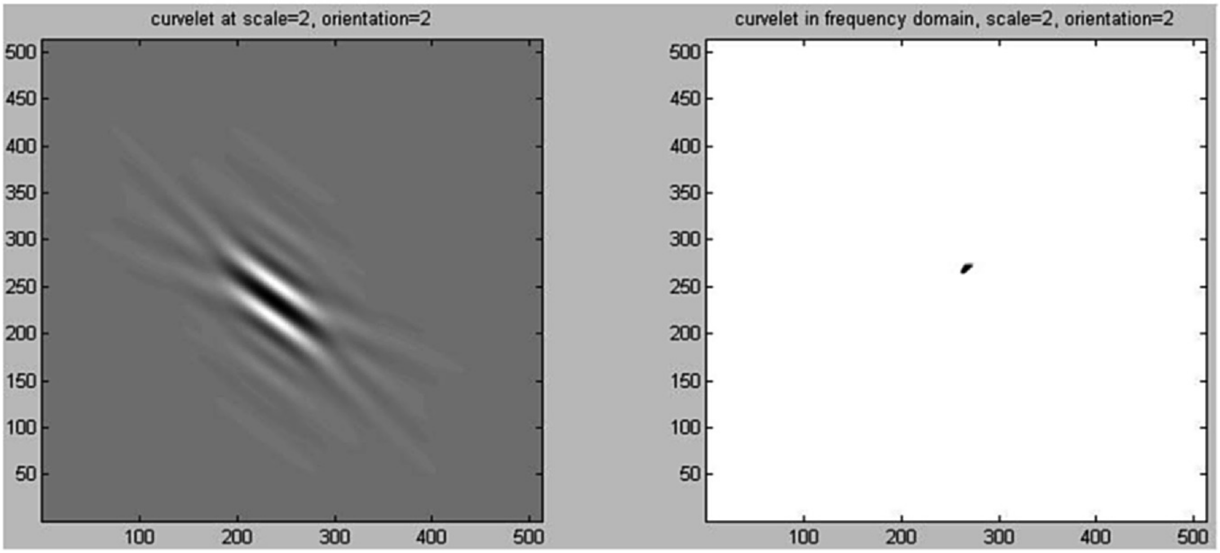
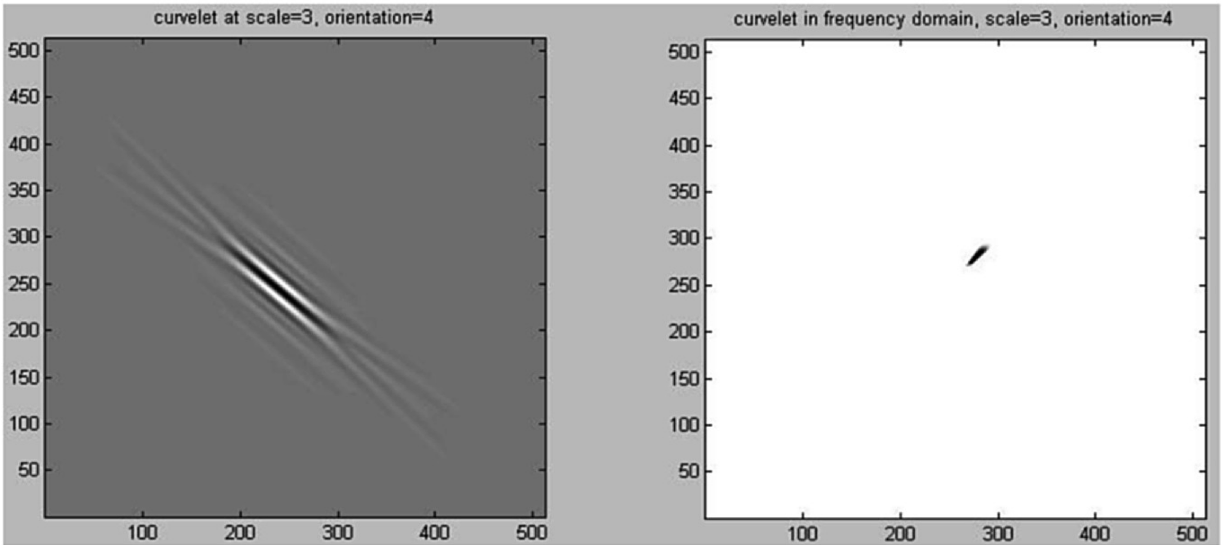

Spectrum at
scale 4 and
orientation 4

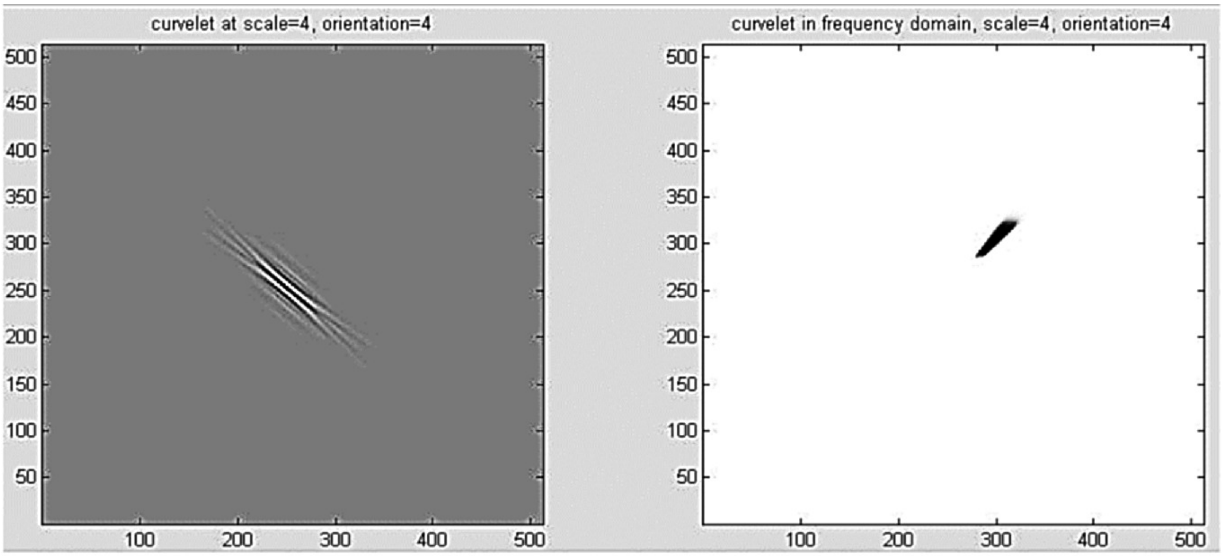
Fig. 5.14 Curvelet tiling of frequency plane with 5-level curvelets

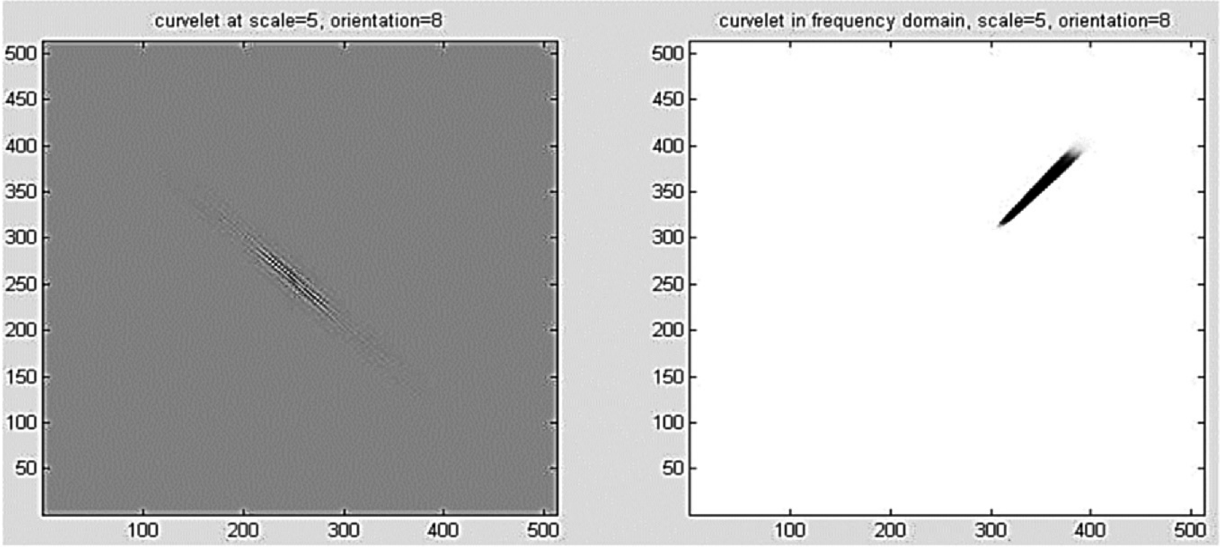
Curvelets exhibit an oscillating behavior in the direction perpendicular to their orientation in frequency domain. A few curvelets at different scales and their frequency responses are shown in Fig. 5.15 [3]; the scales shown on the figure are scales in frequency domain.


curvelet at scale=1
curvelet at frequency domain, scale=1
50
100
150
200
250
300
350
400
450
500


curvelet at scale=2, orientation=2
curvelet in frequency domain, scale=2, orientation=2
50
100
150
200
250
300
350
400
450
500


curvelet at scale=3, orientation=4
curvelet in frequency domain, scale=3, orientation=4
50
100
150
200
250
300
350
400
450
500


curvelet at scale=4, orientation=4
curvelet in frequency domain, scale=4, orientation=4
500
450
400
350
300
250
200
150
100
50
100
200
300
400
500


curvelet at scale=5, orientation=8
curvelet in frequency domain, scale=5, orientation=8
500
450
400
350
300
250
200
150
100
50
100
200
300
400
500

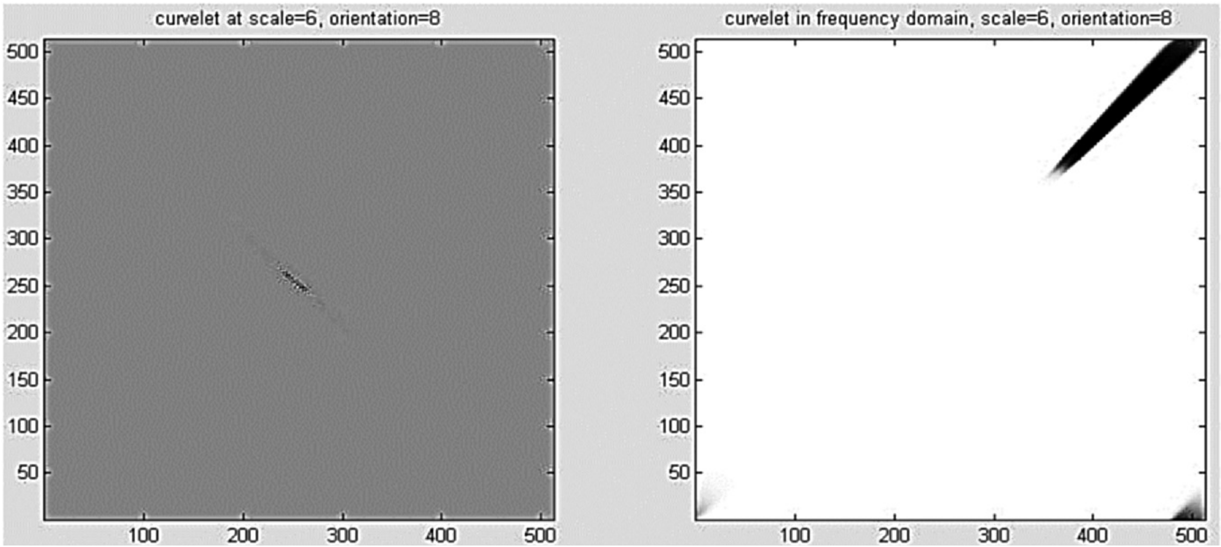

curvelet at scale=6, orientation=8
curvelet in frequency domain, scale=6, orientation=8
500
450
400
350
300
250
200
150
100
50
100
200
300
400
500

Fig. 5.15 Curvelets at different scales are shown in the spatial domain (left) and in the frequency domain (right) respectively

It can be observed that the curvelet is non-directional at the coarsest scale, whereas at highest scales, the curvelet waveform becomes so fine that it looks like a needle-shaped element. With increase in the resolution level, a curvelet becomes finer and smaller in the spatial domain and shows more sensitivity to curved edges which enables it to effectively capture curves in an image.

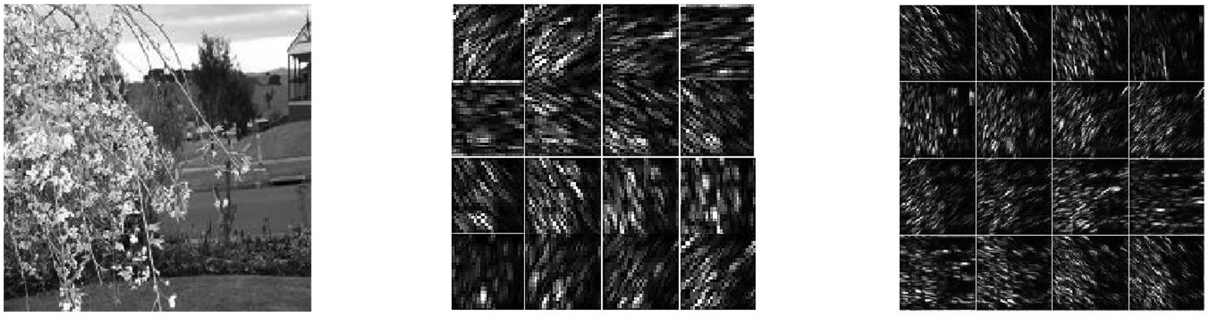
Although curvelet has an advantage of capturing nonlinear edges in an image, the computation of curvelet transform is more complex than both the Gabor filters and wavelet. Similar to Gabor filters, to achieve efficiency, curvelet transform is implemented in the frequency domain. That is, both the curvelet and the input image I are transformed into FT domain using FFT and the two FFTs are then multiplied in the FT domain. The product is then transformed back using the inverse fast Fourier transformed (FFT^{-1}) to obtain the curvelet coefficients. The process can be described as:

$$\text{Curvelet transform } (I) = \mathrm{FFT}^{-1}[\,\mathrm{FFT}(\text{curvelet}) \times \mathrm{FFT}\ (I)\,] \quad (5.37)$$

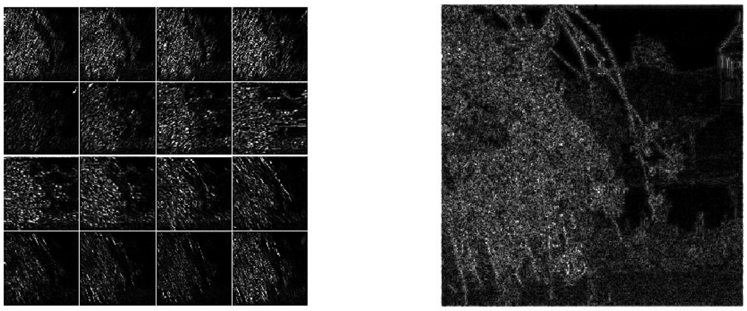
However, due to the FFT of the curvelet is a wedge, the product of the two FFTs needs to be wrapped back into a rectangle before it can be used for the FFT^{-1}. This wrapping process increases the computation cost.

5.3.4.3 Curvelet Spectra

Figure 5.16 shows some of the spectra of the curvelet transform on a flower image at different scales (in frequency domain) and orientations [11, 13]. The size of the spectra is adjusted for better viewing.



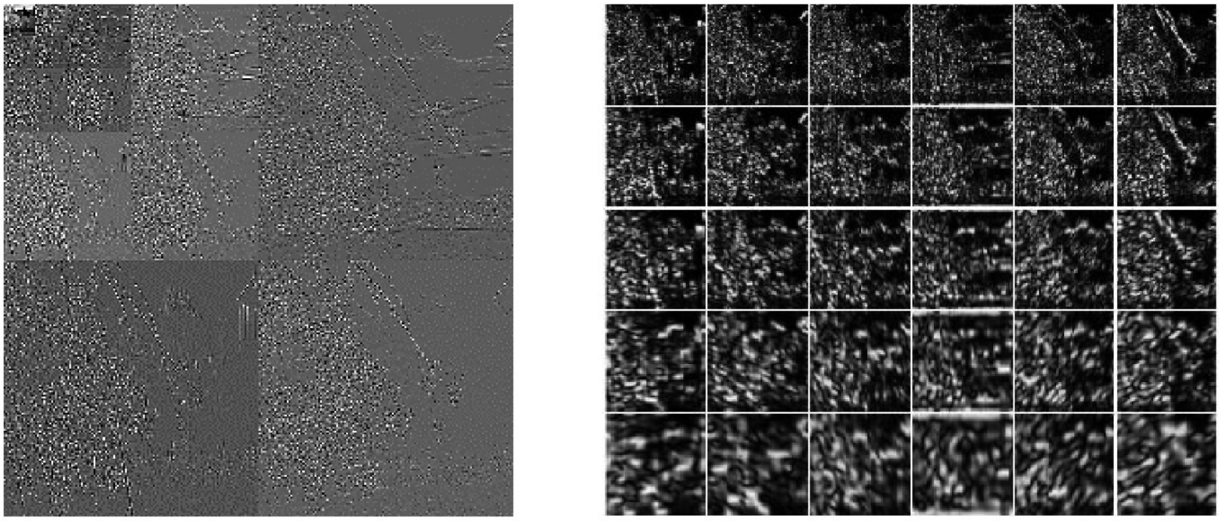
(a) Input image (b) subbands @ scale 3 (c) subbands @ scale 4



(d) subbands @ scale 5 (e) subband @ scale 6

Fig. 5.16 Curvelet subbands at different scales for a flower image (512 × 512). Each subband captures curvelet coefficients of the input image from one orientation

To contrast, the spectra of wavelet and Gabor filters are shown in Fig. 5.17:



(a) (b)

Fig. 5.17 Spectra of wavelets and Gabor filters for the flower image in Fig. 5.16a. **a** Wavelet spectra; **b** Gabor filters spectra

It can be observed from the above two figures, the spectra of Gabor filters have more redundancy than both the wavelet spectra and curvelet spectra due to the use of overlapping windows during the transform. The spectra of Gabor filters also looks more granular than those of both the wavelets and the curvelets. The spectra of wavelets are the most sparse and the most efficient in terms of reducing redundancy; therefore, wavelets are the choice for compression. Curvelet spectra are in between those of wavelet and Gabor filters. Curvelets are more sensitive to edges than Gabor filters and capture edges from more directions than wavelet. Furthermore, curvelets have little redundancy between different subbands. Curvelets also have a complete covering of the spectrum plane; this has overcome the spectra leakage of Gabor filters. However, due to there is a need to wrapping the wedge shape into a rectangle in order to do the invert FFT in (5.37), the computation is more complex than both Gabor filters and wavelets.

5.3.4.4 Curvelet Features

The feature extraction from curvelet transform is similar to Gabor filters. Once the curvelet transform is applied and the coefficients are obtained at each scale and orientation, the mean μ and standard deviation σ are computed for each of the subbands as following.

$$\mu_{s\theta} = \frac{E(s,\theta)}{m \times n}, \quad \sigma_{s\theta} = \frac{\sqrt{\sum_x \sum_y (|C_{s\theta}(x,y)| - \mu_{s\theta})^2}}{m \times n} \tag{5.38}$$

where s is the scale, θ is the orientation, m and n are the dimensions of the corresponding subband and $E(s,\theta) = \sum_x \sum_y |C_{s\theta}(x,y)|$ is the total spectral energy of the subband.

Therefore, for each curvelet, two texture features are obtained. If l curvelets are used for the transform, $2l$ texture features are obtained. A $2l$ dimension texture feature vector is used to represent each image in the database for image retrieval. To mitigate the dynamic range of the spectral energy, both the mean and standard deviation features are normalized using the maximum values of the corresponding features in the database.

Based on the curvelet subband division in Fig. 5.14, with 5 levels curvelet decomposition, 82 (= 1 + 16 + 32 + 32 + 1) subbands of curvelet coefficients are computed (only one subband is chosen from the last scale). However, due to the symmetry property, curvelet at angle θ produces the same coefficients as curvelet at angle $\theta + \pi$. Therefore, half of the subbands at scale 2–4 are discarded. As the result, 42 (= 1 + 18 + 16 + 16 + 1) subbands of curvelet coefficients are computed, and a 2 × 42 = 84 dimension feature vector is generated for each image. This dimension is higher than the feature vector from Gabor filters with the same scales due to Gabor filters usually use fewer orientations.

Rotation invariant curvelet features can also be created by using the circular shift method in Gabor filters.

5.3.5 Discussions

Several texture features based on spectral transforms have been introduced in this section, including DCT, Gabor filters, wavelets and curvelets. Although wavelets are orthogonal and more sensitive to edges, Gabor filters are more directional. This makes Gabor filters a better texture method in many applications. The performance of curvelet-based texture features can be affected by the computation complexity due to the irregular frequency response of curvelets.

Generally, spectral texture methods are much more robust than spatial texture methods when they are applied on homogenous texture images, due to their model simplicity and computation efficiency. However, spectral transforms are usually done in a squared window; therefore, it’s often difficult to apply spectral texture methods in irregular image regions, especially when the region size is not big enough. In these situations, the DCT-based texture method can be used because the 8 × 8 window is small enough to fit with most of image regions.

5.4 Summary

This chapter introduces and discusses a number of widely used texture feature extraction methods. Generally speaking, spectral texture methods such as texture features extracted from Gabor filters, wavelet transform and curvelet transform are much more powerful and robust than spatial methods such as Tamura, GLCM, MRF and FD. This is because spectral methods are based on either multiresolution or multiscale analysis which is more robust to noise and scale changes.

However, spectral and spatial methods both have advantages and disadvantages. Spectral texture methods generally capture edge information well while spatial texture methods can capture local structures well such as corners and shapes. Spatial texture methods are more intuitive than spectral texture methods. The use of different types of texture methods depends on applications. For example, for image classification, spectral texture methods are generally preferred; while for object detection and image registration, spatial texture methods are better choices because they need much more accurate matching.

5.5 Exercises

1. Find a grayscale image, use the Matlab code shown in the following web pages to compute the *mean* and *standard deviation* of the image. Then try them on similar images and different images, explain the pros and cons of the two statistics for image representation.
   https://au.mathworks.com/help/images/ref/mean2.html.
   https://au.mathworks.com/help/images/ref/std2.html.

2. Find a grayscale image and use the Matlab code from the following web page to compute a GLCM of the image: https://au.mathworks.com/help/images/ref/graycomatrix.html. Now calculate the *angular moment*, *contrast* and *correlation* of the GLCM using Eqs. (5.7–5.9). Try GLCM on the images you used in Exercise 1 and compare the effectiveness of the GLCM statistics with the ordinary statistics from Exercise 1.

3. Find a grayscale image and use the Matlab code from the following web page to compute the spectra of Gabor filters at different scales

and orientations. Now, apply the Gabor filters on the same images you used in both Exercises 1 and 2 and compute the mean and standard deviation of the Gabor spectra. Write a short report to compare the effectiveness of Gabor filter statistics with the ordinary statistics and GLCM statistics. https://au.mathworks.com/help/images/ref/imgaborfilt.html.

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6. Shape Representation

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The Creator has a model for every creation.

6.1 Introduction

A shape is a binary image. Mathematically, it is defined as

$$f\left(x,y\right)=\begin{cases}1 & \text{if } \left(x,y\right)\in D\\ 0 & \text{otherwise}\end{cases} \tag{6.1}$$

where D is the domain or area of the binary image.

Most of the objects in this world can be identified by their shapes, such as fruits, trees, plant leaves, buildings, furniture, birds and fishes. Figure 6.1 shows a few examples of shape images; the first two are shapes with a contour, while the last two are shapes with interior content.

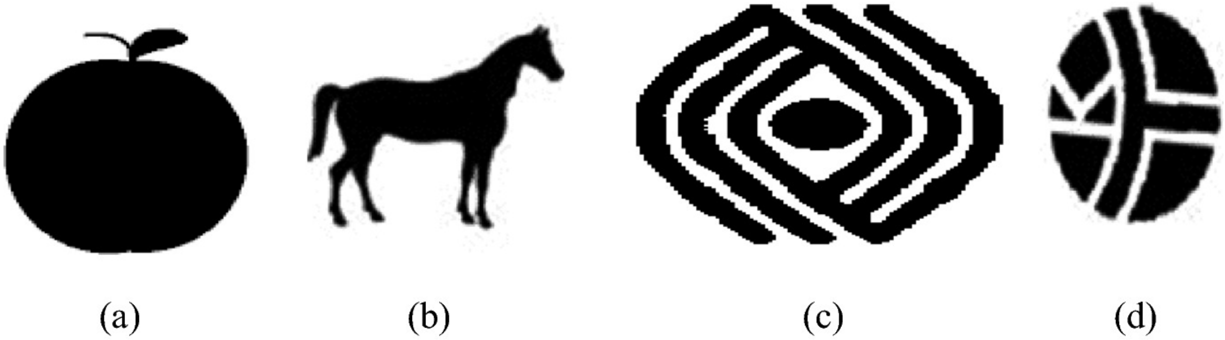

(a) (b) (c) (d)

Fig. 6.1 Examples of shape images

A shape can be defined by its boundary/contour like Fig. 6.1a and b, or by its interior content like Fig. 6.1c and d. There is variety of shape methods, and they can be generally grouped into either contour-based method or region-based method. A number of perceptual shape descriptors have also been proposed to capture both contour and region features. The design of a shape descriptor usually follows the principles suggested by MPEG-7: good retrieval accuracy, compact features, general application, low computation complexity, robust retrieval performance (affine invariance and noise resistance) and hierarchically coarse to fine representation.

However, shape description is a difficult task, because it is difficult to define perceptual shape features and measure the similarity between shapes. To make the problem more complex, shape is often corrupted with noise, defection, arbitrary distortion and occlusion.

6.2 Perceptual Shape Descriptors

There are a number of simple shape descriptors which can be computed according to human perception, such as perimeter, area, compactness, Euler number, circularity, eccentricity, major axis orientation, bending energy and convexity. These individual shape descriptors can be combined to create a more powerful descriptor to represent a shape.

6.2.1 Circularity and Compactness

Circularity represents how a shape is close to a circle, and it also indicates how compact the shape is or not. Mathematically, it is defined as the ratio of the area of a shape (A_s) to the area of a circle (A_c) having the same perimeter:

$$C = A_s / A_c \tag{6.2}$$

Assume the perimeter of the shape is p, and the area of the circle with the same perimeter p is given by

$$A_c = p^2 / 4\pi \tag{6.3}$$

Therefore,

$$C = 4\pi A_s / p^2 \tag{6.4}$$

By this definition, the shape with the largest circularity is a circle with circularity of 1. Since 4π is a constant, circularity can be simply defined as:

$$C = A_s / p^2 \tag{6.5}$$

Rectangularity and *ellipse variance* can be defined in a similar way to circularity.

The circularity descriptor defined in this way can cause confusions at certain situations. For example, the following two shapes would have the same circularity or compactness according to the above definition, although perceptually they look very different. Fig. 6.2

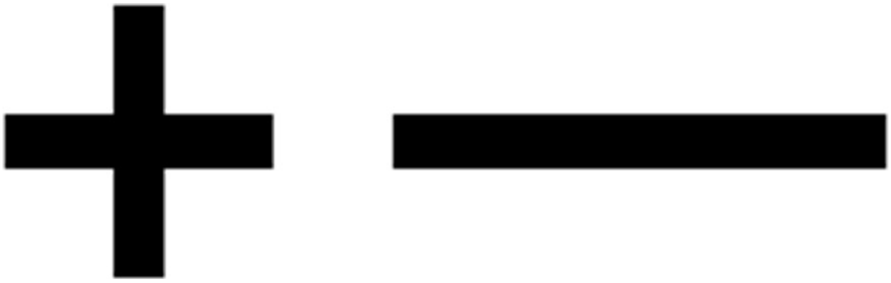


Fig. 6.2 Two different shapes with same circularity

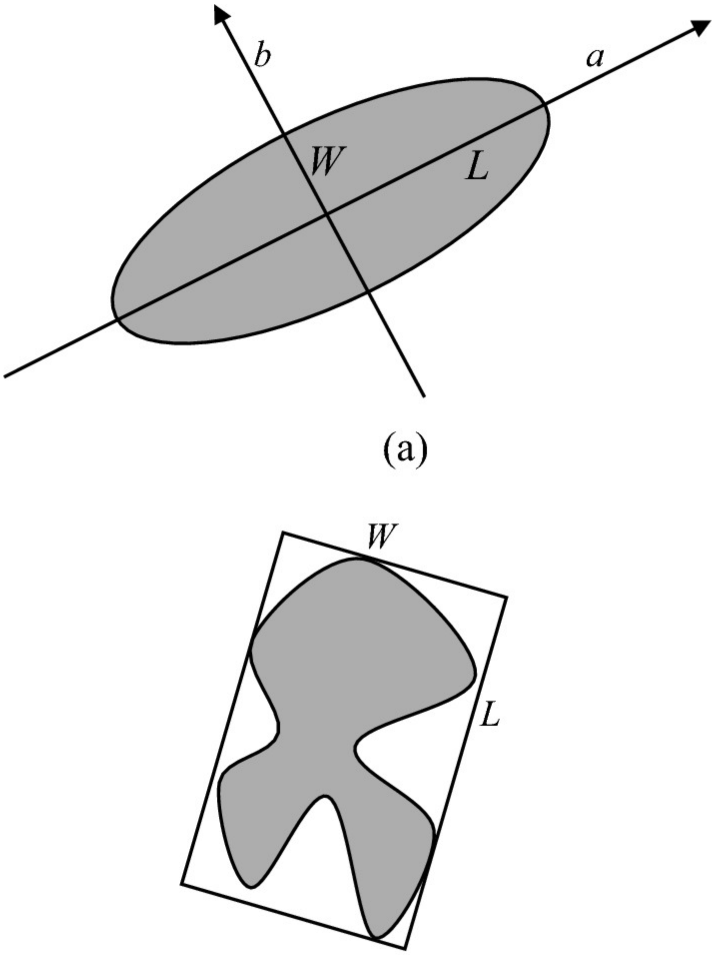
Furthermore, the above circularity is too sensitive to noise and irregularity. Therefore, a more robust circularity descriptor has also been defined. It is defined as the following ratio:

$$C = \sigma_R / \mu_R \tag{6.6}$$

where μ_R stands for the mean of the radial distance from the centroid of the shape to shape boundary points and σ_R stands for the standard deviation of the radial distance from the centroid to shape boundary points.

6.2.2 Eccentricity and Elongation

Eccentricity is defined as the ratio of the length of the longest chord of the shape to the longest chord perpendicular to it. Eccentricity can be computed using either the principle axis method (Fig. 6.3a) or the minimum bounding box method (Fig. 6.3b).



(a)

(b)

Fig. 6.3 Computation of eccentricity. **a** Eccentricity with principle axes; **b** eccentricity with minimum bounding box

In the above figure, the eccentricity of the shapes is given by

$$E = L/W \tag{6.7}$$

The principle axis can also be found using the principle component analysis (PCA) method. *Eccentricity* indicates the *elongation* of a shape; the larger the eccentricity, the more elongated the shape.

Elongation is defined as:

$$El = 1 - W/L \tag{6.8}$$

0 ≤ *El* ≤ 1. A circle, a square or any symmetric shape would have the least elongation (0), while objects like eels, poles, road, etc., would have an elongation close to 1. *Elongation*, however, can fail when an elongated shape is bent. For example, a curled eel (Fig. 6.4) would have a small or even 0 elongation although perceptually it is still an elongated object.

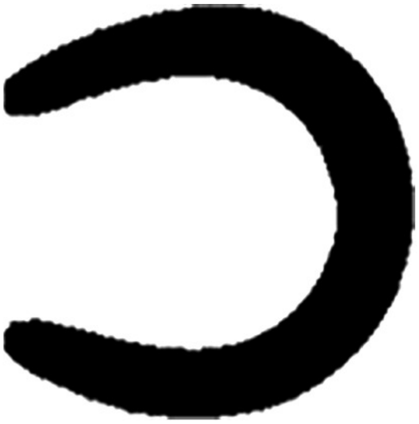


Fig. 6.4 A curled eel with 0 elongation

6.2.3 Convexity and Solidarity

A region is convex if for any two points with the region, the entire line segment linked by the two points is also inside the region. A convex hull of a shape is the smallest convex region that includes the shape. Fig. 6.5

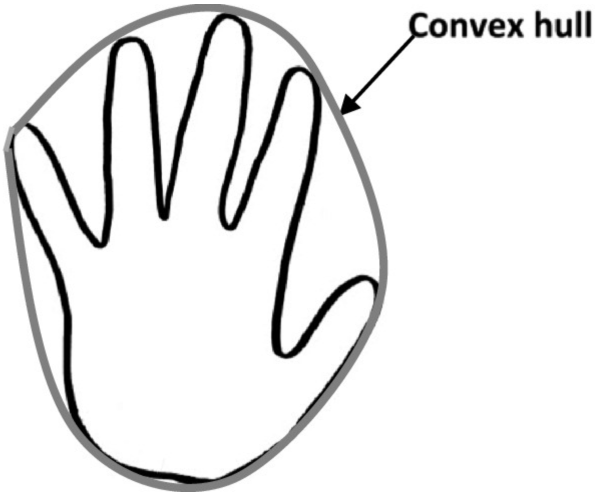


Fig. 6.5 A hand shape and its convex hull

Convexity is then defined as the ratio of the perimeter of the convex hull of the shape (P_h) to the perimeter of the shape (P_s).

$$\text{Convexity} = P_h/P_s \tag{6.9}$$

Solidarity is defined as the ratio of the area of the shape (A_s) to the area of its convex hull (A_h).

$$\text{Solidarity} = A_s/A_h \tag{6.10}$$

The convexity and solidarity of a convex shape are always 1, and convexity and solidarity of non-convex shapes are smaller than 1.

6.2.4 Euler Number

Topology is the study of the properties which are unaffected by any deformation (e.g., rubber-sheet distortion). It is found that when a shape is deformed, the number of holes does not change by the deformation. Therefore, a useful topological descriptor is the *Euler number* which is defined as the difference between the number of holes H and the number of connected components C. A small *Euler number* indicates more holes in a shape.

$$En = C - H \tag{6.11}$$

For example, the Euler numbers of number 3, and letters A and B are 1, 0 and −1, respectively. Fig. 6.6

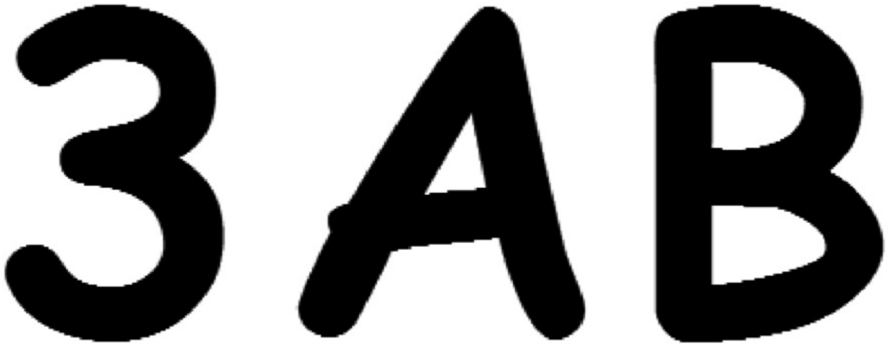


Fig. 6.6 Shapes with different Euler numbers

A hole area ratio (HAR) can also be defined in relation to Euler number:

$$HAR = A_h / A_s \tag{6.12}$$

where A_h is the total area of holes and A_s is the area of the shape.

6.2.5 Bending Energy

The *bending energy* (*BE*) is defined by [1]

$$BE = \frac{1}{N} \sum_{t=0}^{N} K(t)^2 \tag{6.13}$$

and

$$K(t) = (\dot{x}(t)\ddot{y}(t) - \ddot{x}(t)\dot{y}(t)) / (\dot{x}^2(t) + \dot{y}^2(t))^{3/2} \tag{6.14}$$

where $K(t)$ is the curvature function and N is the number of points on a contour. In order to compute a robust bending energy, the shape boundary is usually Gaussian smoothed before the *BE* calculation. It can be shown that a circle is the shape having the minimum bending energy.

The shape descriptors descripted in this section are computed according to human perception of the shape patterns. The advantage of using them is that they usually have a semantic meaning. However, the downside of these descriptors is that they are usually sensitive as shown in the circularity and eccentricity sections. It's difficult to describe a shape effectively using a single shape descriptor. Therefore, these perceptual descriptors are usually used as filters to eliminate shapes of large difference. They are often used together with other more powerful descriptors described in the following sections.

6.3 Contour-Based Shape Methods

Contour shape techniques only exploit shape boundary information. There are generally two types of very different approaches for contour shape modeling: *continuous approach* (global) and *discrete approach* (structural) [1]. *Continuous approaches* do not divide shape into subparts, and a multidimensional feature vector derived from the integral boundary is used to describe the shape. It starts to derive a 1D continuous function, called shape signature, from the shape boundary. After that, variety of techniques from signal processing, time series and statistics can be used to extract a feature vector from the shape signature. The matching between shapes is a straightforward process, which is usually a calculation of the Euclidean distance or city block distance between feature vectors.

Discrete approaches break the shape boundary into segments, called *primitives* using a particular criterion. The final representation is usually a string or a graph (or tree), and the similarity measure is done by string matching or graph matching.

6.3.1 Shape Signatures

The first step of contour-based shape methods is to obtain a 1D function from the shape boundary points, called shape signature. Many shape signatures exist, including *complex coordinates*, *polar coordinates*, *central distance*, *tangent angle*, *cumulative angle*, *curvature*, *area* and *chord length*.

In general, a *shape signature* $u(t)$ is any 1D function representing 2D areas or boundaries. A shape signature captures the perceptual feature of the shape, and it uniquely describes a shape. In the following, we assume the shape boundary coordinates $(x(t), y(t))$, $t = 0, 1, \ldots, N-1$, have been extracted in the preprocessing stage, and t usually means arc length. The preprocessing usually consists of a denoising procedure or a smoothing procedure and a contour tracing procedure.

6.3.1.1 Position Function

Position function, or *complex coordinates*, is simply the complex number generated from the boundary coordinates:

$$z(t) = [x(t) - x_c] + i\,[y(t) - y_c] \tag{6.15}$$

where (x_c, y_c) is the centroid of the shape, which is the average of the boundary coordinates

$$x_c = \frac{1}{N}\sum_{t=0}^{N-1} x(t), \quad y_c = \frac{1}{N}\sum_{t=0}^{N-1} y(t) \tag{6.16}$$

6.24 $z(t)$ is a complex number which captures the spoke features of a shape boundary. $z(t)$ is a translation-invariant signature due to the subtraction of the centroid. Rotation causes a circular shift to $z(t)$, and scaling of shape introduces linear change in $z(t)$. The use of position function as shape signature involves little computation. However, the position function needs to be further processed for matching; for example, a centroid distance signature can be computed from $z(t)$.

6.3.1.2 Centroid Distance

The *centroid distance* function is defined as the magnitude of $z(t)$, and it is expressed by the distance of the boundary points to the centroid (x_c, y_c) of the shape [1]:

$$r(t) = \left([x(t) - x_c]^2 + [y(t) - y_c]^2\right)^{1/2} \tag{6.17}$$

Same as $z(t)$, $r(t)$ is also invariant to translation. Rotation causes $r(t)$ circular shift, and scaling of shape changes $r(t)$ by a linear term. Different from $z(t)$ however, $r(t)$ is a real function which can be used for matching two shapes directly. Figure 6.7 (top) shows the centroid distance signatures of a tree shape. Due to the use of the centroid as the reference point, both $z(t)$ and $r(t)$ attenuate protruding features of a shape. As can be seen, the $r(t)$ function can generally capture the variations of a shape boundary well, like the 8 protruding corners on the tree boundary (marked by black dots). However, it does not capture the most prominent feature in a shape well if it is too thin like the tail of fish or the tail of an apple in Fig. 6.7 (center and bottom).

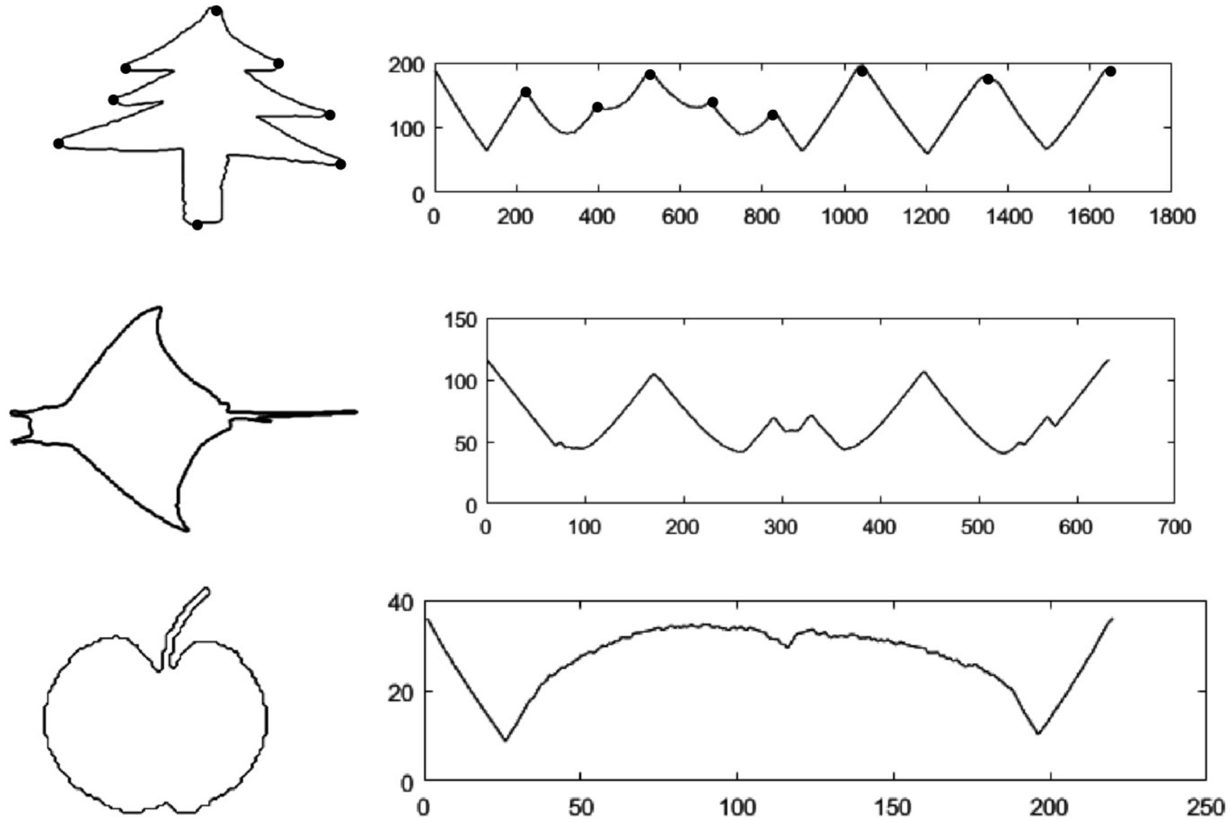
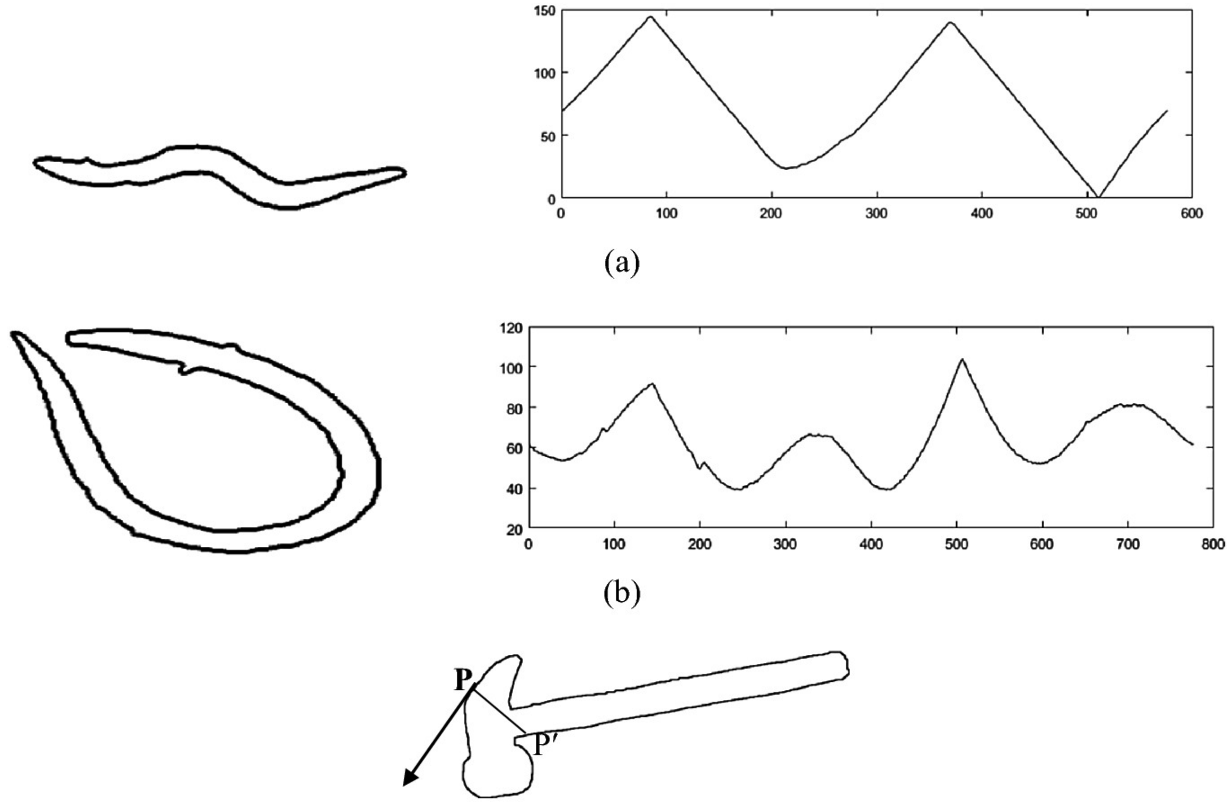


Fig. 6.7 Examples of centroid distance signatures. **Top row**: A tree shape on the left and its centroid distance signature on the right; **middle row**: A ray fish on the left and its signature on the right; **bottom row**: An apple shape on the left and its signature on the right

Another problem with $r(t)$ is that it uses the centroid as reference point. For shapes with high irregularity or low compactness, the centroid often falls outside the shape body. Consequently, the structure of the shape cannot be preserved by $r(t)$ when the shape is under distortion. For example, Fig. 6.8a and b shows, respectively, the $r(t)$ functions of two sea snakes, and it can be seen that the number of peaks in Fig. 6.8b is doubled compared with that of Fig. 6.8a.



(a)

(b)

(c)

Fig. 6.8 Computation of chord length signature. **a** A sea snake shape on the left and its $r(t)$ function on the right; **b** another sea snake shape on the left and its $r(t)$ function on the right; **c** illustration of computing $r^*(t)$ at point **P** of a hammer shape

In order to overcome the reference point problem of $r(t)$, *chord length signature* (CLS) $r^*(t)$ has been proposed. The chord length function $r^*(t)$ is derived from shape boundary without using any reference point. For each boundary point $\mathbf{P}(t)$, its $r^*(t)$ is defined as the distance between **P** and another boundary point **P′** such that **PP′** is perpendicular to the tangent vector at **P** and |**PP′**| is the shortest chord if there are more than one **P′**s perpendicular to **P** (Fig. 6.8c). $r^*(t)$ is invariant to translation. Rotation causes circular shift to $r^*(t)$. Scaling causes linear changes to $r^*(t)$.

$r^*(t)$ is more sensitive to noise than $r(t)$ due to the numeric approximation in computing the tangents at each boundary point and the angles needed to find the chords. To reduce noise sensitivity, an average filter or a median filter can be used to smooth the shape boundary before the signature extraction.

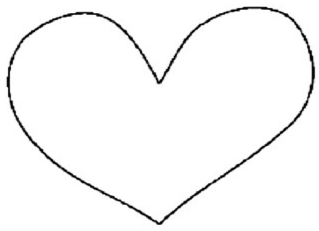
6.3.1.3 *Angular Functions*

Intuitively, the tangent angles of the shape boundary indicate the change of angular directions of the shape boundary. The change of angular directions is important to human perception. Therefore, shape can be represented by its boundary tangent angles:

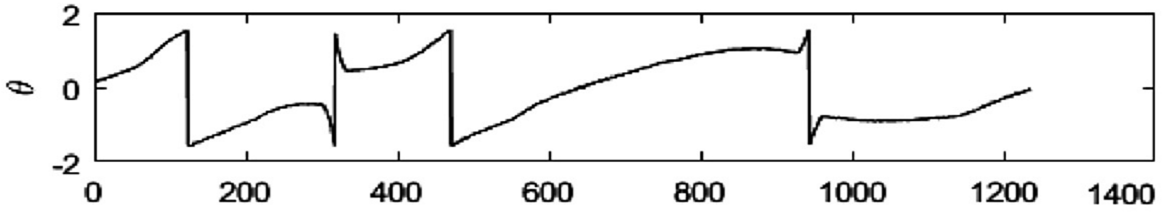
$$\theta(t) = \arctan \frac{y(t) - y(t-w)}{x(t) - x(t-w)} \tag{6.18}$$

where *w*, an integer, is a jump step used in practice to smooth the boundary. However the tangent angle function $\theta(t)$ can only assume values in a range of length π, usually in the interval of $[-\pi/2, \pi/2]$. Therefore $\theta(t)$ in general contains vertical jump/drop discontinuities at $\theta(t) = \pm\pi/2$ (Fig. 6.9b). One solution is to use the absolute function $|\theta(t)|$ instead of $\theta(t)$, as shown in (Fig. 6.9c), the vertical jump/drop discontinuities are removed from $|\theta(t)|$, and the structure of the shape is also preserved. However, the signature function still has sharp corners. Another solution is to use a *cumulative angular function* $\varphi(t)$ which is the net amount of angular bend between the starting position $z(0)$ and position $z(t)$ on the shape boundary

$$\varphi(t) = \theta(t) - \theta(0) \tag{6.19a}$$



(a)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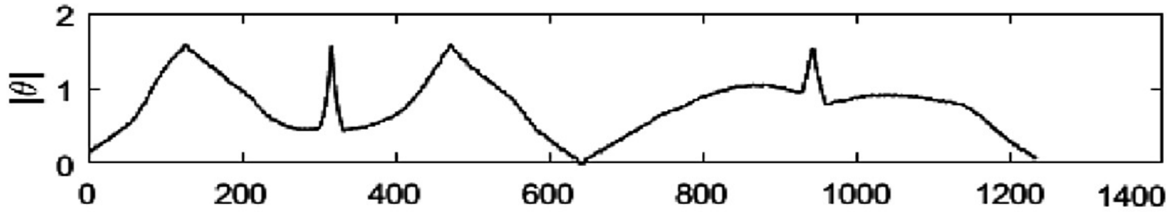
(b)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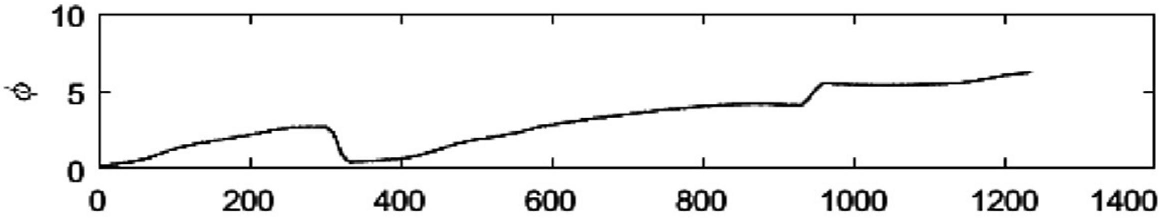
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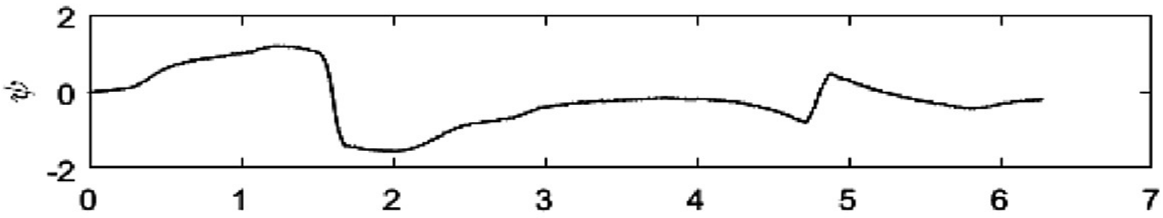
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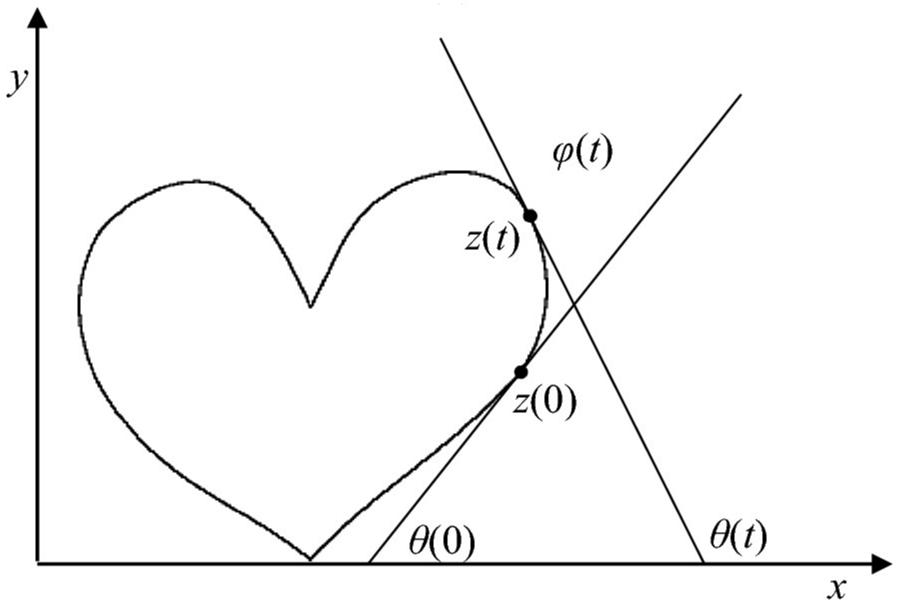


(f)

Fig. 6.9 Computation of angular signatures. **a** A heart shape; **b** $\theta(t)$ of (**a**); **c** $|\theta(t)|$ of (**a**); **d** $\varphi(t)$ of (**a**); **e** $\psi(t)$ of (**a**); **f** illustration of the computation of $\varphi(t)$

The computation of $\varphi(t)$ is illustrated in Fig. 6.9f. As shown in Fig. 6.9d, there is no vertical jump/drop in $\varphi(t)$ at places where $\theta(t) = \pm\pi/2$, and the two sharp angular changes on the heart boundary has been accurately captured. Because of the accumulation, $\varphi(t)$ has captured a linear trend in the function, therefore, a $\psi(t')$ (Fig. 6.9d) can be created by normalizing t into $[0, 2\pi]$ using $t' = \frac{2\pi}{L}t$ and taking away a linear term t' from $\varphi(t')$ if it is obtained in counter clockwise order (or adding t' if it is obtained in clockwise order).

$$\psi(t') = \varphi\left(\frac{L}{2\pi}t'\right) - t' \tag{6.19b}$$

where $t \in [0, L]$, L is the length of the shape boundary and $t' \in [0, 2\pi]$. The cumulative angular signature $\psi(t)$ is invariant to both translation and scaling. Rotation causes a shift in the signature.

6.3.1.4 *Curvature Signature*

Curvature is an important boundary feature. It is used widely for shape representation in the literature. *Curvature function* is given by (6.20):

$$\kappa(t) = \frac{\mathrm{d}\theta}{\mathrm{d}t} \tag{6.20a}$$

$$= \frac{x'y'' - y'x''}{(x'^2 + y'^2)^{\frac{3}{2}}} \tag{6.20b}$$

$$= \frac{\frac{\mathrm{d}^2y}{\mathrm{d}x^2}}{\left(1 + \left(\frac{\mathrm{d}y}{\mathrm{d}x}\right)^2\right)^{3/2}} \tag{6.20c}$$

where θ is defined in (6.18). A perfect circular shape would have a constant $\kappa(t)$ based on the definition of (6.20a). Curvature is an important boundary feature, however due to $\theta(t)$ is typically piecewise continuous and jumps at discontinuities, $\kappa(t)$ is zero almost everywhere and jumps at where $\theta(t)$ jumps. For example, Fig. 6.10 (Top) shows the $\kappa(t)$ of the tree shape in Fig. 6.7, while it successfully captures the 7 shape corners on the shape boundary, and it is jaggy. In order to use $\kappa(t)$ for shape representation, a shape boundary needs to be smoothed before curvature extraction. One way to smooth the shape boundary using a Gaussian filter (Fig. 6.10 Bottom).

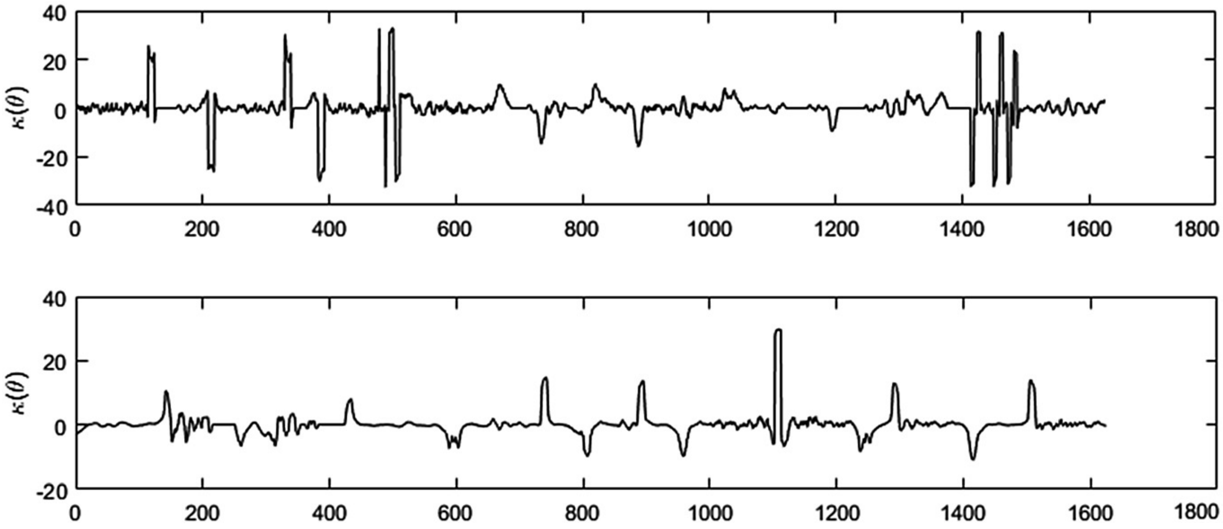


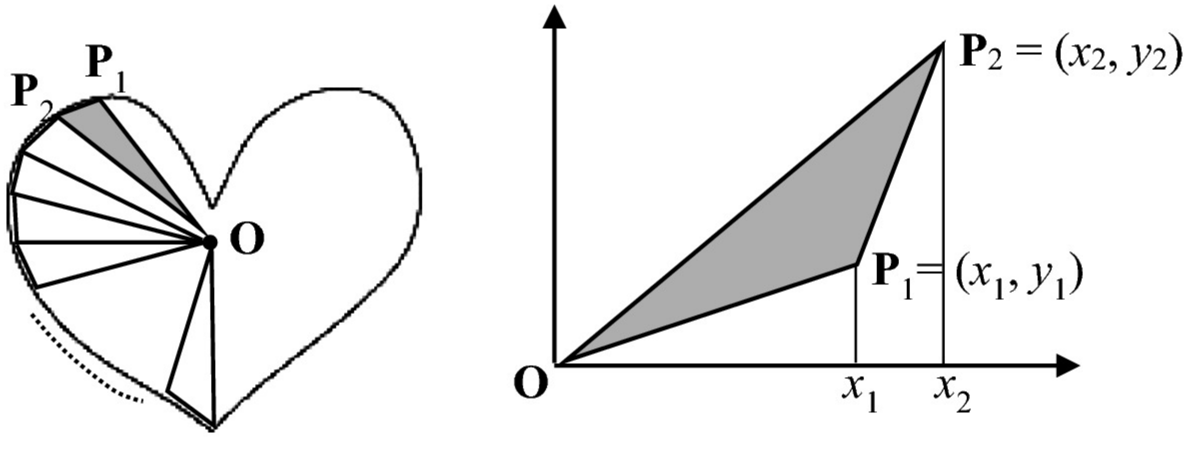
Fig. 6.10 Curvature signatures. Top: curvature signature of a tree shape from Fig. 6.7 without smoothing; bottom: curvature signature of the same tree shape with a Gaussian smoothing

Curvature is invariant to translation, rotation causes circular shift to the signature, and curvature signature is invariant to scaling if all shapes are normalized to the same number of points.

6.3.1.5 Area Function

It is known that the area of a triangle changes linearly under affine transformation. Linearity is a desirable property for shape representation, because normalization of linearity is equivalent to scale normalization which is simple. Therefore, an area signature is used in attempt to acquire a signature invariant to affine distortion [1].

When the boundary points change along the shape boundary, the area of the triangle formed by the two boundary points and the center of gravity also changes (Fig. 6.11a). For each boundary point, the area of the triangle with α degree angle at vertex **o** is calculated (Fig. 6.11b). This forms an *area function* which can be employed as shape representation.



(a) (b)

Fig. 6.11 Computation of area signature. **a** Triangulation of a heart shape; **b** illustration on the calculation of the area of the shaded triangle

For the triangle $\Delta\mathbf{OP}_1\mathbf{P}_2$ formed by **O**, $\mathbf{P}_1$ and $\mathbf{P}_2$ in Fig. 6.11b, its area is given by the following difference:

$$\Delta\mathbf{OP}_1\mathbf{P}_2 = \Delta\mathbf{OP}_2 x_2 - \Delta\mathbf{OP}_1 x_1 - \square x_1\mathbf{P}_1\mathbf{P}_2 x_2$$

Mathematically, the area is given by (6.21):

$$\begin{aligned} A(t) &= \frac{1}{2}x_2y_2 - \frac{1}{2}x_1y_1 - \frac{1}{2}(x_2 - x_1)(y_2 - y_1) - (x_2 - x_1)\,y_1 \\ &= \frac{1}{2}\left|x_1y_2 - x_2y_1\right| \end{aligned} \tag{6.21}$$

Because the area of a triangle and the central distance inside the triangle has a linear relationship, $A(t)$ is similar to $r(t)$ [1]; however, due to the numerical approximation of the area of a triangle, $A(t)$ is usually more jaggy than $r(t)$. Therefore, $A(t)$ needs to be smoothed for further feature extraction. $A(t)$ is linear under affine transformation.

6.3.1.6 Discussions

Shape signatures reduce shape matching in 2D space into 1D space, and this reduces the complexity of feature extraction. Shapes are usually normalized to be translation and scale invariant before signature extraction. Translation invariance is achieved by either using a reference point such as the centroid or using relative positions such as in the cases of curvature, angles and chord length. Scale invariance is achieved by first scaling all shape images to the same size and then normalizing shape boundaries to the same number of points. If shape signatures are used for shape matching, a shift matching is needed to find the best matching between two shapes. Alternatively, a signature can be quantized into a signature histogram, which is rotation invariant and can be used for matching.

Shape signatures are generally sensitive to noise and irregularities. Therefore, a shape boundary is typically smoothed before signature extraction to remove noise and small irregularities. However, significant irregularities can still cause large error in the matching; therefore, it is impractical to use shape signature for direct representation. Further processing is necessary to improve both matching efficiency and accuracy. The following sections describe methods on feature extraction from shape signatures and other robust contour shape methods.

6.3.2 Shape Context

The idea of shape context is similar to the shape signature methods discussed in Sect. 6.3.1. It also computes contour features from a shape boundary point by point. However, instead of computing a single feature value for each boundary point in the shape signature methods, a feature vector (histogram) is computed in shape context. Furthermore, the computation of the feature vector of each boundary point makes use of all the points on the boundary instead of just two points in the shape signature methods. This makes the shape context features more robust to boundary irregularities. The algorithm of shape context computation is summarized in the following.

1. Normalize a shape boundary to N points.

2. For each of the boundary points $\mathbf{P}$, find the vectors between $\mathbf{P}$ and all the other boundary points $\mathbf{P}_n$ (Fig. 6.12a).

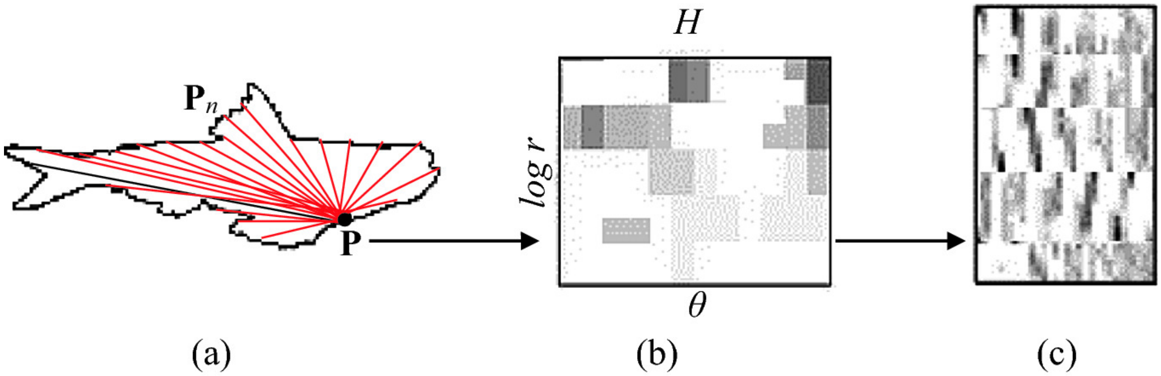


Fig. 6.12 Computation of shape context. **a** A point **P** on a shape boundary and all the vectors started from **P**; **b** the log-polar histogram H of the vectors from **P**, the histogram H is the context of point **P**; **c** the shape context map of shape of (**a**), each row of the context map is the flattened histogram of a point context, the number of rows is the number of sampled points

3. Quantize both the angles θ and the length r of the vectors at $\mathbf{P}$.

4. Create a 2D *logarithmic* histogram H of r on θ for each point $\mathbf{P}$ (Fig. 6.12b).

5. Flat the 2D histogram H into a 1D histogram h by concatenating the rows of H.

6. Concatenate *h*'s from all the boundary points $\mathbf{P}_n$ to form a histogram map which is the shape context (Fig. 6.12c).

The logarithm of *r* is to raise the contribution from neighboring points of **P** which would otherwise contribute too little due to significantly shorter vector length than that of points farther away from **P**. The process of computing a shape context is shown in Fig. 6.12 [2]. In Fig. 6.12a, a point **P** on the shape boundary and its vectors to all the boundary points $\mathbf{P}_n$ are shown. Figure 6.12b shows the logarithmic histogram of the vectors in Fig. 6.12a, and Fig. 6.12c shows the shape context map/matrix of the concatenated flattened histograms from all boundary points.

Shape context is invariant to translation due to the use of relative point position. Scaling invariance can be achieved by normalizing all shape boundaries to N points and normalizing the radial distances by the mean distance between all point pairs. Rotation invariance is done by finding the minimum of all shift matching of two shape context maps.

The matching of two shape contexts is complex. It minimizes the total cost of matching between one context matrix and all the permutations of another context matrix. This can affect the robustness of shape context significantly.

6.3.3 Boundary Moments

Moments can be computed to reduce the dimension of a boundary representation. Assume shape boundary has been represented as a *shape signature* $z(i)$, and the *r*th moment m_r and central moment μ_r can be estimated as [1]

$$m_r = \frac{1}{N}\sum_{i=1}^{N}[z(i)]^r \quad \text{and} \quad \mu_r = \frac{1}{N}\sum_{i=1}^{N}[z(i) - m_1]^r \tag{6.22}$$

where N is the number of boundary points. The normalized moments $\overline{m}_r = m_r/(\mu_2)^{r/2}$ and $\overline{\mu}_r = \mu_r/(\mu_2)^{r/2}$ are invariant to shape translation, rotation and scaling.

Boundary moments can also be computed from the boundary histogram. Suppose the amplitude of shape signature function $z(i)$ is quantized and a histogram $p(v_i)$ is created from the quantized $z(i)$. Then, the rth moment is obtained by

$$\mu_r = \sum_{i=1}^{K} (v_i - m)^r p(v_i) \quad \text{and} \quad m = \sum_{i=1}^{K} v_i p(v_i) \tag{6.23}$$

The advantage of boundary moment descriptors is that they are simple to compute and they are more robust than a shape signature. However, only a few low-order moments have physical meaning. In practice, the following three moment descriptors are usually used for shape description: $F_1 = (\mu_2)^{1/2}/m_1$, $F_2 = \mu_3/(\mu_2)^{3/2}$ and $F_3 = \mu_4/(\mu_2)^2$, which describes the variance, skewness and kurtosis of the boundary.

6.3.4 Stochastic Method

Time-series models and especially autoregressive (AR) modeling have been used for calculating shape descriptors. A linear autoregressive model expresses a value of a function $f(x)$ as a linear combination of a certain number of preceding values. Specifically, each function value in the sequence has some correlation with previous function values and can therefore be predicted through a number of, say, M observations of previous function values. The autoregressive model is a simple prediction of the current radius by a linear combination of M previous radii plus a constant term and an error term:

$$f_t = \alpha + \sum_{j=1}^{m} \theta_j f_{t-j} + \sqrt{\beta}\omega_t \tag{6.24}$$

where θ_j, $j = 1, 2, \ldots, m$ are the AR-model coefficients, m is the model order, and it tells how many preceding function values the model uses. $\sqrt{\beta}\omega_t$ is the current error term or residual, reflecting the accuracy of the prediction. α is proportional to the mean of function values. The parameters $\{\alpha, \theta_1, \cdots, \theta_m, \beta\}$ are estimated by using the *least square* (LS) criterion. The estimated $\{\theta_j\}$ are translation, rotation and scale invariant. Parameters α and β are not scale invariant. But the quotient $\alpha/\sqrt{\beta}$, which reflects the signal-to-noise ratio of the boundary, is regarded as an invariant. Therefore, the feature vector $[\theta_1, \ldots, \theta_m, \alpha/\sqrt{\beta}]$ is used as the shape descriptor.

The AR descriptors can capture the cyclic patterns of a shape, and it works well for a regular and smooth shape. However, AR is an optimization process; for irregular and complex shapes, it may not have a solution. Furthermore, the choice of *m* is a complicated problem and is usually decided empirically.

6.3.5 Scale Space Method

6.3.5.1 Scale Space

The problem of noise sensitivity and boundary variations in most spatial domain shape methods inspire the use of scale space analysis. The scale space representation of a shape is created by tracking the position of *inflection points* in a shape boundary or signature. This is done by repeatedly applying low-pass Gaussian filters of variable widths σ at the signature function $f(x)$.

$$L(x;\sigma) = g(x;\sigma) * f(x) \tag{6.25}$$

The inflection points that remain present in the Gaussian filtered signature functions are expected to be ‘significant’ object characteristics. The result is usually an interval tree, called ‘fingerprint,’ consisting of inflection points shown in Fig. 6.12 [3]. As can be seen from Fig. 6.12a, as the scale σ goes up, the number of inflection points on the function $f(x)$ decreases. However, at each point of the function, the inflection point disappears at different scales, and this feature has been captured in the interval tree shown in Fig. 6.13b.

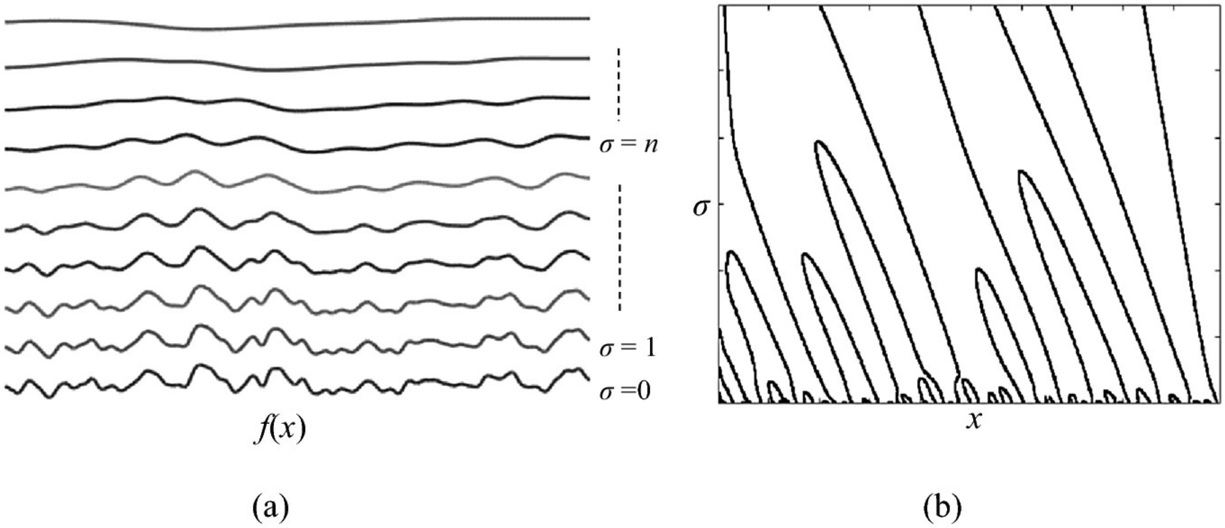


Fig. 6.13 Shape signature in scale space. **a** An original signature function $f(x)$ at the bottom and its successively smoothed versions on the top of it (up to scale 512), where σ is the scale of the smoothed function; **b** the interval tree derived from the zero-crossings of the second derivatives of the smoothed functions at the left, each (x, σ) in the interval tree corresponds to a zero-crossing point at position x and scale σ of the function at left-hand side

6.3.5.2 Curvature Scale Space

The difficulty with scale space method is the interpretation of the interval tree. Mokhtarian and Mackworth [4] developed a *curvature scale space* (CSS) descriptor by finding the peaks of the interval tree. The computation of the CSS descriptor consists of two procedures [5]. The first is to compute a CSS contour map or the interval tree. The second is to extract the branch peaks from the interval tree.

Algorithm of computing CSScontour map:

1. Normalize shape to a fixed number of boundary points.

2. Create an array $ZC[\ ][\ ]$ to record curvature zero-crossing points at each scale.

3. Set $\sigma = 0$.

4. Compute curvatures of each position at scale σ.

5. Record each curvature zero-crossing point at current scale σ to $ZC[\sigma][x]$.

6. Set $\sigma = \sigma + 1$.

7. Smooth the boundary with a Gaussian filter $g(x; \sigma)$.

8. Repeat steps 3–7 until no curvature zero-crossing points are found.

9. Plot $ZC[\sigma][x]$ onto a Cartesian space to create CSS contour map.

Algorithm of extracting CSS contour peaks:

1. Scanning from the top row of CSS contour map.

2. If a zero-crossing point is found at a location (i, j), check the above neighbor points $(i-1, j-1)$, $(i-1, j)$ and $(i-1, j+1)$. If the three above neighbor points are nonzero-crossing points, then the location (i, j) is a peak candidate; find all the peak candidates in row i.

3. For each peak candidate (i, j) at row i, check its neighbor peak candidates, if a neighbor candidate (i, k) is found over 5 points away, then (i, j) is a peak. If a neighbor candidate is found within 5 points, there is a peak at the middle $(i, (j + k)/2)$.

4. Repeat steps 2 and 3 for each row, until all the CSS peaks are found.

Figure 6.14 shows an example of a fish shape, its CSS contour and peaks [1]. The CSS contour successfully captures the 7 major corners of the shape.

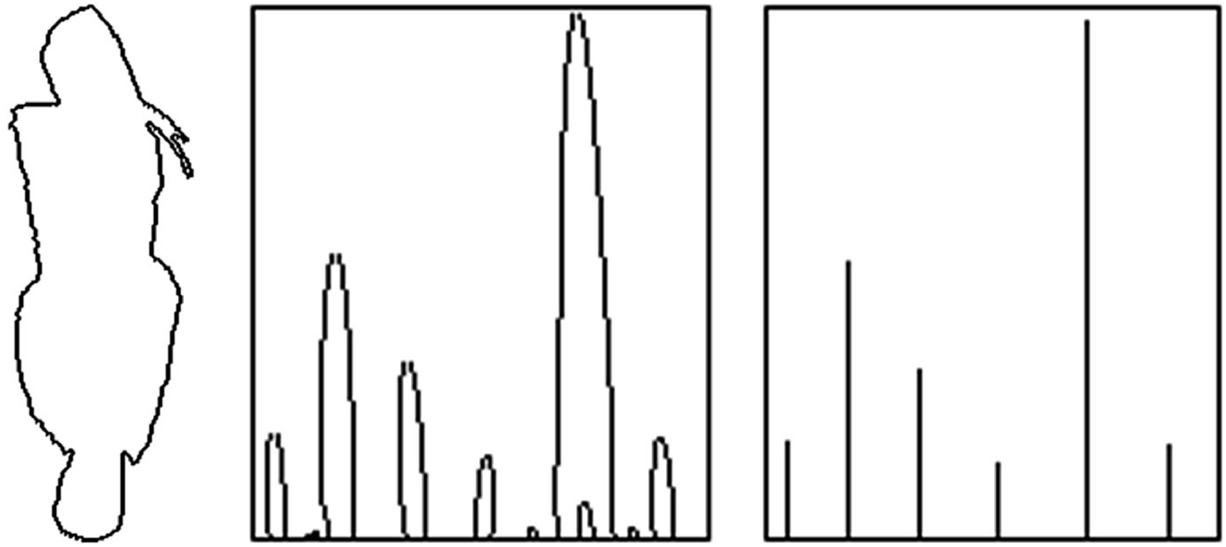


Fig. 6.14 Computation of curvature scale space. A fish shape (**left**), its CSS contour map (**center**) and CSS peaks (**right**)

The morphing of the fish shape in Fig. 6.14 during the Gaussian smoothing process is shown in 6.15. As can be seen from Fig. 6.15, as the scale σ goes up, the shape becomes smoother and smoother until it is completely smoothed.

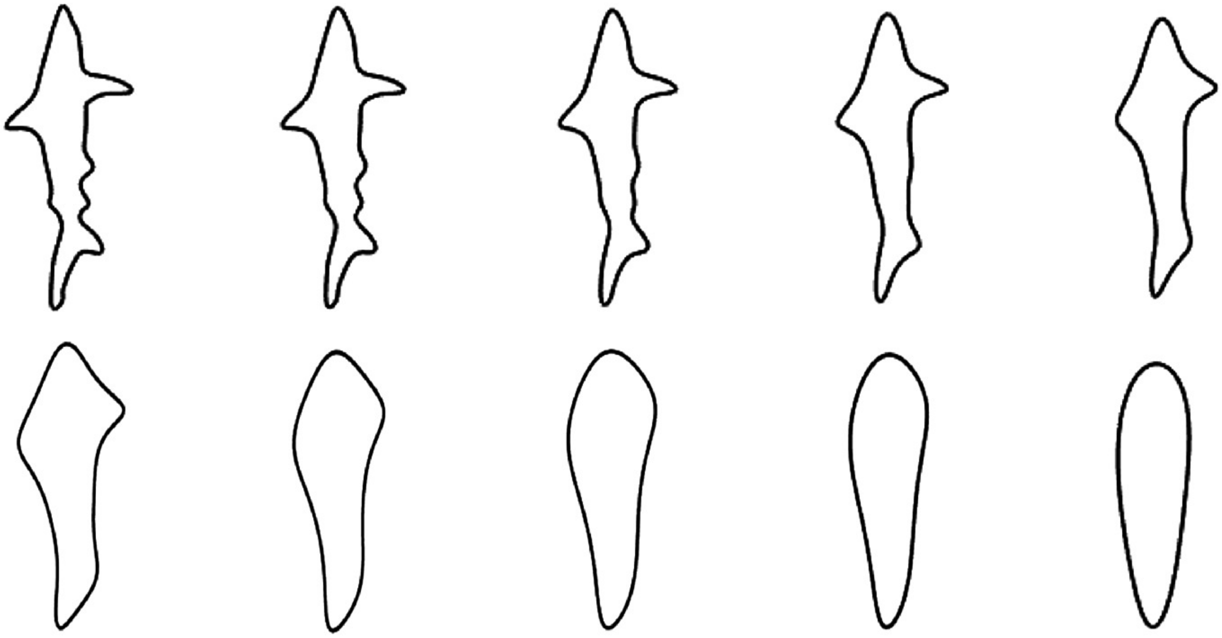


Fig. 6.15 Evolution of shape boundary as scale σ increases

The matching of two CSS descriptors is complex. Assume all shapes have been normalized into the same number of boundary points, and the peaks need to be normalized and circularly shifted to find the best match between two shapes. However, due to the sensitivity of both the height and position of the highest peaks, certain tolerance needs to be accepted during the matching of two peaks. The complex matching can affect the performance significantly. In practice, CSS is combined with a few robust single descriptors such as compactness and elongation [5]. But this introduces a new issue on the weight given to each type of descriptors.

6.3.6 Fourier Descriptor

For any 1D signature function $f(x)$ derived from Sect. 6.3.1, its discrete Fourier transform is given by

$$a_n = \frac{1}{N}\sum_{t=0}^{N-1} f(x)\exp(-j2\pi nx/N), \quad n = 0,\ 1\ , \dots,\ N-1 \tag{6.26}$$

This results in a set of Fourier coefficients $\{a_n\}$, which is a representation of the shape. Since shapes generated through rotation, translation and scaling (called *similarity transformation*) of a same shape are similar shapes, a shape representation should be invariant to these operations. The selection of different start points on the shape boundary to derive $f(x)$ should not affect the representation.

The magnitudes of Fourier coefficients $| a_n |$ are invariant to rotation and starting point, because rotation and starting point only affect the phases of the coefficients. Translation invariance can be achieved by normalizing a shape to its center of gravity or subtraction of the mean. Scale invariance is done by normalizing the magnitudes of the coefficients by the DC component a_0, which is the average energy of the signal and is the largest coefficient:

$$|b_n| = |a_n| / a_0, \quad n = 1, 2, \dots, N-1 \tag{6.27}$$

The set of magnitudes of the normalized Fourier coefficients $\{|b_n|, 1 < n < N{-}1\}$ are used as the shape descriptor, denoted as FD: $\{\mathrm{FD}_n, 1 < n < N{-}1\}$.

FD has several desirable features compared with other shape descriptors. Firstly, it is efficient to compute due to the use of fast

Fourier transform or FFT. Secondly, it provides a coarse to fine representation of a shape. The following examples show how a shape can be reconstructed or represented to different levels of details using different numbers of Fourier coefficients [1]. In practice, only a small number of low-frequency FDs are used to describe a shape to reduce the sensitivity to noise and irregularities. Fig. 6.16

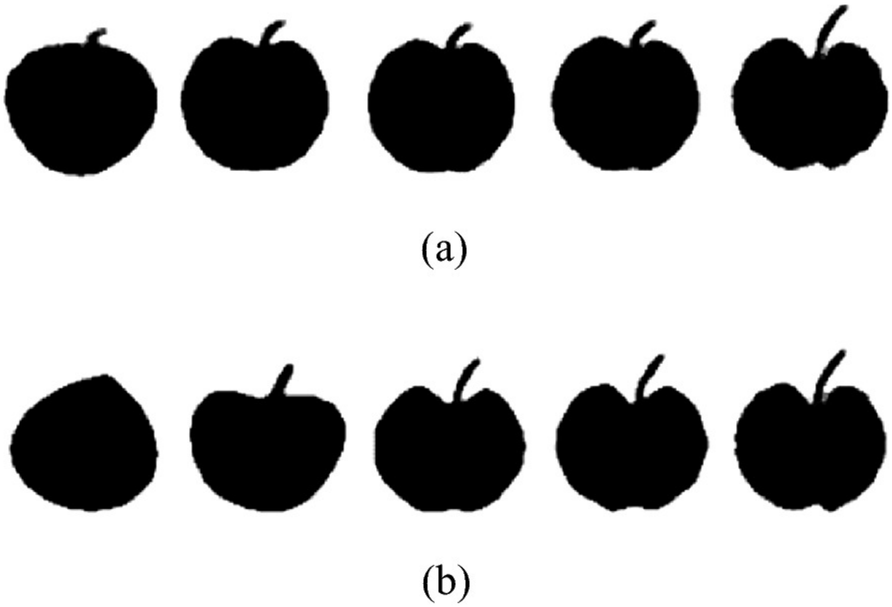


Fig. 6.16 Reconstructed shapes of an apple shape using Fourier coefficients from **a** $r(t)$ and **b** $z(t)$. In both (**a**) and (**b**), from left to right, the shapes are reconstructed using 5, 10, 20, 30 and all the Fourier coefficients, respectively

Thirdly, all FDs have physical meaning, and they capture the different frequency components or different levels of details of a shape boundary. Fourthly, the matching of two FDs is very simple, and it is done by either the city block or Euclidean distance. Because of these desirable features, FD is one of the most robust shape descriptors for contour-based shapes. The study by Zhang et al. [5] shows that FD outperforms CSS descriptor which has been adopted by MPEG-7.

6.3.7 Discussions

The global shape descriptors described above are basically a mathematical summarization of the boundary samples. However, just like any mathematics, it is based on ideal assumptions and constraints. Typically, these descriptors only work on ideal applications where objects are located in isolation and the boundary of the objects can be viewed or kept in completeness. If the objects overlap each other or certain part of the object boundary is missing, these descriptors do not work anymore. For example, an apple with a bite is still perceived as an apple, like the famous Apple Inc. logo. But using the global shape descriptors, the bite on the apple will change the mathematical summarization dramatically and cause mismatch. In such kind of applications, *structural shape methods* can be used to analyze the structure of a shape boundary and match shapes using part of the shape boundary. In the following, different types of *structural shape methods* are described in detail.

6.3.8 Syntactic Analysis

Syntactic analysis is inspired by the phenomenon that composition of a natural scene is analog to the composition of a language; that is, sentences are built up from phrases, phrases are built up from words, words are built up from alphabets, etc. [6, 7]. In syntactic methods, a shape is represented with a set of predefined primitives. The set of predefined primitives is called the *codebook*, and the primitives are called *codewords*. For example, given the codewords in the right of Fig. 6.17, the hammer shape at the left can be represented as a grammatical string of S:

$$S = abbbcbbcbdbb \tag{6.28}$$

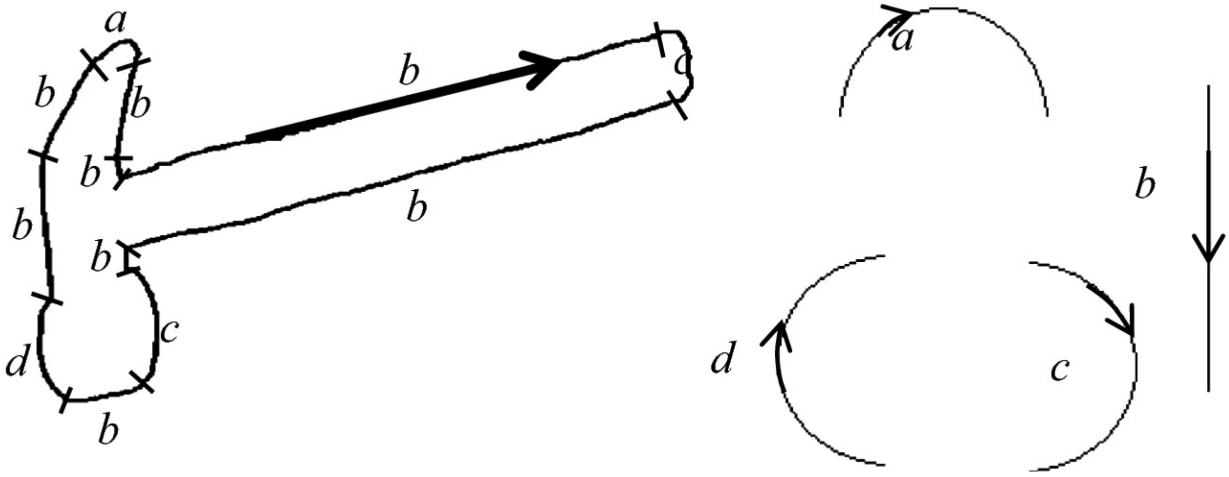


Fig. 6.17 Syntactic analysis of a hammer shape

The matching between shapes can use string matching by finding the minimal number of edit operations to convert one string into another.

A more general method is to formulate the representation as a string grammar. Each primitive is interpreted as an alphabet of some grammar, where a grammar is a set of rules of syntax that govern the generation of sentences formed from symbols of the alphabet. The set of sentences generated by a grammar, G, is called its language and is denoted as $L(G)$. Here, sentences are strings of symbols (which in turn represent patterns), and languages correspond to pattern class. After grammars have been defined, the matching is straightforward. For a sentence representing an unknown shape, the task is to decide in which language the shape represents a valid sentence.

In practice, however, it is difficult to infer a pattern grammar which can generate only the valid patterns. In addition, this method needs a priori knowledge of the database in order to define codewords or alphabets. The knowledge, however, is usually unavailable.

6.3.9 Polygon Decomposition

Polygon can be used to capture the overall shape of a contour and discard the minor variations or noise along the shape boundary. In general, there are two methods to create a polygon from a shape contour: merging and splitting; both are based on applying a distance threshold on the cumulated distance (or errors) between the shape boundary and the polygon line segments [8].

Merging methods add successive pixels to a line segment if each new pixel that is added doesn't cause the segment to deviate too much from a straight line.

In the merging method, it chooses one point as a starting point on the contour, and for each new point to be added, let a line segment go from the starting point to this new point. Then, the total squared error of all the boundary points to the line segment is computed. If the error exceeds some threshold, the line from the starting point to the previous point is kept and new line segment is started. For example, in Fig. 6.18 [8], to find out if the boundary points between $\mathbf{P}_i$ and $\mathbf{P}_k$ should be merged, the total distance or error of all the boundary points to the line segment $\mathbf{P}_i\mathbf{P}_k$ is computed. If the error is larger than the threshold, keep

P$_i$**P**$_j$ and add a new line segment **P**$_j$**P**$_k$. The distance d_j from **P**$_j$ to **P**$_i$**P**$_k$ is given as (6.29) [9]. d_j is equal to twice the area of triangle Δ**P**$_i$**P**$_j$**P**$_k$ divided by the distance between **P**$_i$**P**$_k$, and the area of Δ**P**$_i$**P**$_j$**P**$_k$ is given in (6.21).

$$d_j = \frac{\left|(x_k - x_i)\left(y_j - y_i\right) - \left(x_j - x_i\right)(y_k - y_i)\right|}{\sqrt{(x_k - x_i)^2 + (y_k - y_i)^2}} \tag{6.29}$$

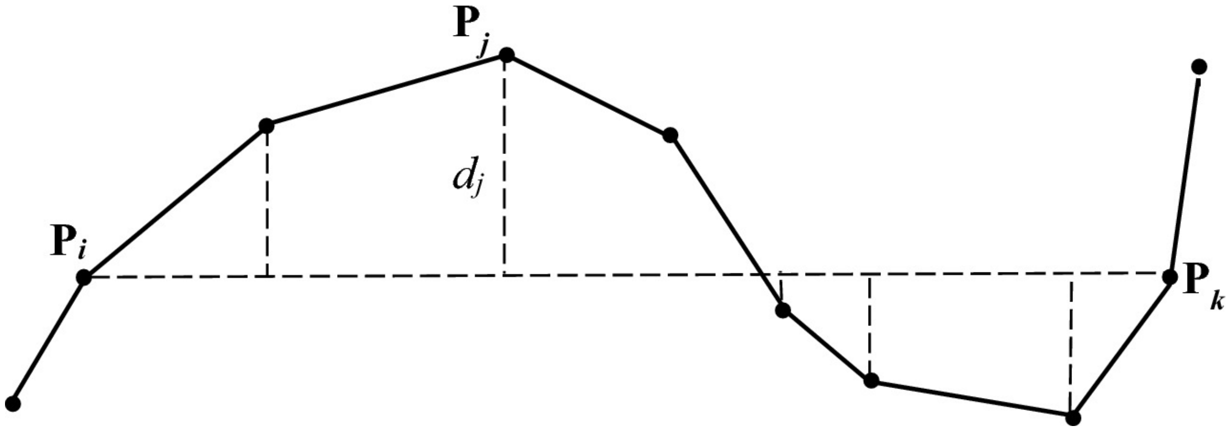


Fig. 6.18 Polygon approximation by merging

Splitting methods work by first drawing a line from the start point of the boundary to the end point of the boundary. Then, the perpendicular distance from each point along the boundary to the line is computed. If this exceeds some threshold, the boundary is broken into two segments with equal length. The process is repeated for each of the two new segments until no boundary segment needs to be broken (Fig. 6.19).

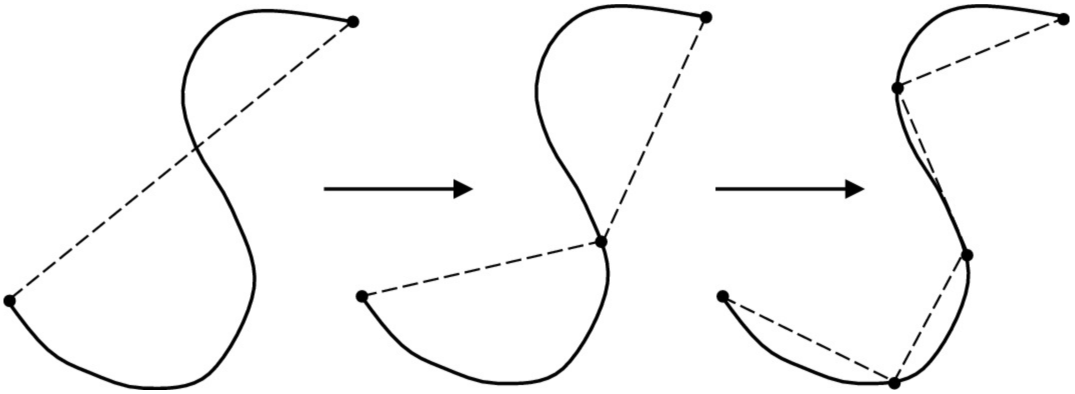


Fig. 6.19 Polygon approximation by splitting

Once a polygon has been approximated, each segment of the polygon is regarded as a primitive and can be described by its *length* and *angle* in relation to the previous segment. Other features can also be used such as *length ratio* and *triangle area* between two adjacent segments. The polygon is then represented as a string of primitives. The length of each primitive is normalized by the shape boundary to achieve scale invariance.

The matching between two shapes involves shift and best match. Typically, the matching between shapes involves two steps: feature-by-feature matching in the first step and model-by-model matching (shape-by-shape matching) in the second step. In the first step, given a feature(s) of a query shape, the feature(s) is searched through the indexed database, and if a particular model feature in the database is found to be similar to the query feature (s), the list of shapes associated with the model feature is retrieved. In the second step, the matching between the query shape and a retrieved model is matched based on the editing distance between the two strings of primitives.

6.3.9.1 Chain Code Representation

Chain codes describe an object by a sequence of unit-size line segments with a given orientation. In the implementation, a digital boundary of an image is superimposed with a grid, the boundary points are approximated to the nearest grid point, and then a sampled image is obtained. From a selected starting point, a chain code can be generated by using a 4-connectivity or an 8-connectivity chain code. Fig. 6.20

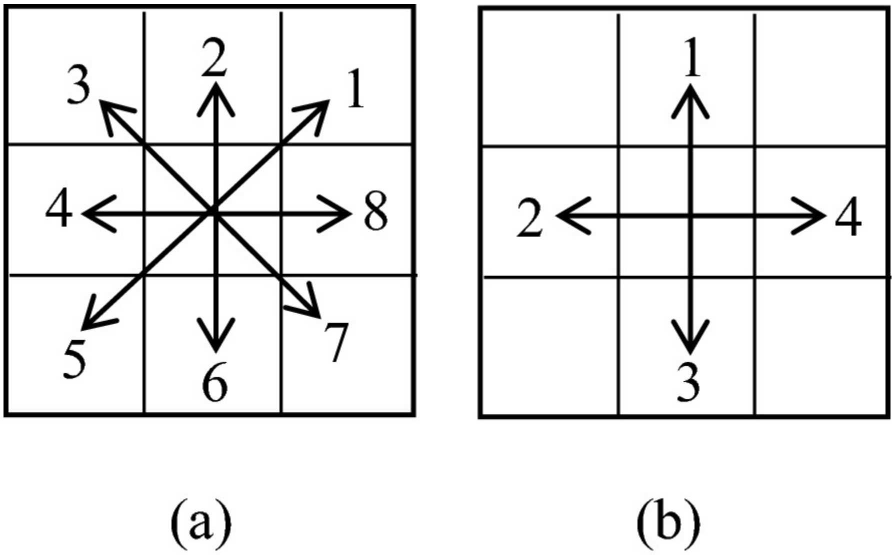


Fig. 6.20 Computation of chain code. **a** Chain code in 8-connectivity; **b** chain code in 4-connectivity

Chain code is invariant to translation because the code values are based on directions only. Rotation invariance can be achieved by finding the pixel in the border sequence which results in the minimum integer number, and that pixel is then used as the starting pixel. For matching, a *chain code histogram* (of directions) normalized by the chain code length is used. This not only reduces the dimensions and sensitivity to noise, but also achieves scaling invariance.

Chain code is itself a fine polygon of equal side length and can be further merged to create a coarse polygon of different side lengths. In other words, chain code can be used to create a polygon of a shape.

6.3.9.2 Smooth Curve Decomposition

A contour shape can also be segmented into boundary segments using curvature threshold. The idea is to first smooth the boundary with a Gaussian filter and then calculate the curvature at each point of the smoothed boundary. The boundary is then segmented at points where the curvature exceeds the threshold [10]. The boundary segments are then regarded as the primitives. An example is shown in Fig. 6.21.

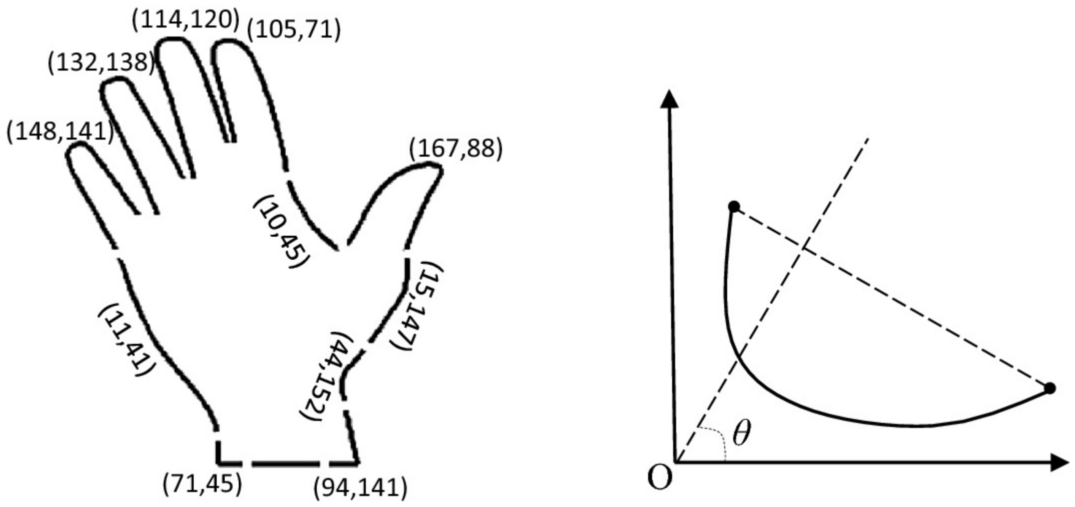


Fig. 6.21 Smooth curve decomposition. **Left**: a horse shape and its boundary segments; **Right**: the calculation of the angle of a segment

The feature for each primitive is its maximum *curvature* and its *orientation*, and the similarity between two primitives is measured by the weighted Euclidean distance. Shapes in database are then indexed with the primitives. Shapes can then be matched using the two-step matching used in the polygon matching.

6.3.9.3 Discussions

The advantage of structural approach is its capability of handling *occlusion* problem in the scene and allowing partial matching. However, structural approach suffers from ambiguity of primitives, expensive computation and complex matching.

Both global and structural approaches are sensitive to boundary noise and irregularity. This can be overcome by extracting features from shape interior content or using region-based feature extraction approaches.

6.4 Region-Based Shape Feature Extraction

In region-based methods, all the pixels within a shape region are taken into account to obtain shape features. Common region-based feature extraction methods are based on shape moments. Other region-based methods include grid method, shape matrix, convex hull and media axis.

6.4.1 Geometric Moments

Mathematically, *geometric moments* are projections of a function onto a polynomial basis in similar way to the FT which is a projection onto a basis of harmonic sinusoid functions. The geometric moment of order $(p + q)$ of a general function $f(x, y)$ is given as (6.30):

$$M_{pq} = \int_{-\infty}^{\infty}\int_{-\infty}^{\infty} x^p y^q f(x, y)\mathrm{d}x\mathrm{d}y, \quad p, q = 0, 1, 2, \ldots \tag{6.30}$$

Two simple properties can be derived from geometric moment:

$$\text{Mass} = M_{00} \tag{6.31}$$

$$\text{Centroid} = \left\{\bar{x} = \frac{M_{10}}{M_{00}}, \bar{y} = \frac{M_{01}}{M_{00}}\right\} \tag{6.32}$$

The *central moments* of order $p + q$ of a shape image $f(x, y)$ are given by

$$\mu_{pq} = \sum_{x}\sum_{y}(x - \overline{x})^p(y - \overline{y})^q f(x, y) \quad p, q = 0, 1, 2 \ldots \tag{6.33}$$

The normalized central moments μ_{pq}/μ_{00} are invariant to both translation and scaling. The following properties can be observed from geometric moments.

- $(m_{10}/m_{00}, m_{01}/m_{00})$ defines the *centre of gravity* or *centroid* of a shape.
- m_{20} and m_{02} describe the distribution of mass of the shape with respect to the coordinate axes. They are also called the *moments of inertia*.
- μ_{10}/μ_{00} and μ_{01}/μ_{00} are the *horizontal mean* and *vertical mean* of the shape, respectively.
- μ_{20}/μ_{00} and μ_{02}/μ_{00} are the *horizontal variance* and *vertical variance* of the shape, respectively.
- μ_{11} is the *covariance* of the shape.

- μ_{30}/μ_{00} and μ_{03}/μ_{00} represent the *horizontal skewness* and *vertical skewness* of the shape, respectively. The *skewness* measures the *symmetry* of a shape. The skewness of a symmetric shape equals to zero.
- μ_{40}/μ_{00} and μ_{04}/μ_{00} represent the *horizontal kurtosis* and *vertical kurtosis* of the shape, respectively. The kurtosis measures the *peakedness* or *sharpness* of the pixel distribution inside the shape.

These are important properties to describe how pixels are distributed inside the shape. Since both x^p and y^q are monomials, they amplify the moment values of pixels farther away from the centroid, and higher-order moments reflect how dramatic a shape changes in relation to its centroid.

However, geometric moments are not rotation invariant and it's difficult to derive moment invariants of high order. Hu [11] has derived seven *moment invariants* up to order three:

$$\left.\begin{aligned}
\Phi_1 &= \eta_{20} + \eta_{02} \\
\Phi_2 &= (\eta_{20} - \eta_{02})^2 + 4(\eta_{11})^2 \\
\Phi_3 &= (\eta_{30} - 3\eta_{12})^2 + (3\eta_{21} - \eta_{03})^2 \\
\Phi_4 &= (\eta_{30} + \eta_{12})^2 + (\eta_{21} + \eta_{03})^2 \\
\Phi_5 &= (\eta_{30} - 3\eta_{12})(\eta_{30} + \eta_{12})\left[(\eta_{30} + \eta_{12})^2 - 3(\eta_{21} + \eta_{03})^2\right] \\
&\quad + (3\eta_{21} - \eta_{03})(\eta_{21} + \eta_{03})\left[3(\eta_{30} + \eta_{12})^2 - (\eta_{21} + \eta_{03})^2\right] \\
\Phi_6 &= (\eta_{20} - \eta_{02})\left[(\eta_{30} + \eta_{12})^2 - (\eta_{21} + \eta_{03})^2\right] \\
&\quad + 4\eta_{11}(\eta_{30} + \eta_{12})(\eta_{21} + \eta_{03}) \\
\Phi_7 &= (3\eta_{21} - \eta_{30})(\eta_{30} + \eta_{12})\left[(\eta_{30} + \eta_{12})^2 - 3(\eta_{21} + \eta_{03})^2\right] \\
&\quad + (3\eta_{12} - \eta_{03})(\eta_{21} + \eta_{03})\left[3(\eta_{30} + \eta_{12})^2 - (\eta_{21} + \eta_{03})^2\right]
\end{aligned}\right\} \tag{–}$$

where $\eta_{pq} = \mu_{pq}/(\mu_{00})^{\gamma}$ and $\gamma = 1 + (p + q)/2$ for $p + q = 2, 3, \ldots$.

The geometric moment transform can be extended to generalized form by replacing the conventional transform kernel $x^p y^q$ with a more general kernel of $P_p(x)P_q(y)$.

6.4.2 Complex Moments

The rotation invariance issue of the geometric moments can be easily addressed by using *complex moments* and polar sampling, because the magnitude of a complex function is invariant to rotation and polar sampling is also invariant to rotation. The idea is to replace the real polynomials in the geometric moment with complex polynomials and sample the shape in a polar coordinate system. The general form of complex moments is defined as (6.35):

$$C_{pq} = \int_{-\infty}^{\infty} \int_{-\infty}^{\infty} (x + jy)^p (x - jy)^q f(x, y)\,\mathrm{d}x\mathrm{d}y \tag{6.35}$$

where $j = \sqrt{-1}$. The orthogonal *Zernike moments* are derived from

Zernike polynomials:

$$V_{nm}(x, y) = V_{nm}(\rho\cos\theta, \rho\sin\theta) = R_{nm}(\rho)\exp(jm\theta) \tag{6.36}$$

where

$$R_{nm}(\rho) = \sum_{s=0}^{(n-|m|)/2} (-1)^s \frac{(n-s)!}{s!\left(\frac{n+|m|}{2} - s\right)!\left(\frac{n-|m|}{2} - s\right)!}\rho^{n-2s} \tag{6.37}$$

where ρ is the radius from (x, y) to the shape centroid, θ is the angle between ρ and x-axis, and n and m are integers and subject to n-$|m|$ = *even*, $|m| \le n$. Zernike polynomials are a complete set of complex-valued function orthogonal over the unit disk, i.e., $x^2 + y^2 = 1$. Therefore, a shape is first normalized into a unit disk to compute Zernike moments.

For example, the first six real Zernike polynomials are given in the following:

$$\begin{array}{lll} R_{00}(\rho) = 1, & R_{11}(\rho) = \rho, & R_{20}(\rho) = 2\rho^2 - 1 \\ R_{22}(\rho) = \rho^2, & R_{31}(\rho) = 3\rho^3 - 2\rho, & R_{33}(\rho) = \rho^3 \end{array}$$

The first 10 real Zernike polynomials of up to order 5 are shown in Fig. 6.22.

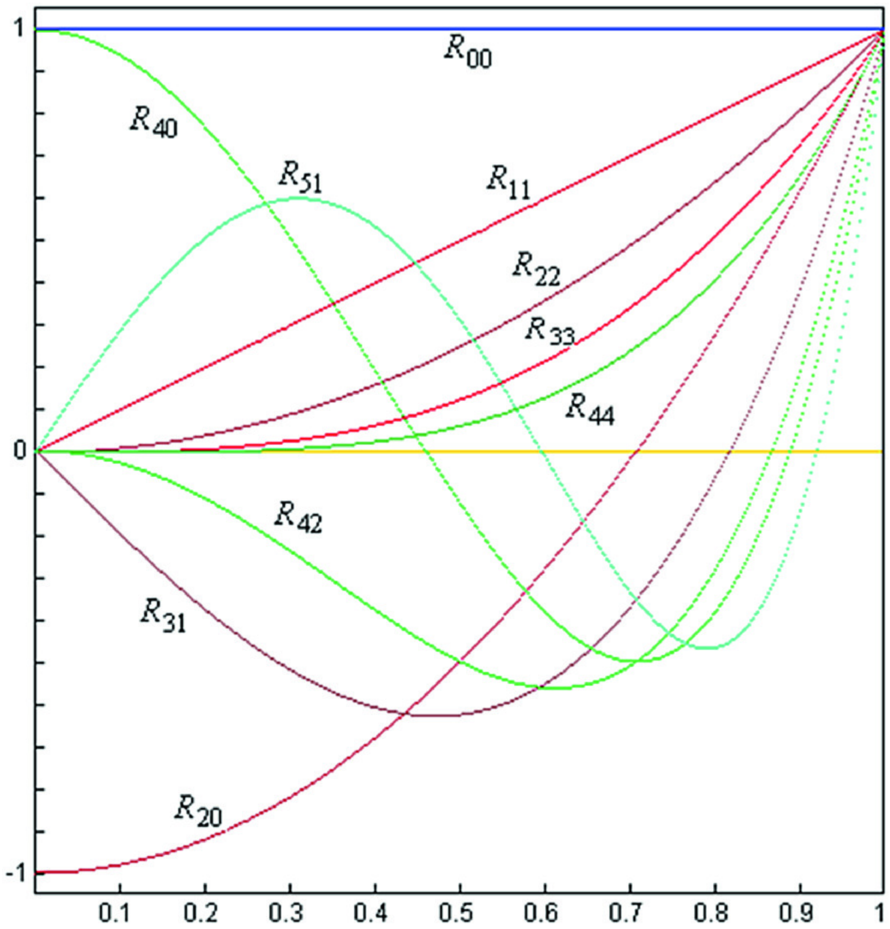


Fig. 6.22 First ten real Zernike polynomials

The complex Zernike moments of order n with repetition m are thus defined as:

$$A_{nm} = \frac{n+1}{\pi} \sum_x \sum_y f(x, y) V^*_{nm}(x, y), \quad x^2 + y^2 \leq 1 \tag{6.38}$$

or

$$A_{nm} = \frac{n+1}{\pi} \sum_\rho \sum_\theta f(\rho\cos\theta, \rho\sin\theta) R_{nm}(\rho) \exp(jm\theta), \rho \leq 1 \tag{6.39}$$

where * means complex conjugate. Due to the constraint of $n-|m|$ = *even* and $m < n$, there is $[n/2]$ repetition of moments in each order n. As an example, the first 36 Zernike moments of up to order 10 are given in Table 6.1. The table only shows the moments with positive m, and the moments of negative m are just the rotational versions of the moments of positive m. It can be seen from the table, from the second order (row), there are $[n/2]$ repetition of moments which capture different circular frequencies. The images of Zernike moment functions from order 1 to 10 are shown in Fig. 6.23 [12].

Table 6.1 List of Zernike moments up to order 10

Order (n)	**Zernike moment of order n with repetition m (A_{nm})**	**Number of moments in each order n**	**Total number of moments up to order 10**
0	$A_{0,0}$	1	36
1	$A_{1,1}$	1	
2	$A_{2,0}, A_{2,2}$	2	
3	$A_{3,1}, A_{3,3}$	2	
4	$A_{4,0}, A_{4,2}, A_{4,4}$	3	
5	$A_{5,1}, A_{5,3}, A_{5,5}$	3	
6	$A_{6,0}, A_{6,2}, A_{6,4}, A_{6,6}$	4	
7	$A_{7,1}, A_{7,3}, A_{7,5}, A_{7,7}$	4	
8	$A_{8,0}, A_{8,2}, A_{8,4}, A_{8,6}, A_{8,8}$	5	
9	$A_{9,1}, A_{9,3}, A_{9,5}, A_{9,7}, A_{9,9}$	5	
10	$A_{10,0}, A_{10,2}, A_{10,4}, A_{10,6}, A_{10,8}, A_{10,10}$	6	

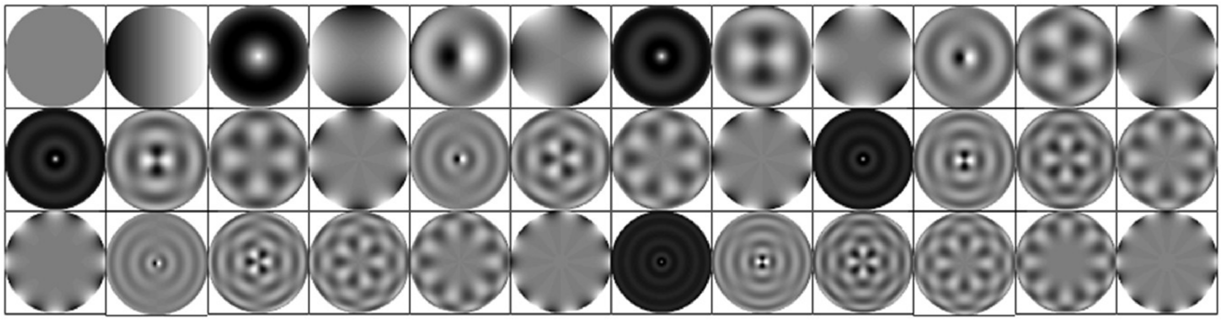


Fig. 6.23 First 36 Zernike moments from order 1 to 10

A simplified complex moment is used by MPEG-7, called *angular radial transformation* (ART).

$$\mathrm{ART}_{nm} = \frac{1}{2\pi}\sum_{\rho}\sum_{\theta} f(\rho\cos\theta, \rho\sin\theta)\, V_{nm}(\rho,\theta), \quad \rho \le 1 \qquad (6.40)$$

where V_{nm} is the ART basis function

$$V_{nm} = R_n(\rho)\exp(jm\theta) \tag{6.41}$$

and R_n(\rho) is the radial basis function

$$R_n(\rho) = \begin{cases} 1 & \text{if } n = 0 \\ 2\cos(n\pi\rho) & \text{if } n \neq 0 \end{cases} \tag{6.42}$$

The real part of the first 36 ART basis functions is shown in Fig. 6.24.

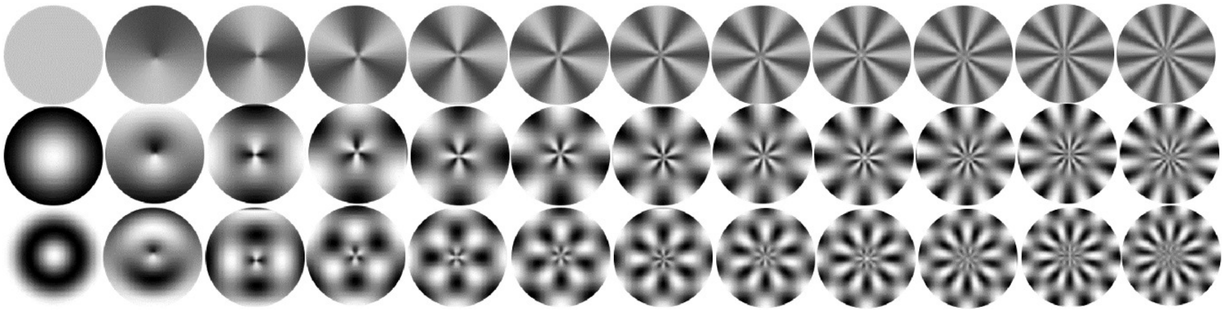


Fig. 6.24 Real parts of the ART basis functions

Compared with geometric moments, complex moments are invariant to rotation and they are also more robust due to capturing the spatial information within a shape. They have minimum information redundancy due to orthogonal basis.

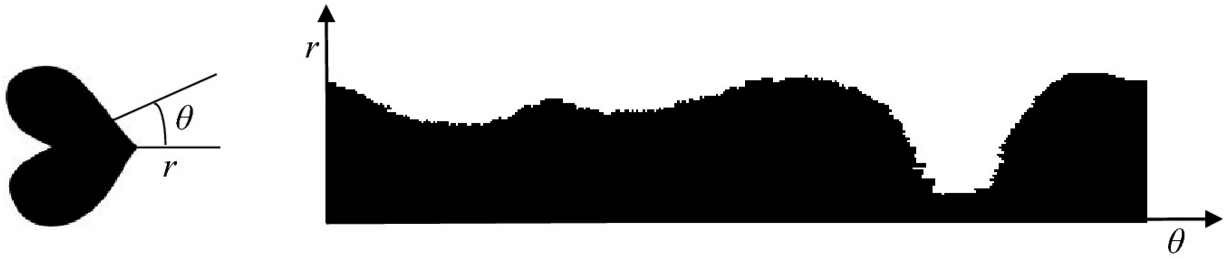
However, the computation of complex moments is more expensive than geometric moments. The image needs to be normalized to a unit disk. For an irregular shape, this may either cut out part of the shape if an interior circle is used or include irrelevant part if an exterior circle is used. Depending on how much the shape is cut out or irrelevant part is included, the unit disk normalization can affect the accuracy.

6.4.3 Generic Fourier Descriptor

Complex moment improves the geometric moment with three advantages: rotation invariance, spatial or frequency information and orthogonality. These three features can be achieved more naturally and efficiently using Fourier transform. The generic Fourier descriptor or GFD is a method just based on this idea [13].

The idea is to first transform a shape into a rectangular polar image with sides r and θ by a polar raster sampling around the shape centroid. Next, a 2D Fourier transform is applied on the transformed rectangular image. The normalized Fourier coefficients are then used as the shape descriptor.

Figure 6.25 demonstrates the polar raster transform [13]. For example, Fig. 6.25a shows the original shape image in polar space, and Fig. 6.25b shows the polar raster-sampled image plotted into Cartesian space.



(a)

(b)

Fig. 6.25 Polar raster transform. **a** An original shape image in polar space; **b** polar raster-sampled image (**a**) plotted into Cartesian space

Given a shape image $I = \{f(x, y); 0 \le x < M, 0 \le y < N\}$. To apply the polar Fourier transform or PFT, the shape image is converted from Cartesian space to polar space $I_p = \{f(r, \theta); 0 \le r < R, 0 \le \theta < 2\pi\}$, and R is the maximum radius of the shape. The origin of the polar space is set to be the centroid of the shape, so that the shape is translation invariant. The centroid (x_c, y_c) is given by (6.43):

$$x_c = \frac{1}{M}\sum_{x=0}^{N-1} x, \quad y_c = \frac{1}{N}\sum_{y=0}^{M-1} y \tag{6.43}$$

and (r, \theta) is given by

$$r = \sqrt{(x - x_c)^2 + (y - y_c)^2}, \quad \theta = \arctan\frac{y - y_c}{x - x_c} \tag{6.44}$$

The shape image is then polar raster sampled around the centroid and transformed into a rectangular polar image. The polar image, e.g., Fig. 6.25b, is a normal rectangular image. Therefore, a 2D FT is applied on this polar rectangle (PFT). The PFT has the similar form to the normal discrete 2D FT in Cartesian space and is defined as:

$$PF(\rho,\theta) = \sum_r \sum_i f(r,\theta_i) \exp\left[j2\pi \left(\frac{r}{R}\rho + \frac{2\pi i}{T}\theta \right) \right] \tag{6.45}$$

where $0 \le r < R$ and $\theta_i = i(2\pi/T)$ $(0 \le i < T)$; $0 \le \rho < R$, $0 \le \theta < T$. R and T are the radial frequency resolution and angular frequency resolution, respectively.

In addition to the three advantages of complex moment, the PFT has another desirable feature of capturing shape information in a smaller number of low-frequency coefficients. This is particularly suitable for shape representation. Figure 6.26 shows an example of PFT on two shape images with different orientations. Conventional 2D FT on the two images results in two different spectra, as they are rotated each other. It can be observed from the middle row of Fig. 6.26 that rotation of shapes in Cartesian space results in circular shift in polar space. However, the circular shift does not change the spectra distribution on polar space, e.g., the bottom row of Fig. 6.26.

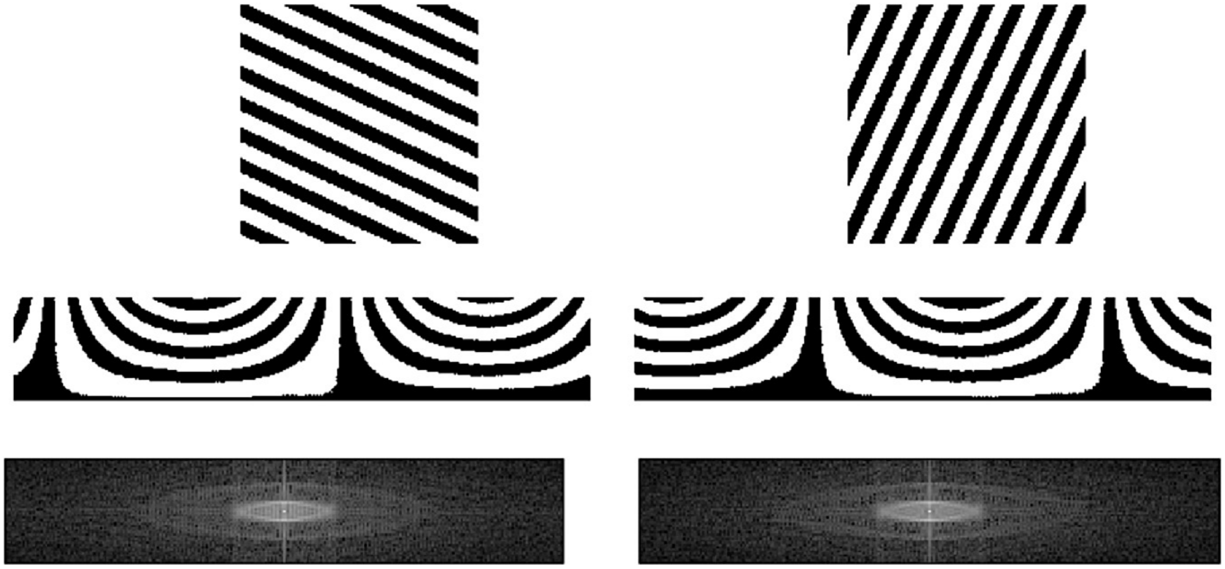


Fig. 6.26 Rotation-invariant GFD. **Top row**: Two shape images with different orientations; **Middle row**: The polar raster-sampled images of the two corresponding shapes at the top row; **Bottom row**: The Fourier spectra images of the two corresponding images at the middle row

Since $f(x, y)$ is a real function, the spectra is circularly symmetric, and only the first quarter of the spectra features is needed to describe the shape.

The acquired coefficients of the PFT are translation invariant due to the use of centroid as polar space origin. Rotation invariance is achieved by ignoring the phase information in the coefficients and only retaining the magnitudes of the coefficients. To achieve scale invariance, the first magnitude value is normalized by the area of the circle (*area*) in which the polar image resides or the mass of the shape (*mass*), and all the other magnitude values are normalized by the magnitude of the first coefficient. The translation, rotation and scale-normalized PFT coefficients are used as the shape descriptor. To summarize, the shape descriptor derived from the PFT is shown as follows

$$\mathbf{GFD} = \left\{ \frac{|PF(0,0)|}{\text{area}}, \frac{|PF(0,1)|}{|PF(0,0)|}, \ldots, \frac{|PF(0,n)|}{|PF(0,0)|}, \ldots, \frac{|PF(m,0)|}{|PF(0,0)|}, \ldots, \frac{|PF(m,n)|}{|PF(0,0)|} \right\} \quad (6.46)$$

where m is the maximum number of the radial frequencies selected and n is the maximum number of angular frequencies selected. m and n can be adjusted to achieve hierarchical coarse to fine representation requirement. Normally, the first coefficient or the *DC* component is used as the normalization factor and is discarded after normalization. However, this component is used as an additional feature in a shape descriptor, because it reflects the average energy (scale) of the shape which is useful for shape description.

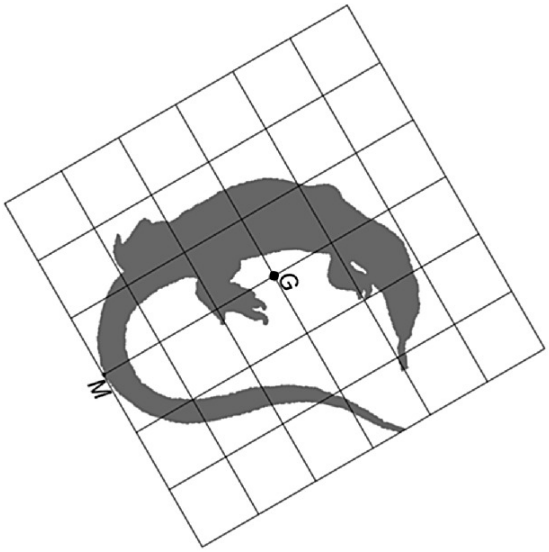
For efficient shape description, only a small number of the acquired GFD features are selected for shape representation. The selected GFD features form a feature vector which is used for indexing the shape.

Compared with Zernike moment descriptor (ZMD), GFD is simpler and more efficient to compute.

6.4.4 Shape Matrix

The most intuitive way to represent a shape is simply to binarize the shape within a bounding box, and the result is a binary *shape matrix*. To acquire the shape matrix of a shape *S*, a square is centered at the *center of gravity* *G* of *S* (Fig. 6.27). The side length of the square is equal to 2*L*, where *L* is the maximum distance from *G* to a point *M* on the boundary of the shape, or $L = \overline{GM}$. All shape squares are normalized with the same length L and are aligned with line L. The square is then divided into N x N blocks b_{ij}, and the shape matrix is defined as $SM = [c_{ij}]$ where c_{ij} is given by:

$$c_{ij} = \begin{cases} 1 & \text{if } A\left(S \cap b_{ij}\right) > A\left(b_{ij}\right)/2 \\ 0 & \end{cases} \tag{6.47}$$



$$SM = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 1 & 0 & 0 \\ 1 & 1 & 1 & 1 & 1 & 0 \\ 1 & 0 & 0 & 0 & 1 & 0 \\ 0 & 1 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Fig. 6.27 Computation of a shape matrix. A shape on the left and its shape matrix on the right

where $A(\cdot)$ is the area function.

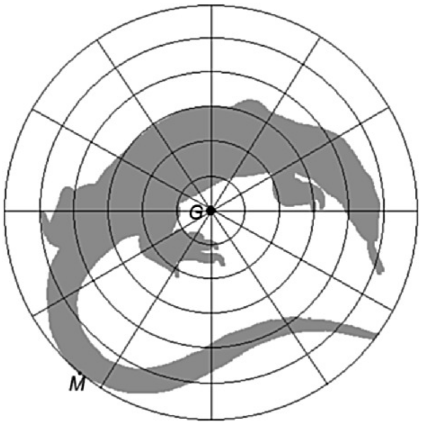
It is easy to show that the shape matrix acquired this way is invariant to translation, scale and rotation. The similarity of two shape matrices $A = [a_{ij}]$ and $B = [b_{ij}]$ is given by

$$d(A, B) = 1 - \frac{1}{N^2} \sum_{i=0}^{N} \sum_{j=0}^{N} \left|a_{ij} - b_{ij}\right| \tag{6.48}$$

In [14], a binary shape number is created by concatenating the rows of a shape matrix into a vector.

The shape matrix acquired this way is sensitive to boundary noise because the size and orientation of the square bounding box can easily be influenced by the noise. In practice, there need multiple guesses of longest radii; therefore, the best matching of multiple shape matrices is needed.

A more robust shape matrix can be created by using a polar grid [15]. The idea is similar to the square shape matrix; however, instead of using a square grid, a polar grid is used. For example, the polar shape matrix of a shape is shown in Fig. 6.28.



$$SM = \begin{bmatrix} 0 & 0 & 1 & 1 & 1 & 1 & 0 & 1 & 1 & 1 & 0 & 0 \\ 0 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 0 & 0 \\ 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 0 & 0 \\ 1 & 1 & 1 & 0 & 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 1 & 1 & 1 & 1 & 1 & 1 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 1 & 0 & 1 & 1 \end{bmatrix}$$

Fig. 6.28 Computation of a polar raster shape matrix. **Left**: Polar raster sampling of a shape; **Right**: Its polar shape matrix

The polar model of shape matrix is more robust than the square model because rotation of a shape only causes a horizontal shift of the shape matrix, and the matching becomes simply a shift best matching. However, since the sampling density of the polar raster is not constant at all rings, a weighed shape matrix is necessary.

6.4.5 Shape Profiles

6.4.5.1 Shape Projections

Shape profiles can be extracted from the projections of the shape. The profiles are the projections of the shape onto *x*-axis and *y*-axis on Cartesian coordinate system. By vertical and horizontal projections, two 1D functions are obtained:

$$\left.\begin{aligned} P_v(x) &= \sum_{y_{\min}}^{y_{\max}} f(x, y) \\ P_h(y) &= \sum_{x_{\min}}^{x_{\max}} f(x, y) \end{aligned}\right\} \tag{6.49}$$

The vertical profile $P_v(x)$ counts the number of pixels on each column of the shape, and the horizontal profile $P_h(y)$ counts the number of pixels on each row of the shape (Fig. 6.29). The profiles are unique to each type of objects, and they can be used as shape signatures to describe shapes.

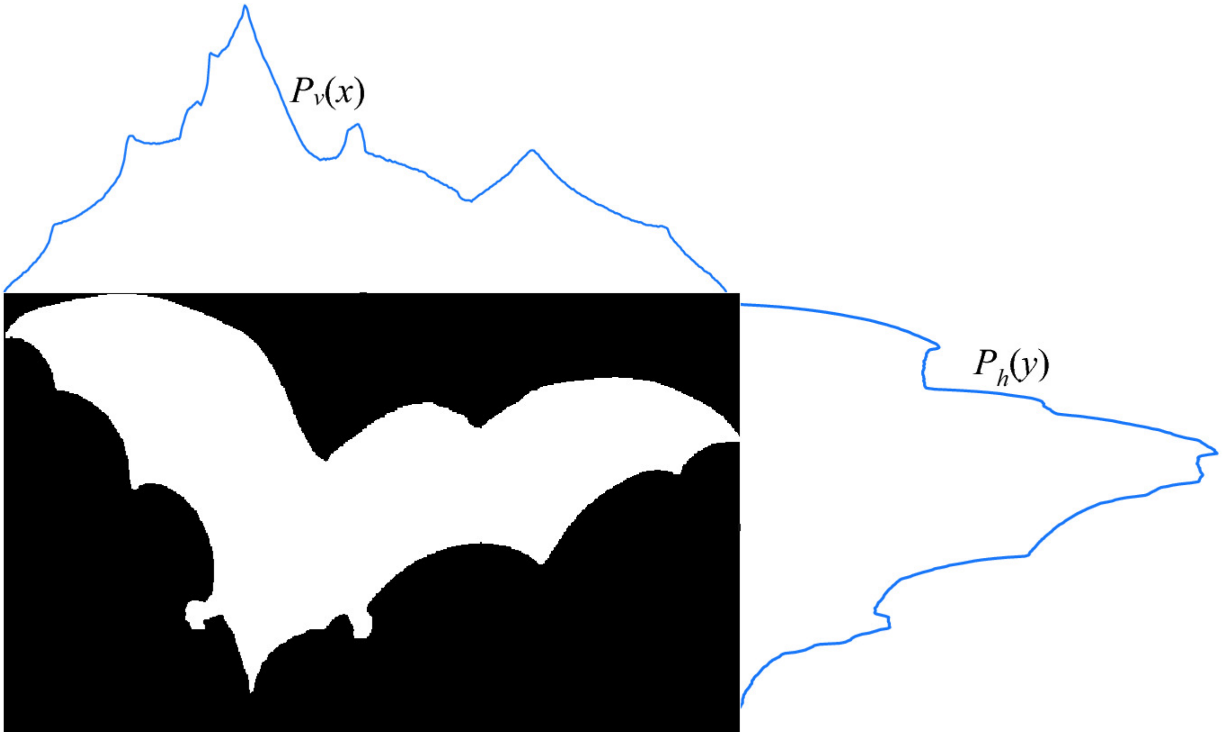


Fig. 6.29 Computation of shape profiles. A binary shape image with its vertical profile $P_v(x)$ (**top**) and horizontal profile $P_h(y)$ (**right-hand side**)

Polar shape profiles can also be obtained in the similar way by counting the number of pixels at each angle and radius on polar coordinates.

6.4.5.2 Radon Transform

Multiple shape profiles projected from different directions θ can be obtained using the *Radon transform*. When all these profiles are aligned on the θ-axis in 3D, they create a Radon spectrum of the shape and the spectrum captures the content information of the shape region.

A Radon transform works by creating a shape profile at each angle. Formally, it is defined as

$$R(\rho,\theta) = \iint_{-\infty}^{\infty} f(x,y)\,\delta(x\cos\theta + y\sin\theta - \rho)\,\mathrm{d}x\mathrm{d}y \tag{6.50}$$

where $\rho = x\cos\theta + y\sin\theta$ is the line the shape is to be projected; θ and ρ are the angle of the line and distance of the line to the origin, respectively. $\delta(x)$ is the Dirac delta function and is given by (6.51):

$$\delta(x-a) = 0 \quad \text{for} \quad x \neq a \tag{6.51}$$

$$\int_{-\infty}^{\infty} f(x)\,\delta(x-a)\,\mathrm{d}x = f(a) \tag{6.52}$$

The projection of a shape image at a particular angle θ is shown in Fig. 6.30.

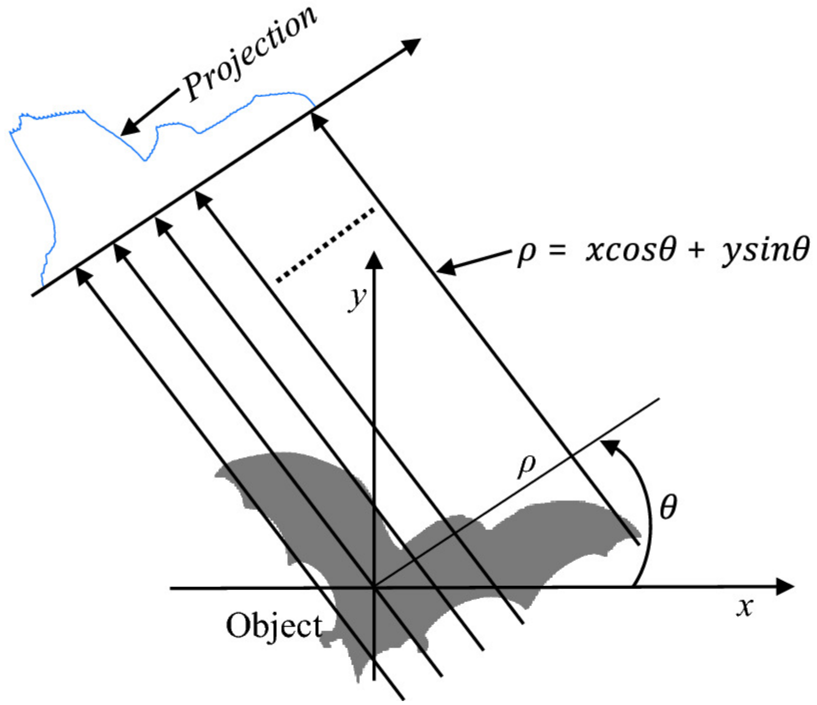
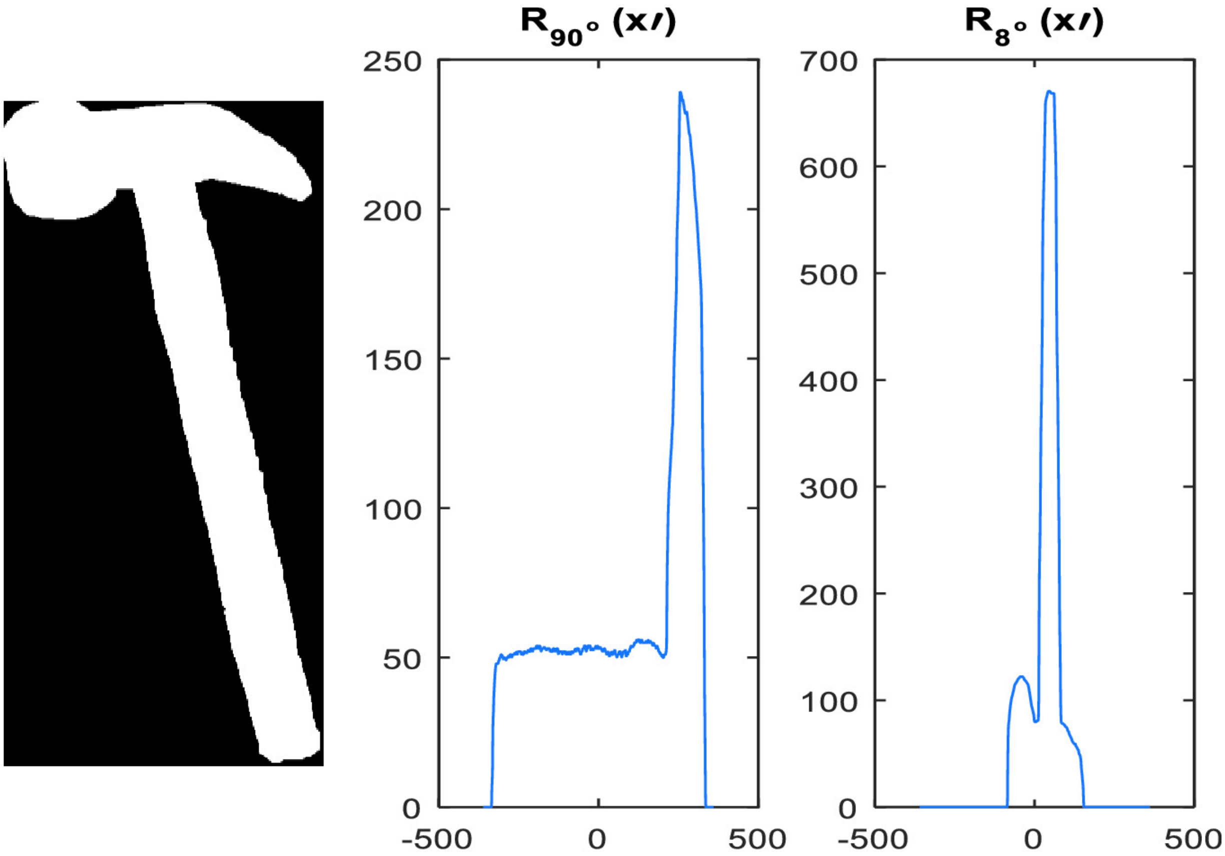

Projection
$\rho = x\cos\theta + y\sin\theta$
y
ρ
θ
x
Object

Fig. 6.30 A shape profile from Radon transform

The top row of Fig. 6.31 shows the projections of a hammer shape from two different directions. It can be seen the projection at 8° has a much higher amplitude than that at 90° because the projection at 8° captures the profile of the long handle. The two profiles are shown at the bottom row of Fig. 6.31 after zooming in and realignment with the projection angles.


$R_{90^\circ}(x')$
$R_{8^\circ}(x')$
250
200
150
100
50
0
-500
0
500
700
600
500
400
300
200
100
0
-500
0
500

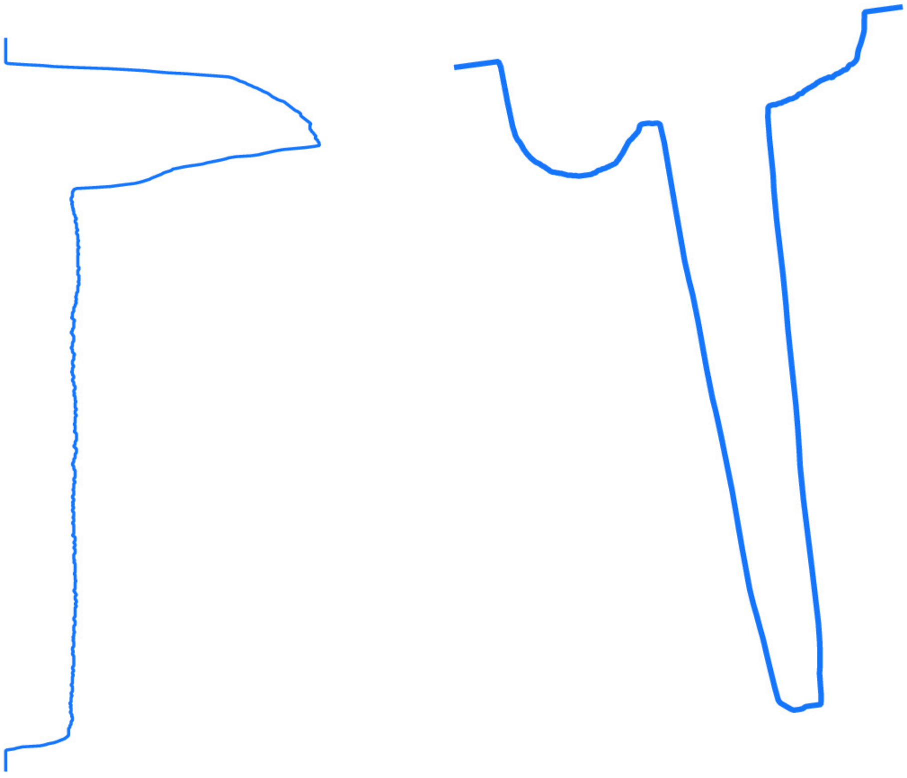


Fig. 6.31 Shape profiles of a hammer image. **Top row**: A hammer shape and its Radon transforms at 90° and 8°; **bottom row**: the 90° and 8° profiles of the hammer shape after zooming in and realignment

In order to capture the complete information of a shape, projections from all directions are created. If the projections from all directions are created and plotted into an angle–magnitude plane, it creates a spectrum of the transformed shape image. For example, the Radon transform spectrum of the hammer shape is shown in Fig. 6.32. The bright spots on the spectrum indicate high amplitudes on the projections. In this case, there is a single brightest spot at around 8°, and it exactly captures the handle angle of the hammer. The next brightest area is around 100°, pointing to the hammer head. Another Radon transform example is shown in Fig. 6.33, where the most bright spots are at 0° and 90°, pointing to the vertical legs and horizontal body of the dog.

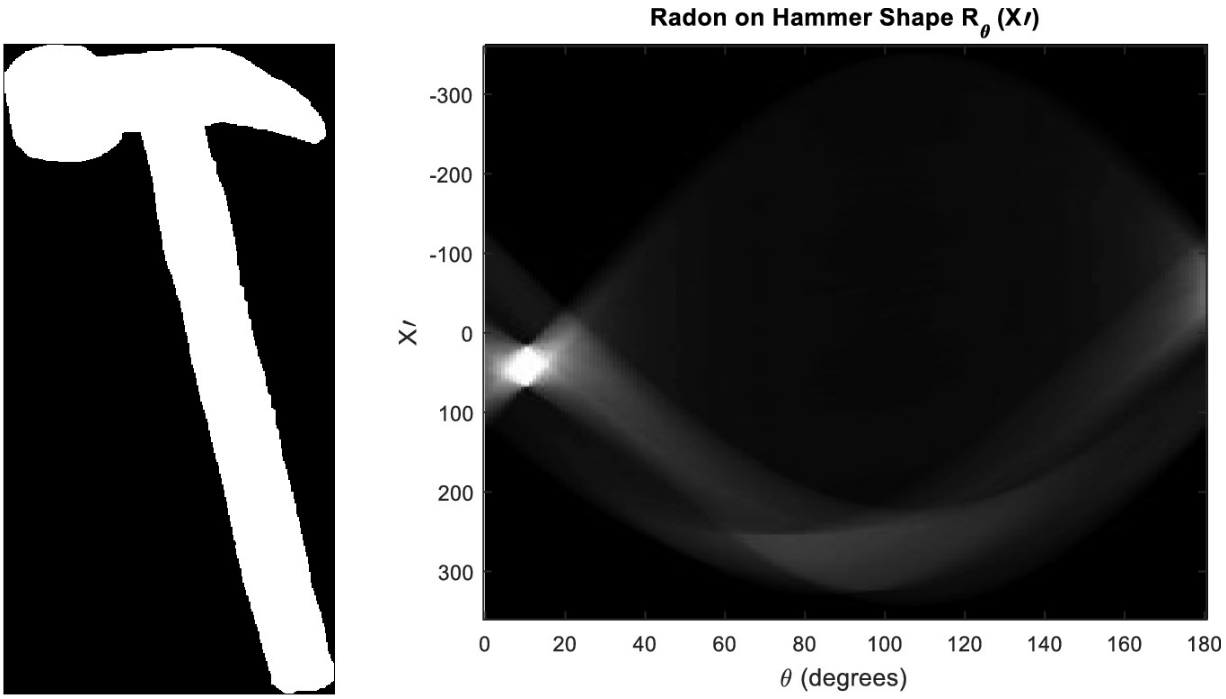


Fig. 6.32 Radon transform of hammer shape. A hammer shape (**left**) and its Radon transform spectrum (**right**)

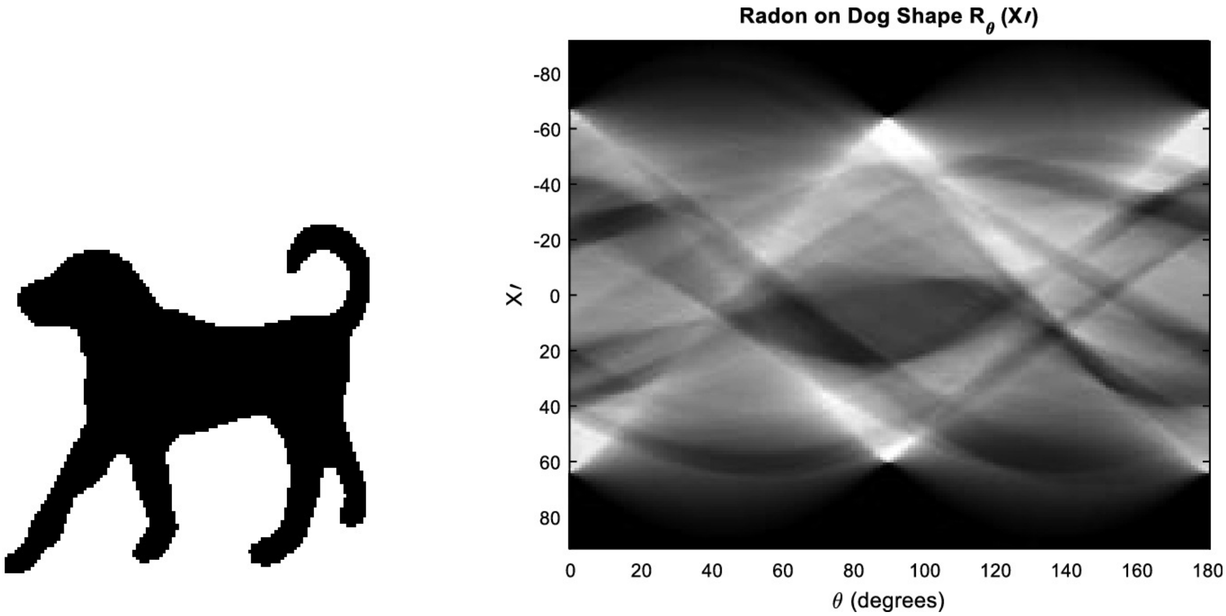


Fig. 6.33 A dog shape and its Radon transform spectrum

A histogram or a GFD can be computed from the Radon spectrum image as a shape descriptor to match between two shapes.

6.4.6 Discussions

Global region-based methods treat a shape region as a whole instead of just using the boundary and make effective use of all the pixel information within the region. These methods measure *pixel distribution* within the shape region, which are less likely affected by noise and variations. This makes them more robust than contour-based methods. Methods like complex moments and GFD are more powerful region shape descriptors than conventional moments, because they not only capture the pixel distribution within a shape, but also capture the spatial details or spatial relationship between pixels. This spatial feature gives them a significant advantage over other region-based methods, such as geometric moments, shape matrix and shape profiles.

However, similar to the global boundary-based methods, global region-based methods cannot deal with overlapped shapes or shapes with missing parts. To address this issue, structural methods are used. Similar to the contour structural methods, *region-based structural methods* decompose a shape region into individual parts which are then used for shape representation and description. In the following, we discuss two of the region-based structural methods.

6.4.7 Convex Hull

A region R is convex if and only if any two points $\mathbf{x}_1, \mathbf{x}_2 \in R$, the whole line segment $\mathbf{x}_1\mathbf{x}_2$ is inside the region. The *convex hull* of a region is the smallest convex region H which satisfies the condition $R \subset H$. The difference H-R is called the *convex deficiency* D of the region R. Methods of computing a convex hull from a shape include morphological methods [16, 17] and polygon approximation. Shape boundaries tend to be irregular because of digitization, noise and variations in segmentation, and these irregularity and noise usually result in a convex deficiency that has small, insignificant components scattered randomly throughout the boundary. Common practice is to first smooth a boundary prior to convex hull computation. The polygon approximation is particularly attractive, because it reduces the computation of extracting convex hull from $O(n^2)$ to $O(n)$.

The extracting of convex hull features can be a single process which finds the most significant convex deficiencies along the boundary. The shape can then be represented by a string of concavities. A fuller representation of the shape may be obtained by a recursive process which results in a concavity tree. To do this, the convex hull of an object is first obtained and its convex deficiencies are detected, and they are level 1 convex hull and convex deficiencies. Next, the convex hulls and deficiencies of the level 1 convex deficiencies are found. Then, the convex hulls and deficiencies of the level 2 convex deficiencies are found. So on so forth until all the derived convex deficiencies are convex.

Figure 6.34a illustrates the computation of convex hull and concavities [7]. The shape is then represented as a concavity tree in Fig. 6.34b. Each concavity can be described by its area, bridge length which is the line connecting the cut of the concavity, maximum curvature, distance from maximum curvature point to the bridge. The matching between shapes becomes a string matching or a graph matching. A shape boundary needs to be smoothed to remove small irregularities before convex hull and concavity extraction; otherwise, the concavity tree would be very complex and sensitive. For example, if the boundary of the apple shape in Fig. 6.34a had been smoothed, the concavity tree would only have four branches S_1–S_4, which accurately represent the shape boundary.

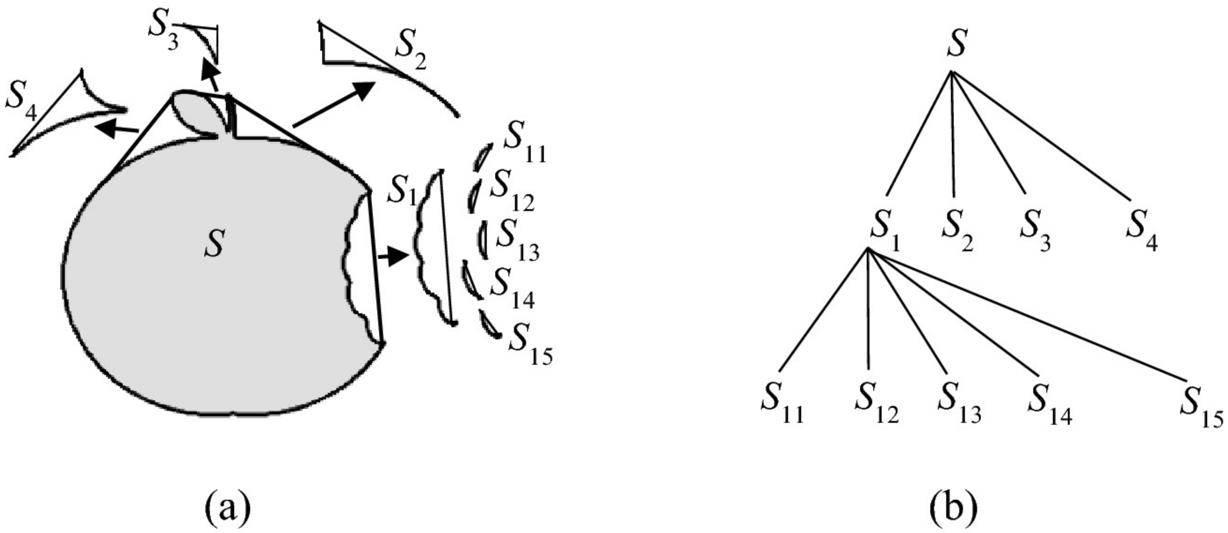


Fig. 6.34 Convex hull and concavity tree of an apple shape. **a** The convex hull of an apple shape and its concavities; **b** concavity tree representation of the convex hull

6.4.8 Medial Axis

Like the convex hull, region *skeleton* can also be employed for shape representation and description. A skeleton may be defined as a connected set of medial lines along the limbs of a figure [17]. For example, in the case of thick hand-drawn characters, the skeleton may be supposed to be the path traveled by the pen. The basic idea of the skeleton is that eliminating redundant information while retaining only the topological information concerning the structure of the object that can help with recognition.

Shape skeleton can be found by using Blum's *medial axis transform* (MAT) [18]. In MAT, the medial axis is the locus of centers of maximal disks or bi-tangent circles that fit entirely within the shape as illustrated in Fig. 6.35. The bold line in the figure is the skeleton of the hand shape. The skeleton can then be decomposed into segments and represented as a graph according to certain criteria. The matching between shapes becomes a graph matching problem.

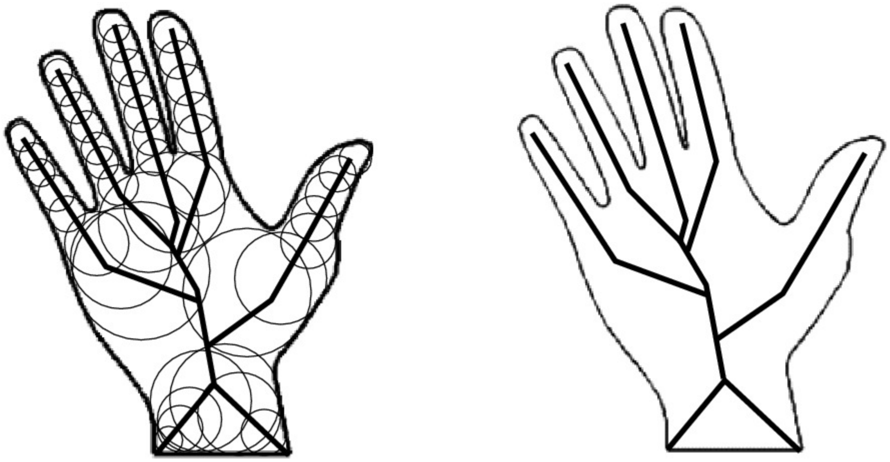


Fig. 6.35 Computation of media axis. **Left**: Construction of medial axis of a rectangle shape using locus of circles; **Right**: The medial axis or skeleton of the hand shape

The computation of medial axis in this way is a rather challenging problem. In addition, medial axis tends to be very sensitive to boundary noise and variations. Therefore, it is suggested that the contour of a shape be smoothed before the media axis computation.

The medial axis can be computed from scale space. The medial axis acquired in this way is called the core of the shape [19].

An alternative way of finding the medial axis is to use a distance transform (calculate the distance from each shape point to the background) to convert the binary shape into a gray-level distance map (Fig. 6.36b). A ridge detection is then applied on the distance map followed by a linking process. The ridge points are local extrema which can be found by scanning the distance map both horizontally and vertically. An extremum is found at where the gradient changes from positive (uphill) to negative (downhill). The skeleton of the shape is finally shown up after the linking process (Fig. 6.36c).

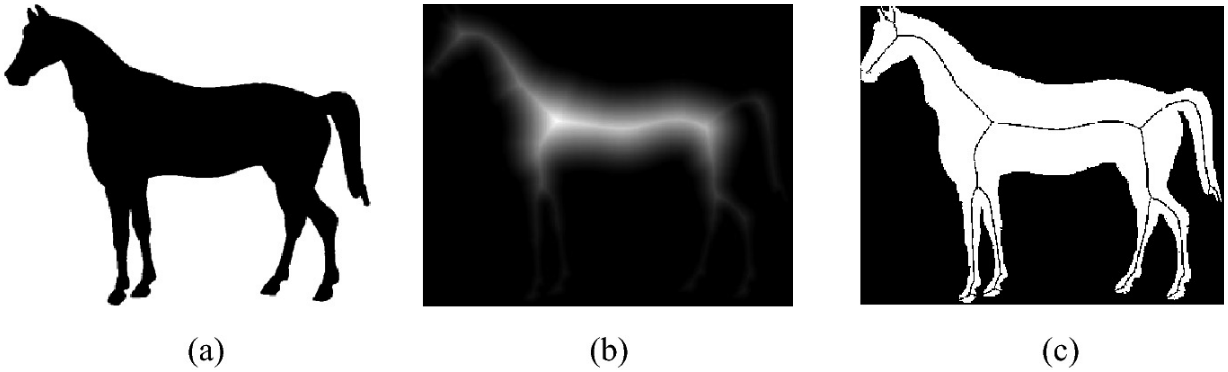


Fig. 6.36 Computation of a shape skeleton. **a** A horse shape image; **b** distance map of (**a**); **c** skeleton of the shape

The limbs and spine of the skeleton are then detected, and features of the limbs and spine such as *length*, *angle* and *curvature* are computed for indexing.

The region structural methods are useful in applications which require partial matching due to object overlapping and missing parts. However, they suffer from similar drawbacks to the contour base structural approaches. Apart from complex computation and implementation, the graph matching is also a complex issue. These issues can affect the performance of region structural methods significantly.

6.5 Summary

This chapter describes three types of shape descriptors: perceptual, contour-based and region-based. Perceptual shape descriptors are very intuitive and easy to understand; however, they are not powerful enough to be used alone. Typically, they are used as filters to eliminate large number of irrelevant shapes before other shape descriptors are used to refine the retrieval list.

Generally, contour shape descriptors are more sensitive to noise and variations than region shape descriptors due to using less information to extract the features. The sensitivity issue can be alleviated by using spectral transform such as Fourier descriptor. Region-based methods are usually more robust, because they make use of all the information within the shape region instead of just the boundary.

For image description and retrieval, MPEG-7 has set a set of principles to evaluate the suitability of shape technique: good retrieval accuracy, compact features, general application, low computation complexity, robust retrieval performance and hierarchical coarse to fine representation. Based on these principles, methods like FD, GFD, ZMD are desirable descriptors.

However, every shape technique has its advantages and disadvantages. The choice of shape techniques often depends on applications and datasets. For example, for shapes with solid interior, contour-based methods are usually preferred, such as fish sorting and tool recognition. In applications with overlapped objects which require partial matching, structural methods are a preferred choice.

6.6 Exercises

1. Find a binary shape with connected boundary, and use the boundary trace code and area code from the following Web pages to compute the *circularity*/*compactness* of the shape. Try more shape images and explain the effectiveness of circularity/compactness.
   https://au.mathworks.com/help/images/boundary-tracing-in-images.html
   https://au.mathworks.com/help/images/ref/bwarea.html

2. Find a binary shape image and use the following Matlab code to extract the bounding box of the shape (change *image_name* to your own image name). Then calculate the elongation of the shape.

```
I = imread(‘image_name’);
h = bwconvhull(I);
stats = regionprops(h, ‘BoundingBox’, ‘MajorAxisLength’,
‘MinorAxisLength’);
imshow(I);
hold on;
rectangle(‘Position’, stats.BoundingBox,‘EdgeColor’, ‘b’);
stats.
```

3. Find a binary image and use the following Matlab code to compute the Radon transform of the image (replace the image *I* with your own image using the *imread*() function shown in the above code): https://au.mathworks.com/help/images/ref/radon.html. Examine the Radon spectrum, and match the bright spots on the spectrum and their corresponding features on the binary image.

4. Use the methods shown in Exercise 1 of both Chaps. 4 and 5 to compute the mean, standard deviation and the histogram of the Radon spectrum from Exercise 3.

5. Find more binary shape images, compute the Radon spectra of these images, and then compute the statistics and histograms of the Radon spectra. Write a short report on how well the features from Radon spectra describe the images and compare them with the features computed from Exercises 1 and 2.

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Part III
Image Classification and Annotation

Dripping water penetrates the stone

III.1 Introduction

Due to the rapid digitisation and development of the Web, the world is full of digital images. However, without proper classification, these mammoth amount of images are not going to be much helpful, instead, it has caused a huge waste of resources.

Vast amount of research has been done in the past decades to organize digital images into categories so that they can be searched and retrieved conveniently. However, despite the tremendous effort, we are still at the early stage of understanding images.

Basically, image classification is to organize images into different classes based on the features of the images. Image annotation is to label images with different semantic class names, such as trees, air planes, lake, etc. The difference between image classification and image annotation is that image annotation attempts to annotate an image with multiple labels or classify an image into multiple classes. Image annotation is done through *multiple instance learning* (MIL). With MIL, an image is represented with a *bag of features* (BOF), and an image is labelled as positive if any of the instances in the bag is positive. Image classification and annotation are close related, because if an image is correctly classified, it can be annotated and if an image is correctly annotated, it can be properly classified into a class.

Given an image as in Fig. III.1, what we want is to classify it into one of the semantic classes, such as, ‘mountain’ or ‘plants’ or ‘nature’, with a probability or likelihood.

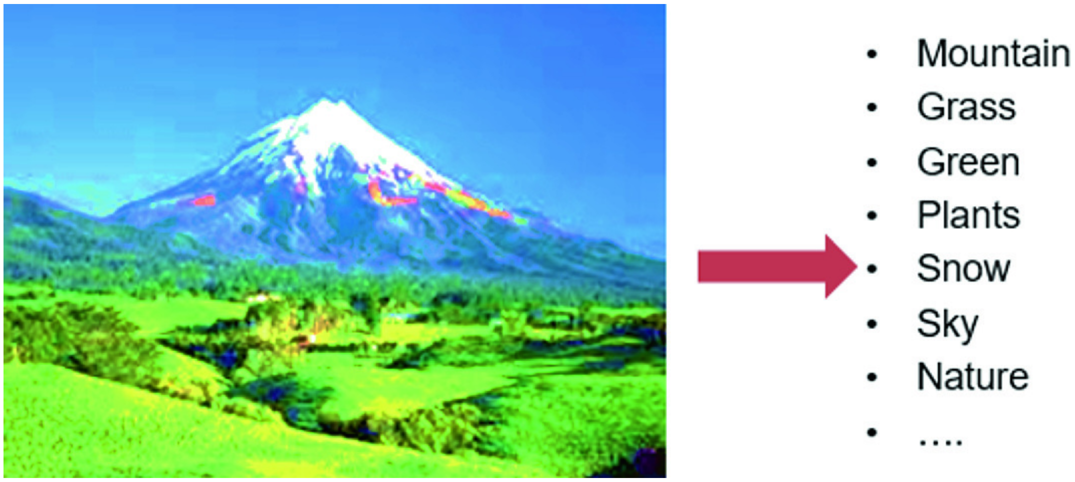

Fig. III.1 An image to be classified into one of the classes

However, what we have is usually a sequence of numeric features computed through certain feature extraction methods described in Part II, such as, a color histogram, or a feature vector (Fig. III.2).

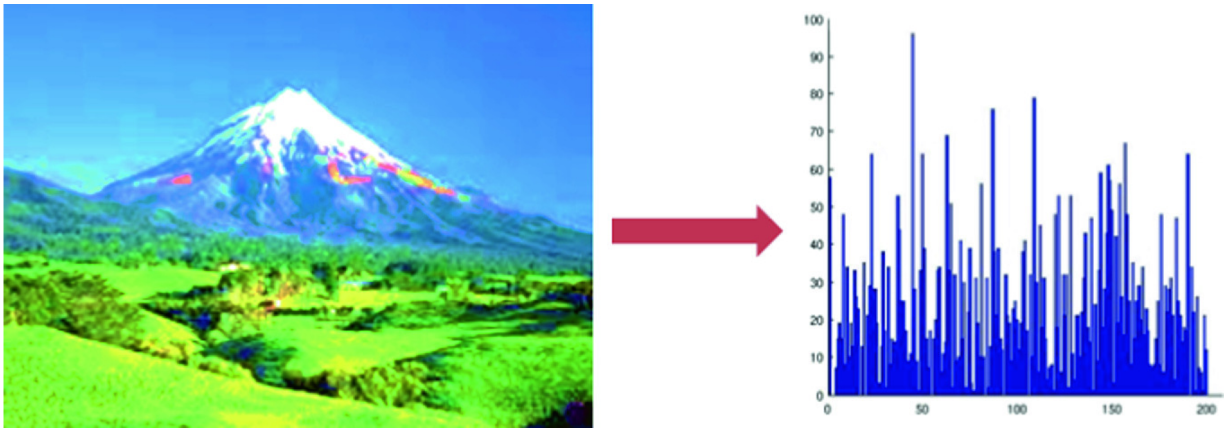

Fig. III.2 An image on the *left* and its color histogram on the *right*

What we can do is to learn from experience or prior knowledge like a human being. Suppose we know the above image is a mountain image, given an unknown image, we can compare its features with the features of the mountain image. If there is a good match (e.g., high probability) between the two feature vectors, we would label or classify the unknown image also as 'mountain' (Fig. III.3).

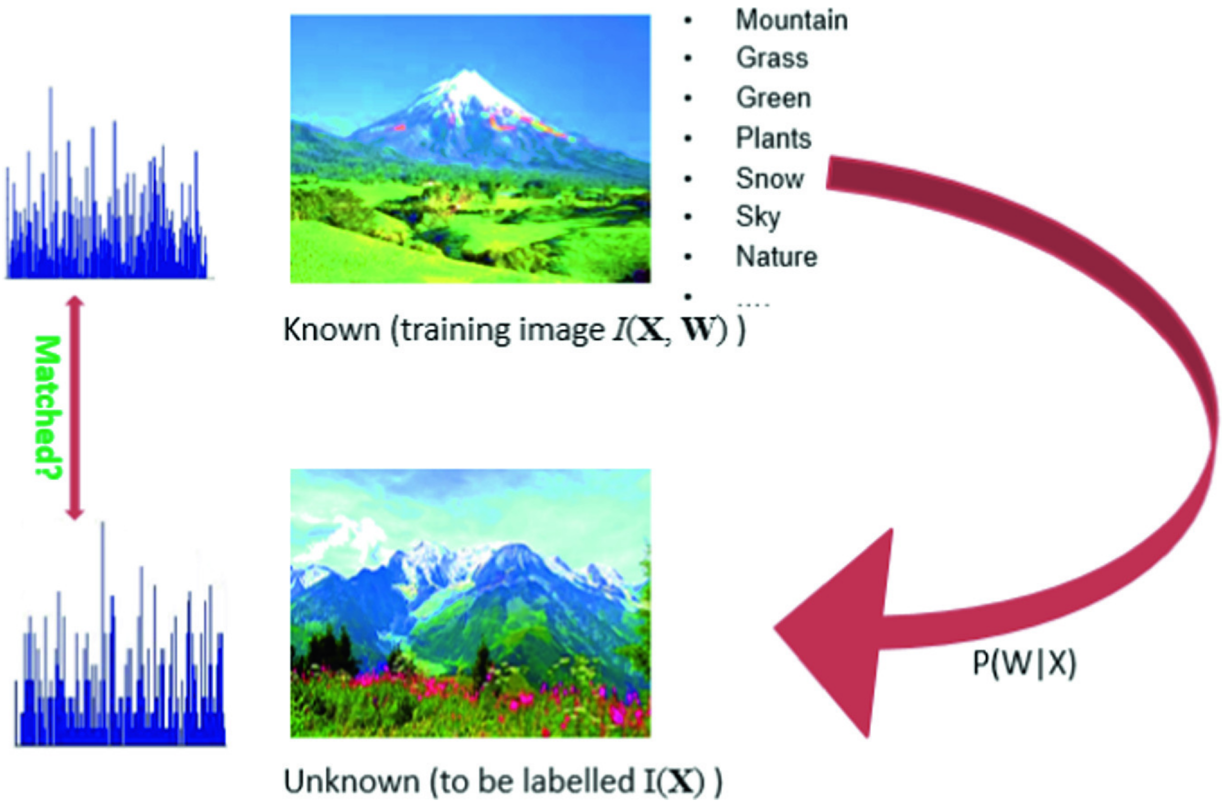
Mountain
Grass
Green
Plants
Snow
Sky
Nature
....
Known (training image $I(\mathbf{X}, \mathbf{W})$)
Matched?
P(W|X)
Unknown (to be labelled $I(\mathbf{X})$)

Fig. III.3 Matching between an unknown image with a labelled image

We could use this simple method to identify or retrieve all the mountain images from the database (Fig. III.4). However, this is not going to work well, because the single known image is not a good representation of all the mountain images in the database. Consequently, many mountain images in the database will be misclassified or not retrieved.

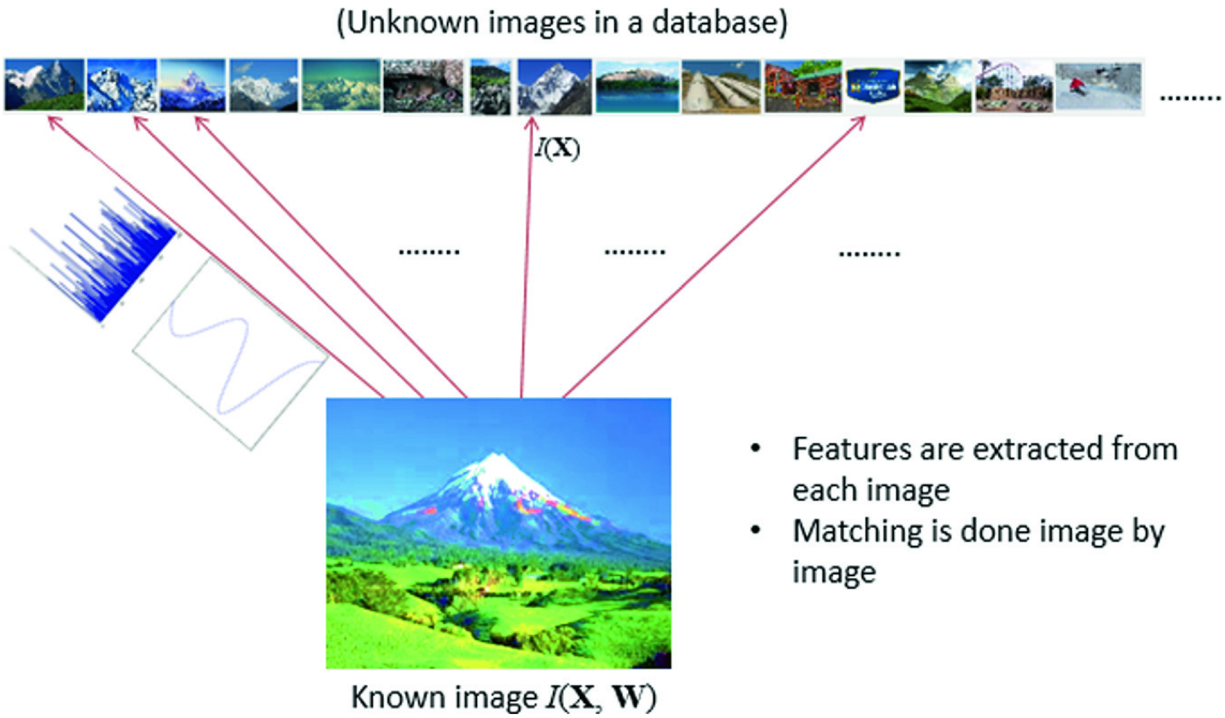
(Unknown images in a database)
....
$I(\mathbf{X})$
....
....
....
• Features are extracted from each image
• Matching is done image by image
Known image $I(\mathbf{X}, \mathbf{W})$

Fig. III.4 Use a labelled image to identify all the mountain images in a database

A much better way to identify all mountain images in a database is to collect large number of sample mountain images and use them to train a classifier. Once trained, the classifier will be able to memorize these sample images and use them to recognize unknown images.

There are generally two types of approaches on training or building a classifier, *generative* versus *discriminative*.

III.1.1 Generative Model

The generative approach is based on an idea similar to Platonic philosophy that there is an abstract concept or model behind every type of objects in this world, such as trees, apples, dogs, human beings etc. It is believed that when people try to recognize a specific type of objects in this world, they actually compare them with this abstract model. Therefore, it is possible to create or work out this abstract model for every type or class of objects. The simplest way to create this kind of model is to collect a set of real world samples and average them, for example, an average apple (Fig. III.5).

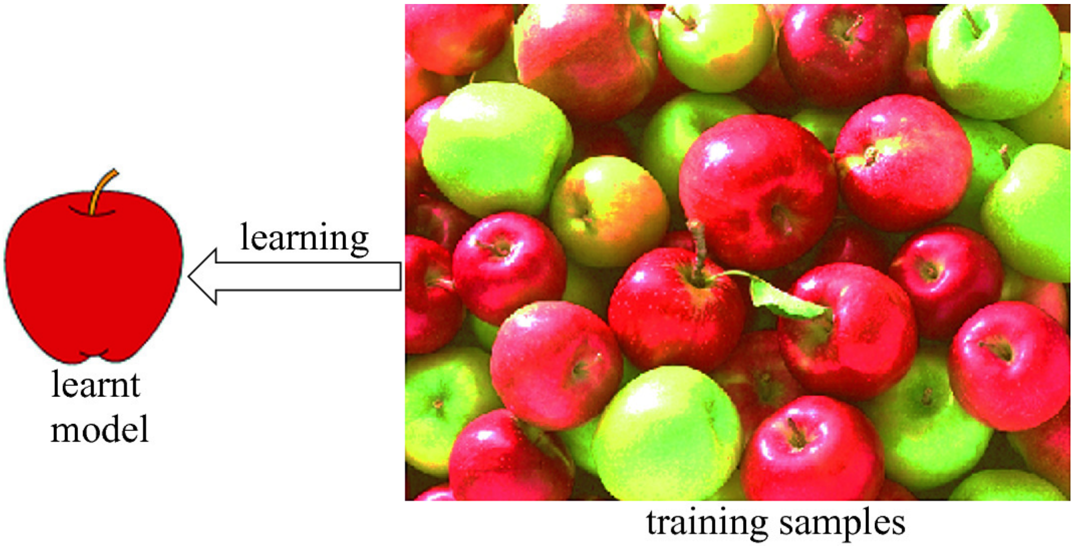

Fig. III.5 Sample apples (*right*) and the learnt apple model (*left*)

However, this can only do simple classification by distinguishing apples from non-fruit objects, while it would be difficult to distinguish apples from other fruits such as peaches, or pears. In practice, a probabilistic distribution is learnt from the collected samples and the distribution is used as the model representing the objects (Fig. III.6). The variety of those probabilistic methods follow the generative approach, including the typical Gaussian mixture model and Bayesian methods.

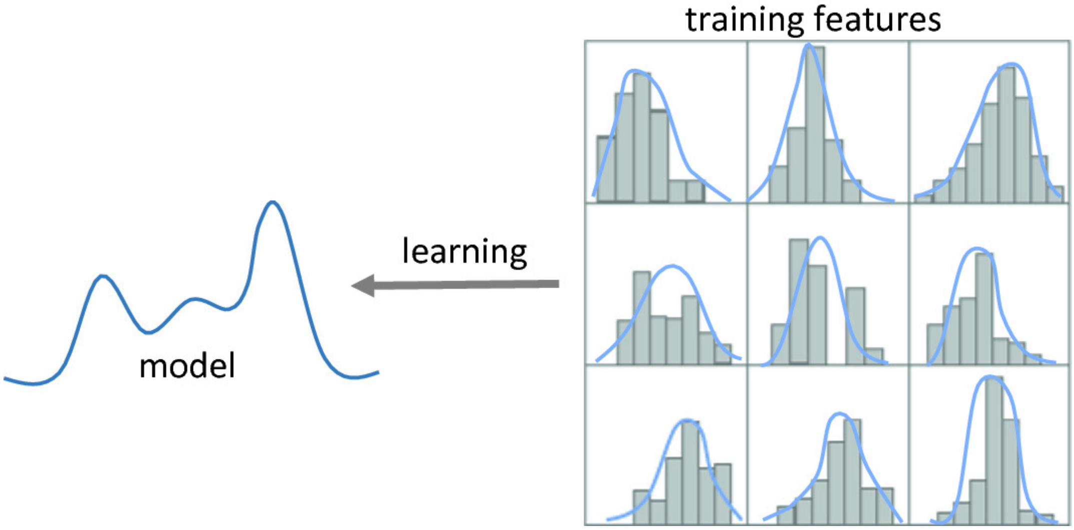

Fig. III.6 Computation of a generative model. Sample images are represented as features (*right*); a mixture distribution model is learnt from those sample features (*left*)

III.1.2 Discriminative Approach

In contrast to the generative approach, the discriminative approach doesn’t believe or is unaware of the model behind every type of objects. Instead, discriminative methods do classification by comparing different objects based on their similarity or difference, as opposed to comparing objects with a model in the generative approach. In practice, a large number of sample training data are collected from different classes, and an optimal hyper plane, called the classifier or a machine, is fitted between two classes in a high dimensional feature space (Fig. III.7). The optimal hyper plane is found through a trial and error process by keeping testing the similarity or difference between the training data.

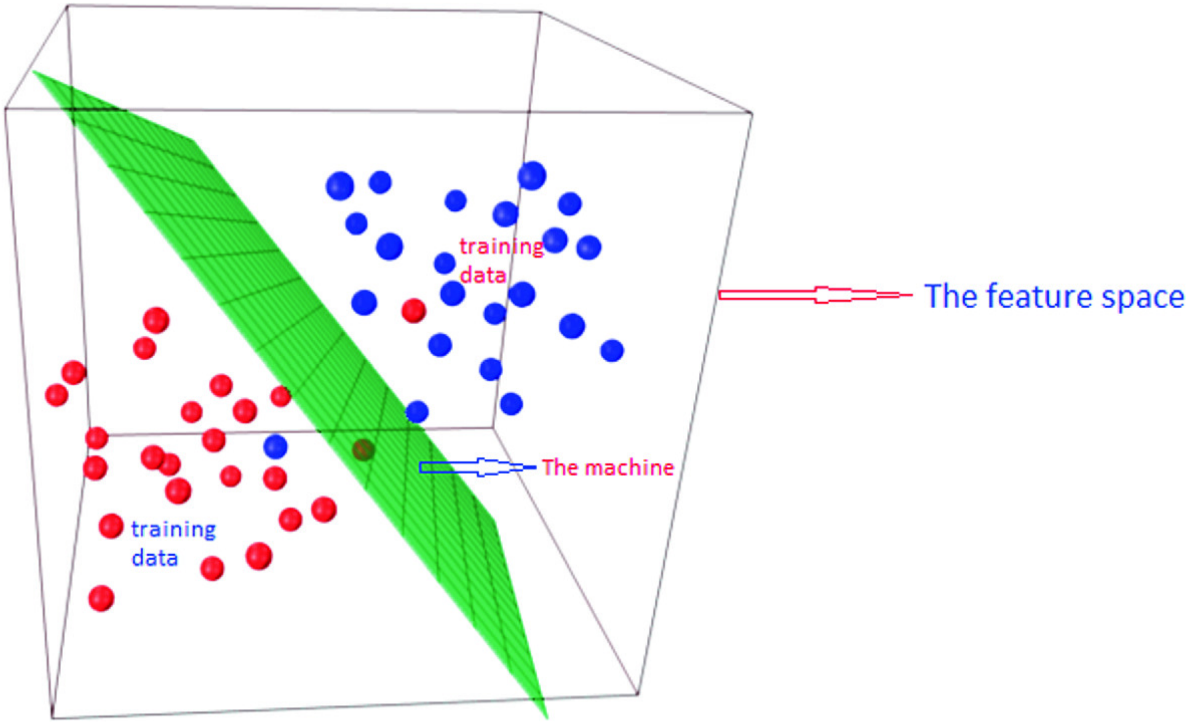

Fig. III.7 A machine is fitted between two classes of data

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7. Bayesian Classification

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History tells the future.

7.1 Introduction

All Bayesian classification methods are based on the Bayes' theorem:

$$P\left(A|B\right)=\frac{P(B|A)P\left(A\right)}{P\left(B\right)}=\frac{P(B|A)P\left(A\right)}{P(B|A)P\left(A\right)+P(B|\bar{A})P\left(\bar{A}\right)} \tag{7.1}$$

where

- A and B are random events, and $\bar{A}$ is the complement of A.
- A is a hypothesis to be tested or predicted.
- B is the new data or observation, and it is the new evidence to predict A.
- $P(A)$ is called the *prior* probability, and $P(B|A)$ is called the *likelihood*; they represents our experience or prior knowledge.
- $P(B)$ is the observation probability or the chance to observe event B.
- $P(A|B)$ is called the *posterior* probability.

The idea of Bayes' theorem is to convert the computation of probability of $P(A|B)$ to $P(B|A)$ which is easier to compute. This is extremely helpful when two random events A and B are dependent each other, and the prediction of event A is difficult due to lack of evidence or information; in this situation, the information about *B* can be employed to help predicting *A* more accurately. The information about *B* can usually be obtained from historical data or experience.

This idea of predicting one event using other related events have been practiced by human beings all the time; for example, we use symptoms to predict a disease, use cloud to predict rain, use a man's culture/background to predict his behavior, use rainfall to predict harvest, etc. In the following, we use two simple examples to get some firsthand understanding of how Bayesian theorem works in real-world applications.

For the first example, we are planning for a sports event at a weekend in a local club and we want to know if the weather will be fine at the weekend. We know the weather and humidity are highly related; we can use humidity to help us predicting if the weather is fine so that the sports can go ahead. Formally, let

$$R = \text{Rain} \quad \bar{R} = \text{No rain} \quad H = \text{High humidity} \ \ (\text{humidity} > 80\%)$$

Suppose we know from history (e.g. bureau of meteorology) the following prior information:

$$P(R) = 35\% \quad P(\bar{R}) = 65\% \quad P(H|\bar{R}) = 30\%$$

Suppose further we know there will be high humidity at the weekend based on the most recent day weather, then we can predict the chance of no rain at the weekend by the Bayes' theorem:

$$P\left(\bar{R}|H\right) = \frac{P(H|\bar{R})P\left(\bar{R}\right)}{P(H)} = \frac{P(H|\bar{R})P\left(\bar{R}\right)}{P(H|\bar{R})P\left(\bar{R}\right) + P(H|R)P(R)}$$
$$= \frac{0.3 \times 0.65}{0.3 \times 0.65 + 1 \times 0.65} = \frac{0.195}{0.845} \approx 23\%$$

This information is useful for making a reasonable decision on if the sports event should go ahead. Notice that without the prior information of $P(\bar{R})$ and $P(H|\bar{R})$, the prediction and decision would have been made arbitrarily. In practice, factors such as humidity, temperature and atmospheric pressure are combined to obtain an even more accurate prediction.

Another example is the application of the Bayes' theorem on image classification. Suppose we have detected some black and white strips (through feature extraction) in an image; based on our experience, we believe it's likely a zebra image. But how likely the image is a zebra, 70% of the chance, 80% or 99%? For many other cases like financial, economic or military situations, this likelihood is crucial to make a right decision. It's clear we need more evidence to determine the accurate likelihood. The answer is in statistics.

If we were able to sample all the images in the world just like a population census in a country, we would be able to calculate the statistics and tell how many non-zebra images would have the black and white strips. This statistic would help us to determine how likely the image with black and white strips is a zebra image. Unfortunately, we are not able to do a census on all the images in the world; all we can do is to sample part of the image population and create an image database, then use the statistics calculated from the image database to approximate those in the image population.

Formally, let

$$Z = \text{ Zebra image} \quad \bar{Z} = \text{non} - \text{Zebra image} \quad BWS = \text{Black and white strips}$$

Now, suppose we know the following probabilities from a training set or an image database (our experience or prior information):

$$P\,(\text{BWS}|Z) = 1.0 \quad P\,(Z) = 0.05 \quad P(\text{BWS}|\bar{Z}) = 0.01$$

Then, given the black and white strips in an image, we can predict if there is a zebra in the image by the Bayes' theorem:

$$P\,(Z|\text{BWS}) = \frac{P(\text{BWS}|Z)P\,(Z)}{P\,(\text{BWS})} = \frac{P(\text{BWS}|Z)P\,(Z)}{P\,(\text{BWS}|Z)\,P\,(Z) + P(\text{BWS}|\bar{Z})P\left(\bar{Z}\right)}$$
$$= \frac{1.0 \times 0.05}{1.0 \times 0.05 + 0.01 \times 0.95} = \frac{0.05}{0.0595} \approx 84\%$$

Therefore, we can say there is a high chance that the image is a zebra image and we have high confidence to classify the image into the zebra image category.

Bayes' theorem can be extended to multiple events $A_1, A_2, \ldots, A_n$:

$$P\left(A_i|B\right) = \frac{P(B|A_i)P\left(A_i\right)}{P\left(B\right)} = \frac{P(B|A_i)P\left(A_i\right)}{P(B|A_1)P\left(A_1\right) + \ldots + P(B|A_n)P\left(A_n\right)} \quad (7.2)$$

In this case, B is related to or dependant on multiple other events A_i, and based on what we know about the relationship or dependency between B and each A_i: $P(B|A_i)$, we can predict if a new observation of B is from any of the events A_i.

For example, fever (B) can be caused by many diseases or medical conditions (A_i), such as infection, flu, pneumonia, chickenpox, measles, HIV, meningitis, cancers, malaria and dengue. However, each disease or medical condition has different chances of causing fever: $P(B|A_i)$. Now, given a patient with fever, (7.2) can be used to determine if the patient has flu: $P(A_i|B)$. In clinical practice, however, symptoms are typically combined to nail a disease; e.g. by combining fever with running nose and headache, flu can be diagnosed with very high accuracy.

7.2 Naïve Bayesian Image Classification

7.2.1 NB Formulation

The *naïve Bayesian* (NB) methods are based on a simple application of the above Bayes' theorem on numerical and high-dimensional image data.

- Given a set of N images: $I = \{I_1, I_2, \ldots, I_N\}$
- And a set of n semantic classes $C = \{C_1, C_2, \ldots, C_n\}$ (events).
- $I \in C$.
- Each image I is represented by a feature vector $I \sim \mathbf{x} = (x_1, x_2, \ldots, x_m)$ (observation).

According to Bayes' theorem, the classification or annotation of image I to class C_i is given by

$$P\left(C_i|I\right) = P\left(C_i|\mathbf{x}\right) = \frac{P(\mathbf{x}|C_i)P\left(C_i\right)}{P\left(\mathbf{x}\right)} = \frac{P(\mathbf{x}|C_i)P\left(C_i\right)}{P(\mathbf{x}|C_1)P\left(C_1\right) + \ldots + P(\mathbf{x}|C_n)P\left(C_n\right)} \quad (7.3)$$

Or

$$P(C_i|I) = P(C_i|\mathbf{x}) = \frac{P(\mathbf{x}|C_i)P(C_i)}{\sum_{k=1}^{n} P(\mathbf{x}|C_k)P(C_k)} \tag{7.4}$$

Because the denominator $P(\mathbf{x}) = \sum_{k=1}^{n} P(\mathbf{x}|C_k) \times P(C_k)$ is independent of class C_i ($i = 1, 2, \ldots, n$) and is a constant, (7.4) can be written as:

$$P(C_i|I) = P(C_i|\mathbf{x}) = \frac{1}{Z} P(\mathbf{x}|C_i) P(C_i) \tag{7.5}$$

where $Z = \sum_{k=1}^{n} P(\mathbf{x}|C_k)P(C_k)$ is a scaling factor. The class of image I can be decided using the *maximizing a posterior* (*MAP*) criterion

$$P\left(C_j|I\right) = \hat{C} = \arg\max_i P(C_i|\mathbf{x}) = \arg\max_i \{P(\mathbf{x}|C_i)P(C_i)\} \tag{7.6}$$

The prior probabilities $P(C_i)$ is usually uniform for all classes; otherwise, they can be found by the frequency or proportion of samples belonging to class C_i among all classes. Therefore, the classification of image I comes down to modeling the likelihood probability of $P(\mathbf{x}/C_i)$.

Since image features are typically numerical and continuous, they need to be discretized before the likelihood modeling. In practice, the following procedure is used to compute the $P(\mathbf{x}|C_i)$ in (7.6).

Training:

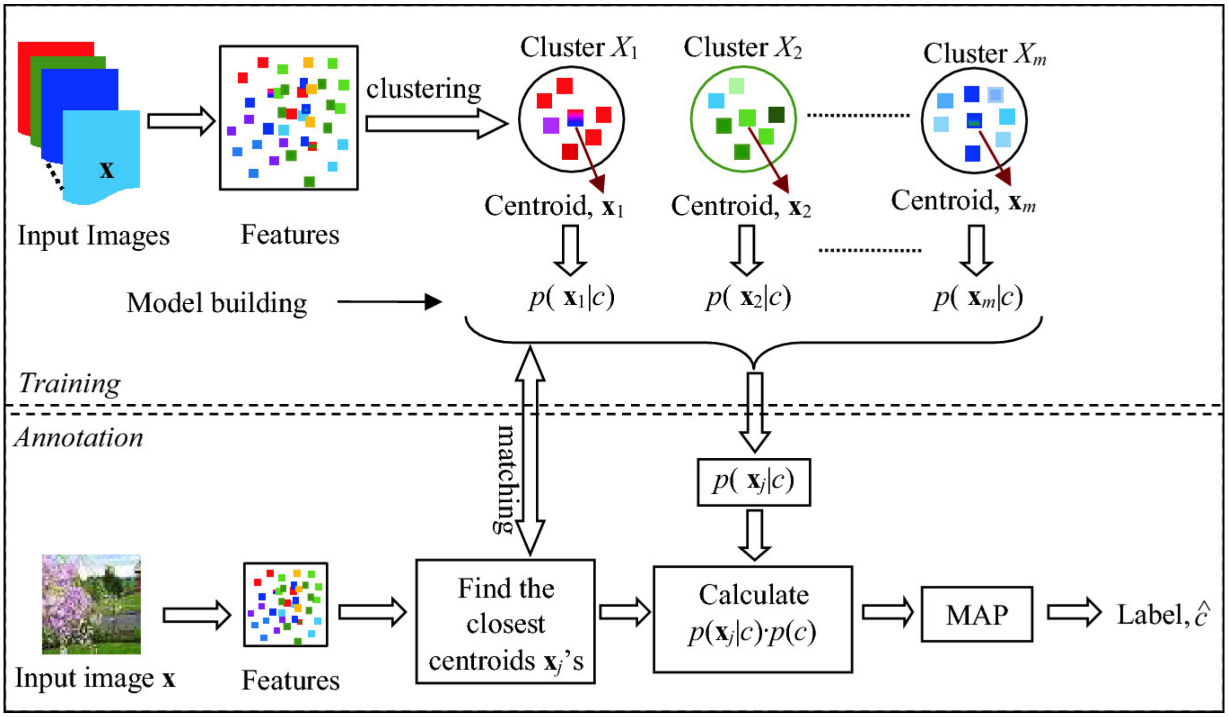
- A training database of images from all the n classes $\{C_1, C_2, \ldots, C_n\}$ are created.
- Image features from the training database are clustered into m clusters X_j using a certain vector quantization algorithm.
- Next, a cluster centroid $\mathbf{x}_j$ is computed for each of the clusters $X_{j:}$ $\mathbf{x}_j$, $j = 1, 2, \ldots, m$.
- Then, the likelihood $P(\mathbf{x}_j|C_i)$ is calculated by finding the frequency of samples in X_j belonging to class C_i.

$$P\left(\mathbf{x}_j|C_j\right) = \frac{\text{No. of samples in } X_j \text{ which are from class } C_i}{\text{Total no. of samples in cluster } X_j} \tag{7.7}$$

Classification/Annotation:

- Given a new image I with feature $\mathbf{x}$.
- Match feature $\mathbf{x}$ to the closest cluster centroids $\mathbf{x}_j$*'s*.
- Apply the *MAP* of (7.6) by replacing the likelihood $P(\mathbf{x}|C_i)$ with (7.7) to obtain the posterior probability $P(C_j \mid I)$.

The classification and annotation of an image with naïve Bayesian method is illustrated in Fig. 7.1 [1, 2]. There are two major modules in a NB classifier: *training* and *annotation*, and each of the major modules consists of three submodules. The training module consists of *feature extraction*, *clustering* and *model building*; while the annotation consists of *feature extraction*, *matching* and *decision making* using MAP.



x
Input Images
Features
clustering
Cluster X_1
Cluster X_2
Cluster X_m
Centroid, $\mathbf{x}_1$
Centroid, $\mathbf{x}_2$
Centroid, $\mathbf{x}_m$
Model building
$p(\mathbf{x}_1|c)$
$p(\mathbf{x}_2|c)$
$p(\mathbf{x}_m|c)$
Training
Annotation
matching
$p(\mathbf{x}_j|c)$
Input image $\mathbf{x}$
Features
Find the closest centroids $\mathbf{x}_j$'s
Calculate $p(\mathbf{x}_j|c)\cdot p(c)$
MAP
Label, $\hat{c}$

Fig. 7.1 Image classification with naïve Bayesian method

7.2.2 NB with Independent Features

Assume $x_1, x_2, \ldots, x_m$ are independent each other; then the likelihood is given as:

$$P(\mathbf{x}|C_i) = \prod_{j=1}^{m} P(x_j|C_i) \tag{7.8}$$

There are many situations where the features of a data are independent each other, e.g., nominal features extracted by a web crawler, tree, grass, sand and water. Suppose we are using a set of nominal features $\mathbf{x} = (sand, water, sky, people)$ to classify a collection of images into 'beach' and 'non-beach' categories; then, (7.8) can be employed to modeling the likelihood in the Bayes' theorem. Often different types of numerical image features are combined into a more powerful feature vector, e.g. $\mathbf{x} = (color, shape, texture)$; again, the likelihood probability in the Bayes' theorem can be computed using (7.8).

7.2.3 NB with Bag of Features

If an image I is segmented into k regions, and each region is represented as a feature vector $\mathbf{x}_j$, $j = 1, 2, \ldots, k$, I can be represented as a *bag of features*: $I = \{\mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_k\}$. Typically, regions in an image are independent each other; therefore, the conditional probability of $P(I \mid C_i)$ is given by:

$$P(I|C_i) = P(\mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_k|C_i) = \prod_{j=1}^{k} P(\mathbf{x}_j|C_i) \tag{7.9}$$

7.3 Image Annotation with Word Co-occurrence

In the above naïve Bayesian classification, images are not individually labeled; instead, they are simply classified into categories. The categories can be regarded as *implicit image annotation* or collective image annotation. However, individual images can be pre-labeled and the annotation of images can be done explicitly. Vast amount of labeled images are available on the web; they can be employed to annotate new images. One of the earliest works on *explicit image annotation* or individual image annotation is the *word co-occurrence model* (WCC) introduced by Mori et al. [3]. The idea is to establish the relationship between image features and the labels and use the relationship as a likelihood model to label new images. Specifically, features from pre-labeled image are clustered into clusters and a *word histogram* is computed from each cluster as the likelihood model. The idea of their method can be summarized as follows:

1. Collecting training images with pre-labeled key words.
2. Divide each image into parts and extract features from each part.
3. Each divided part inherits all words from its original image.
4. Make clusters from all divided images using vector quantization.
5. Accumulate the frequencies of words of all partial images in each cluster and calculate the likelihood for every word.
6. For an unknown image, divide it into parts, extract their features and match the image parts with the above clusters. Combine the likelihoods of the image parts and determine which words are most plausible.

The *algorithm* of the word co-occurrence model is given as following:

- **Collect and label training images**. Given a training dataset of n images $\mathbf{I} = (I_1, I_2,, ..., I_n)$ and each image I_i is pre-labeled with a set of semantic words $\mathbf{w}_i$:

$$(\mathbf{I}, \mathbf{w}) = \{(I_1, \mathbf{w}_1), (I_2, \mathbf{w}_2), \ldots, (I_n, \mathbf{w}_n)\}$$

- **Obtain the vocabulary of the training images**. The semantic vocabulary of the dataset consists of m words:

$$\mathbf{w} = (w_1, w_2, \ldots, w_m)$$

- **Divide training images into blocks**. Each training image is divided into small blocks, and each block inherits all the annotations from its parent image.
- **Vector Quantization (VQ)**.
  - – Blocks from all the training images are clustered into v clusters represented by the centroids c_1, c_2, ..., c_v.
  - – Each cluster c_i is represented as a feature vector $\mathbf{x}_i$ (each cluster is called a *visual word* or VW, which is corresponding to a region in the training images):

$$\mathbf{c} = (c_1, c_2, \ldots, c_v) = (\mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_v)$$

- **Obtain a word histogram in each cluster**. Because each block has inherited a set of words from its parent image, by counting the occurrence of words, a histogram of words from the vocabulary can be created:

$$P(w_j|c_i) = P\left(w_j|\mathbf{x}_i\right) = (W_1, W_2, \ldots, W_m) \tag{7.10}$$

  where W_j represents the frequency of word w_j in cluster c_i, $P(W_j|c_i)$ represents the likelihood of word w_j.

- **Annotate an unknown image**
  - – Given an unknown image I_u, it is also divided into small blocks and the blocks of the unknown image is also clustered into clusters.
  - – Each unknown cluster is matched with the VWs, and the nearest l VWs are found for the unknown image.
  - – The matching is done by calculating the distance between each feature of the unknown image $\mathbf{x}_u$ and each VW $\mathbf{x}_i$: $\|\mathbf{x}_u - \mathbf{x}_i\|$

– The annotation of image I_u to a semantic word w_j (j = 1, 2, ..., k) is given by first summing up the histograms of matched clusters c_i (i = 1, ..., l) and then selecting the top k bins as the annotations:

$$P\,(w_1, \ldots, w_k|I_u) = \text{top}\,k\,\text{bins}\,(\sum_{1}^{l} P(w_j|c_i)) \tag{7.11}$$

The co-occurrence annotation method can be illustrated in Fig. 7.2 [1, 2]. There are two key differences between Figs. 7.2 and 7.1. The first is in the training module; while the NB builds a model of $p(\mathbf{x}_i|c)$, the WCC builds a model of $p(w|c)$. The second difference in the annotation module; while the NB makes a decision based on MAP, the WCC makes a decision based on top histogram bins which means an image can be classified into several classes.

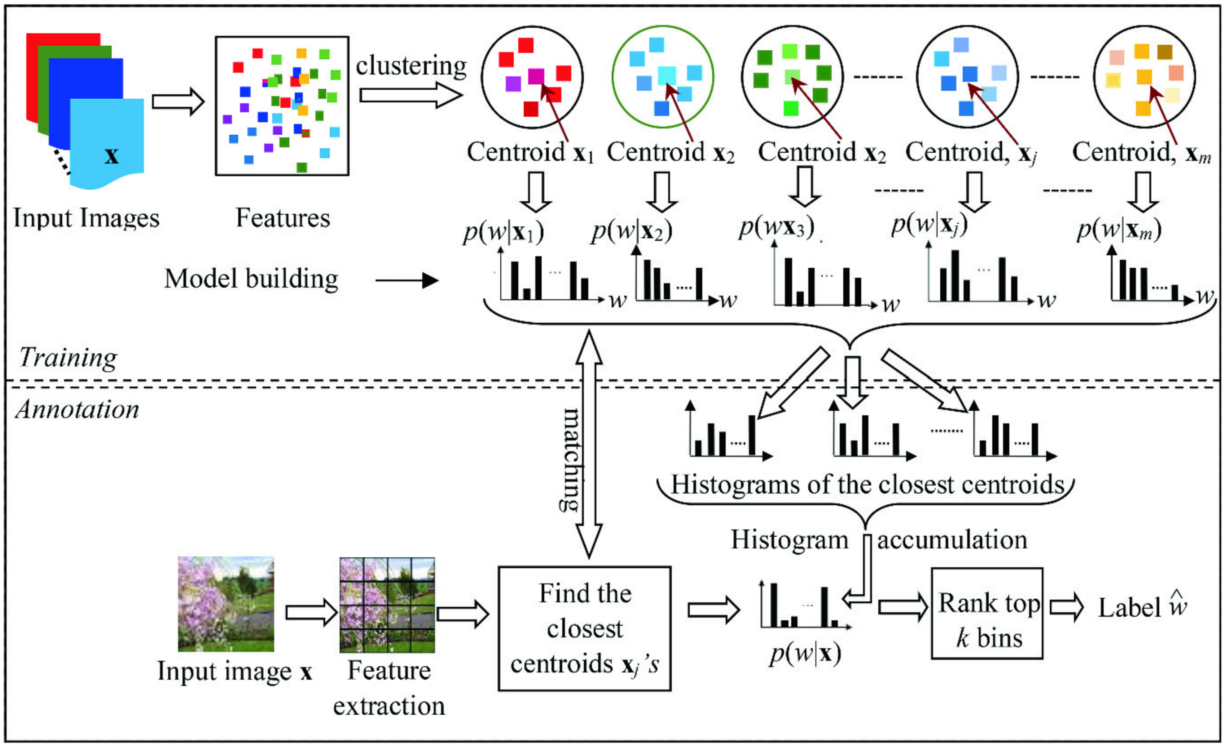

x
Input Images
Features
clustering
Centroid $\mathbf{x}_1$
Centroid $\mathbf{x}_2$
Centroid $\mathbf{x}_2$
Centroid, $\mathbf{x}_j$
Centroid, $\mathbf{x}_m$
$p(w|\mathbf{x}_1)$
$p(w|\mathbf{x}_2)$
$p(w\mathbf{x}_3)$
$p(w|\mathbf{x}_j)$
$p(w|\mathbf{x}_m)$
Model building
w
w
w
w
w
Training
Annotation
matching
Histograms of the closest centroids
Histogram accumulation
Input image $\mathbf{x}$
Feature extraction
Find the closest centroids $\mathbf{x}_j$'s
$p(w|\mathbf{x})$
Rank top k bins
Label $\hat{w}$

Fig. 7.2 Image annotation with co-occurrence of words

Although the co-occurrence method uses image blocks for the VQ, the blocks can be replaced with pre-segmented image regions. This is because regardless blocks or regions, they are all represented with a feature vector **x**, and the VQ is done based on feature vector **x**.

7.4 Image Annotation with Joint Probability

The word co-occurrence model is a significant development to traditional image classification; it can be generalized into a joint probability model which is described in the following.

- Given a training dataset of *n* pre-annotated images:

$$(\mathbf{I}, \mathbf{w}) = (I_1, \mathbf{w}_1), (I_2, \mathbf{w}_2), \ldots, (I_n, \mathbf{w}_n)$$

- The semantic vocabulary of the dataset consists of *m* words:

$$\mathbf{w} = (w_1, w_2, \ldots, w_m)$$

- The annotation or association of an unknown image *I* to a word *w* in the vocabulary can be found by the joint probability of $P(w, I)$ or $P(w, \mathbf{x})$, where **x** is the feature of *I*.
- In order to compute $P(w, I)$, a latent variable *c* is introduced

$$P(w|I) = P(w, I) = P(w|c) \times P(c|I) \tag{7.12}$$

The computation of conditional probabilities $P(w \mid c)$ and $P(c \mid I)$ is given in the following procedure:

- The training images are clustered into *v* clusters or VWs (*the latent variables*):

$$\mathbf{c} = (c_1, c_2, \ldots, c_v) = (\mathbf{x}_1, \mathbf{x}_2, \ \ldots, \mathbf{x}_v)$$

- An image to be annotated is represented as a histogram or distribution of VWs:

$$P(c_i|I) = (X_1, X_2, \ldots, X_v) \tag{7.13}$$

  where X_i is the frequency of VW $\mathbf{x}_i$ in image *I*.

- Each cluster is represented as a histogram or distribution of vocabulary words:

$$P\left(w_j|c_i\right) = (W_1, W_2, \ldots, W_m) \tag{7.14}$$

where W_j represents the frequency of word w_j in cluster c_i,

- Finally, the annotation of image I to a word w_j is given by

$$P\left(w_j|I\right) = P\left(w_j|c_i\right) \times P\left(c_i|I\right) \tag{7.15}$$

As discussed in Sect. 7.2, images can be segmented into regions and represented as a *bag of features* for annotation.

- If an image I is represented as a *bag of features* (pre-clustered): $I = \{\mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_k\}$
- The conditional probability of $P(c_i|I)$ in (7.15) can be computed using *MAP*:

$$P\left(c_i|I\right) = \arg\max_{c_j} P(c_j|I) = \arg\max_{c_j}\{P(I|c_j) \times P(c_j)\} \tag{7.16}$$

where

$$P\left(I|c_j\right) = P\left(\mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_k|c_j\right) = \prod_{l=1}^{k} P(\mathbf{x}_l|c_j) \tag{7.17}$$

The key idea of image annotation based on the joint probability model is the association of semantic words with visual words. This is achieved through the VQ process. Once image features are clustered, each cluster (VW) and the semantic words are bound together or associated because each image feature inherits the semantic word(s) from its parent image. This idea can be illustrated in Fig. 7.3.

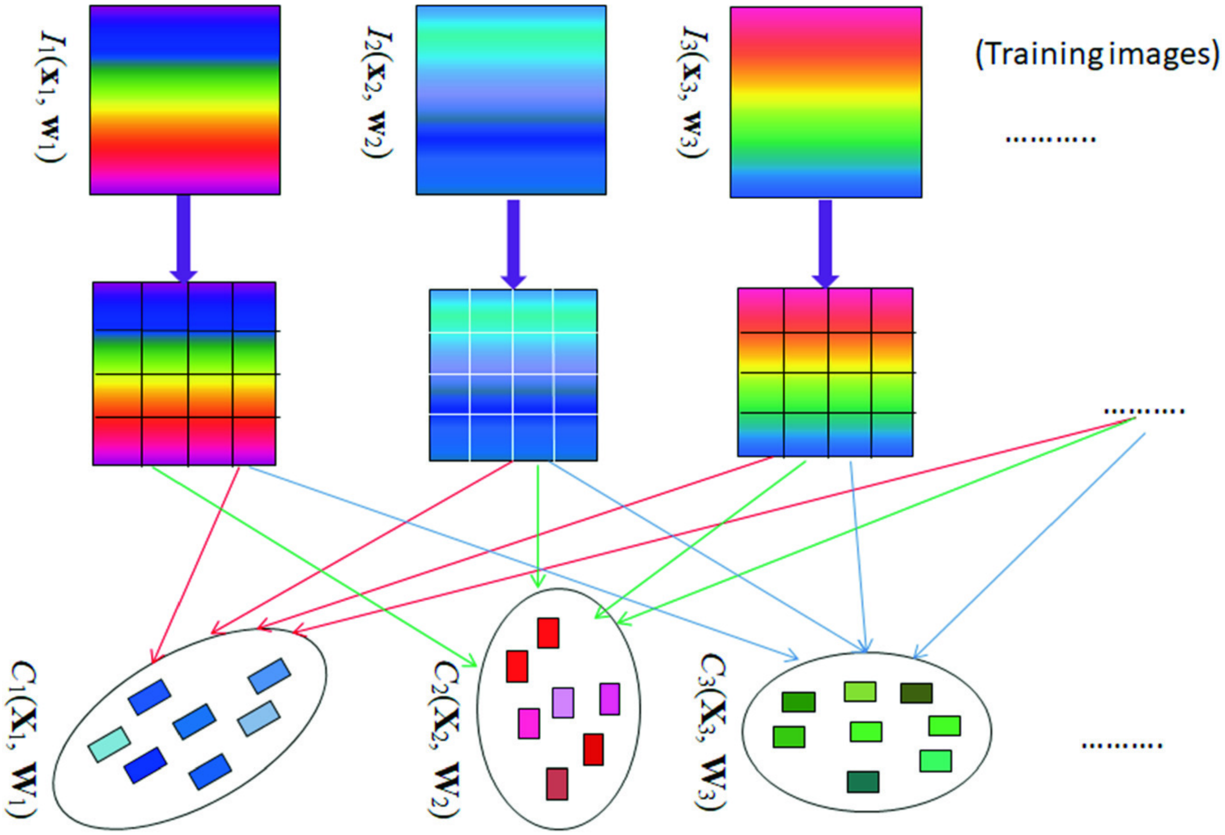

$I_1(\mathbf{x}_1, \mathbf{w}_1)$
$I_2(\mathbf{x}_2, \mathbf{w}_2)$
$I_3(\mathbf{x}_3, \mathbf{w}_3)$
(Training images)
....
....
$C_1(\mathbf{X}_1, \mathbf{W}_1)$
$C_2(\mathbf{X}_2, \mathbf{W}_2)$
$C_3(\mathbf{X}_3, \mathbf{W}_3)$
....

Fig. 7.3 Association of semantic words with block features

Once image features are clustered and visual words are generated, two types of distribution can be created from each cluster: $P(\mathbf{x}|c_i)$ and $P(w|c_i)$. $P(w|c_i)$ is the word distribution in cluster c_i, and it connects the VWs to the semantic vocabulary. $P(\mathbf{x}|c_i)$ is the feature distribution in cluster c_i, and it connects each VW with each of the images in the database (Fig. 7.4). By combining these two important information, new image can be annotated as shown in the above sections.

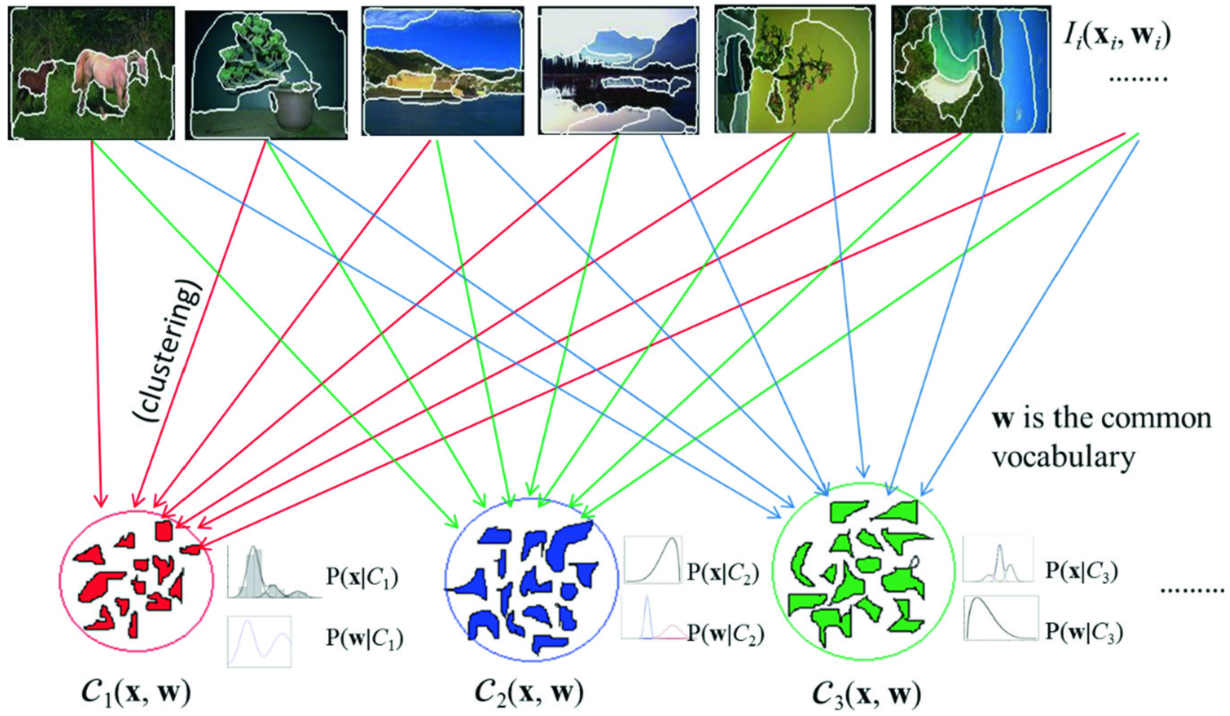

$I_i(\mathbf{x}_i, \mathbf{w}_i)$
....
(clustering)
w is the common vocabulary
P(**x**|C_1)
P(**w**|C_1)
P(**x**|C_2)
P(**w**|C_2)
P(**x**|C_3)
P(**w**|C_3)
....
$C_1(\mathbf{x}, \mathbf{w})$
$C_2(\mathbf{x}, \mathbf{w})$
$C_3(\mathbf{x}, \mathbf{w})$

Fig. 7.4 Association of semantic words with region features

7.5 Cross-Media Relevance Model

Although VQ is typical in building the likelihood models, models can also be built 'on the fly' by a set of training images which are relevant to the new observation. The *cross-media relevance model* (CMRM) [4] provides an alternative method to the VQ and is another joint probability model.

Given an image which is represented by a set of blobs: $I = \{\mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_m\}$, the association of I with concept c is given by the joint probability of $p(c, \mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_m)$:

$$\begin{aligned} p(c, \mathbf{x}_1, \cdots \mathbf{x}_m) &= \sum_{J\in T} p(J)\times p(c, \mathbf{x}_1, \cdots \mathbf{x}_m|J) \\ &= p(J)\times \sum_{J\in T} p(c|J)\times \prod_{i=1}^{m} p(\mathbf{x}_i|J) \end{aligned} \tag{7.18}$$

where

$$p(c|J) = (1 - \alpha_J) \times \frac{\#(c, J)}{|J|} + \alpha_J \times \frac{\#(c, T)}{|T|} \tag{7.19}$$

$$p(\mathbf{x}_i|J) = (1 - \beta_J) \times \frac{\#(\mathbf{x}_i, J)}{|J|} + \beta_J \times \frac{\#(\mathbf{x}_i, T)}{|T|} \tag{7.20}$$

where

- J is an image in the training set T.
- α_J and β_J are the interpolation parameters.
- $\#(c, J)$ is the number of times concept c appears in J.
- $\#(\mathbf{x}_i, J)$ is the number of times blob $\mathbf{x}_i$ appears in J.
- $\#(c, T)$ is the number of times concept c appears in T
- $\#(\mathbf{x}_i, T)$ is the number of times blob $\mathbf{x}_i$ appears in T.

It can be seen from (7.18), given a new observation $I = \{\mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_m\}$, CMRM attempts to find all the relevant images in the training set that have both concept c ($p(c|J) \neq 0$) and feature $\mathbf{x}_i$ ($p(\mathbf{x}_i|J) \neq 0$). A joint probability model is built by aggregating all the models from the relevant images. This is equivalent to build a class model for concept c ‘on the fly’. From (7.19) and (7.20), it can be seen that the performance of this model depends on the choice of the weight α_J and β_J. In practice, this can be a difficult decision to make.

7.6 Image Annotation with Parametric Model

One of the classic ways of model building is the parametric method using the *expectation-maximization* (EM) algorithm. The idea of image annotation with parametric model is similar to the CMRM method, that is, to build a model for each of the individual images and aggregate the similar individual models into a class model. However, instead of combining training and annotation into a single process as in the CMRM method, parametric model separates training and annotation into two different processes.

During the training, images in the training set are pre-labeled and pre-classified into different classes. A class model is then built by aggregating individual image models in each class. During the annotation, the model of the new image is built and matched with the class models and the closest classes are selected as the annotations. The procedure of parametric method is shown in Fig. 7.5. The algorithm of this method is as the following:

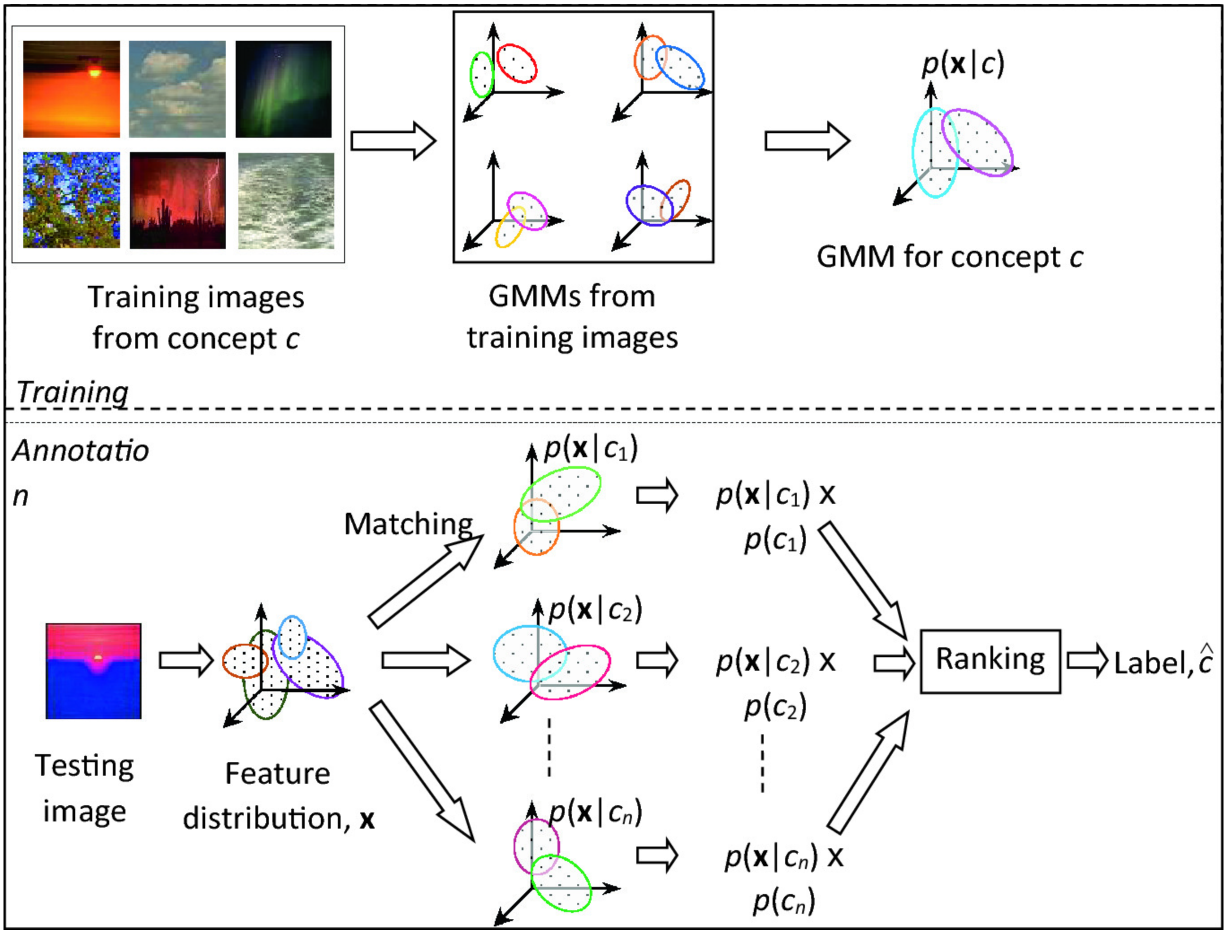

Training images from concept c
GMMs from training images
p(x|c)
GMM for concept c
Training
Annotation
Testing image
Feature distribution, x
Matching
p(x|c1)
p(x|c2)
p(x|cn)
p(x|c1) x p(c1)
p(x|c2) x p(c2)
p(x|cn) x p(cn)
Ranking
Label, ĉ

Fig. 7.5 Image annotation with parametric model

- Given a set of N training images: I_1, I_2, ..., I_N and a set of n classes C_1, C_2, ..., C_n
- Features (e.g., block features) from each training image I are clustered within the image
- A Gaussian mixture model (GMM) is learned from the clustering using the EM algorithm:

$$P(\mathbf{x}|I) = \sum_{i=1}^{l} \pi_I^i \mathcal{G}\left(\mathbf{x}, \mu_I^i, \Sigma_I^i\right) \tag{7.21}$$

where

- l is the number of components in the mixture model of image *I.*
- π_I^i is the weight for the *i*th component of the mixture model.
- μ_I^i is the mean of the *i*th component of the mixture model.
- Σ_I^i is the standard deviation of the *i*th component of the mixture model.

- A Gaussian mixture model for each class C_i is learnt by aggregating (e.g., weighted averaging) all the image models within the class:

$$P(\mathbf{x}|C_i) \sum_{k=1}^{K} \pi_{C_i}^k \mathcal{G}\left(\mathbf{x}, \mu_{C_i}^k, \Sigma_{C_i}^k\right) \tag{7.22}$$

where

- K is the number of components in the mixture model of class C_i.
- $\pi_{C_i}^k$ is the weight for the *k*th component of the mixture model.
- $\mu_{C_i}^k$ is the mean of the *k*th component of the mixture model.
- $\Sigma_{C_i}^k$ is the standard deviation of the *k*th component of the mixture model.

- Given a new observation image $I_u = \mathbf{x}_u$, the annotation of image I_u is given by the *MAP*:

$$\begin{aligned} P\left(C_j|\mathbf{x}_u\right) = \hat{c} &= \arg\max_{C_i} P(C_i|\mathbf{x}_u) \\ &= \arg\max_{C_i} \{P(\mathbf{x}_u|C_i) \times P(C_i)\} \end{aligned} \tag{7.23}$$

The algorithm of the parametric annotation method is illustrated in Fig. 7.5 [2, 5].

7.7 Image Classification with Gaussian Process

In Gaussian mixture, each multidimensional feature vector $\mathbf{x} = (x_1, x_2, \ldots, x_n)$ is regarded as a data point in a R^n space and the mixture model is built based on the statistics of the data points in a cluster.

But a multidimensional data $\mathbf{x} = (x_1, x_2, \ldots, x_n)$ can also be regarded as a discretized function f: $X \rightarrow R$ and $y = f(\mathbf{x}) = \{x_i = f(d_i) \mid i = 1, 2, \ldots, n\}$. A typical example of such a data is a histogram feature vector. Figure 7.6 shows three normalized histograms (vertical bars) from the same class in red, green and blue, respectively. The corresponding functions approximating the three histograms are shown as colored curves at the top of the histograms.

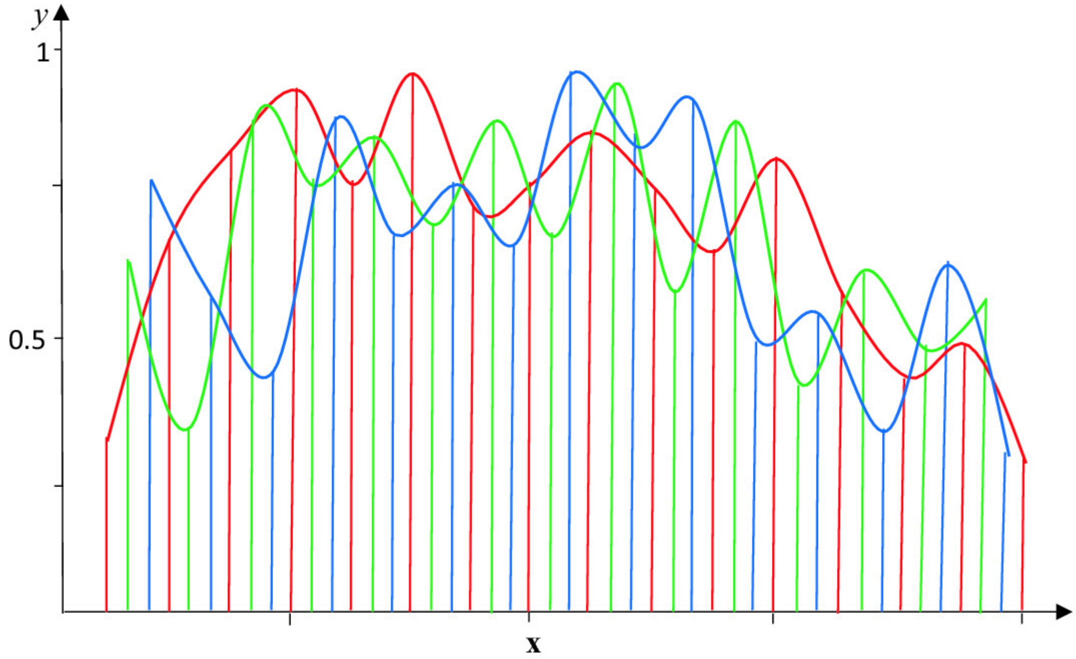


Fig. 7.6 Feature vectors shown as functions. Three histograms shown as vertical color bars and their respective functions shown as colored curves on the top

If we plot all the histogram features $f(\mathbf{x}_i)$ from a class in a single coordinate system, we would see all the data fall within a band and form a cluster. Like in the linear regression which attempts to fit a line to a cluster of data points, we can also fit a curve to this cluster of data points and use this curve as the model to predict new instances. This approach is the idea behind the Gaussian process or GP, which is demonstrated in Fig. 7.7 [6].

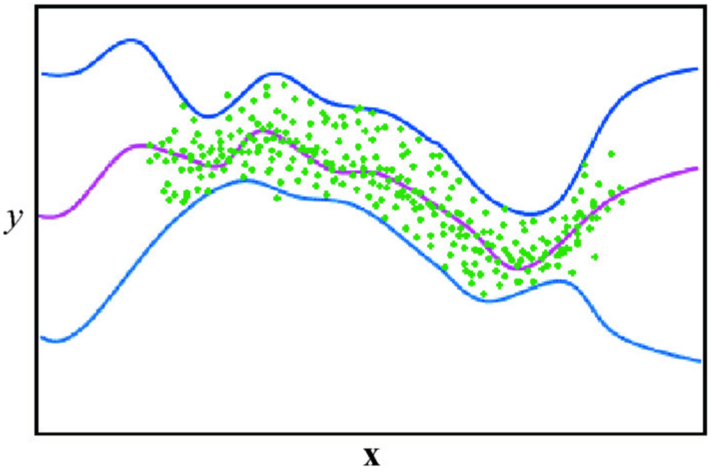


Fig. 7.7 Cluster of multidimensional data (green) and the approximation function of the data shown in pink

Now, given a set of data $\mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_N$ from a certain class C and each feature vector $\mathbf{x}_i$ is a D-dimensional data point in space $\mathbf{x}_i = (x_{i1}, x_{i2}, \ldots, x_{iD})$. A matrix $\mathbf{X} = D \times N = (\mathbf{d}_1, \mathbf{d}_2, \ldots, \mathbf{d}_D)^{\mathrm{T}}$ can be created as following:

$$\mathbf{X} = \begin{bmatrix} x_{11}, x_{21}, \ldots\ldots, x_{N1} \\ x_{12}, x_{22}, \ldots\ldots, x_{N2} \\ \ldots\ldots\ldots \\ x_{1D}, x_{2D}, \ldots\ldots, x_{ND} \end{bmatrix} = \begin{bmatrix} \mathbf{d}_1 \\ \mathbf{d}_2 \\ \ldots \\ \mathbf{d}_D \end{bmatrix} \tag{7.24}$$

where $\mathbf{d}_j$ is a jth-dimensional vector. Since the elements of each $\mathbf{d}_j$ are samples from (or follow) a normal distribution, $N(\mu_j, \sigma_j)$, $\mathbf{X}$ is a Gaussian process and $\mathbf{X} \sim N(\boldsymbol{\mu}_{\mathbf{X}}, \mathbf{K}_{\mathbf{XX}})$, where $\boldsymbol{\mu}_{\mathbf{X}}$ and $\mathbf{K}_{\mathbf{XX}}$ are the *mean* and *variance* which are determined by (7.25) and (7.26), respectively.

$$\boldsymbol{\mu}_{\mathbf{X}} = \begin{bmatrix} \mu(\mathbf{d}_1) \\ \mu(\mathbf{d}_2) \\ \ldots \\ \mu(\mathbf{d}_D) \end{bmatrix} \tag{7.25}$$

$$\mathbf{K}_{\mathbf{XX}} = \begin{bmatrix} k(\mathbf{d}_1, \mathbf{d}_1), k(\mathbf{d}_1, \mathbf{d}_2) \ldots\ldots, k(\mathbf{d}_1, \mathbf{d}_D) \\ k(\mathbf{d}_2, \mathbf{d}_1), k(\mathbf{d}_2, \mathbf{d}_2) \ldots\ldots, k(\mathbf{d}_2, \mathbf{d}_D) \\ \ldots\ldots\ldots \\ k(\mathbf{d}_D, \mathbf{d}_1), k(\mathbf{d}_D, \mathbf{d}_2) \ldots\ldots, k(\mathbf{d}_D, \mathbf{d}_D) \end{bmatrix} \tag{7.26}$$

where $k(\mathbf{d}_i, \mathbf{d}_j)$ is a *kernel* function which is typically the *covariance* function.

To predict a new data or a new set of data $\mathbf{X}_*$, $\mathbf{X}$ and $\mathbf{X}_*$ are concatenated and the concatenated data is a new GP which follows the following normal distribution:

$$f\begin{pmatrix} \mathbf{X}_* \\ X \end{pmatrix} \sim \mathcal{N}\left(\begin{pmatrix} \mu_{\mathbf{X}_*} \\ \mu_{\mathbf{X}} \end{pmatrix}, \begin{pmatrix} \Sigma_{\mathbf{X}_*\mathbf{X}_*}, \Sigma_{\mathbf{X}_*\mathbf{X}} \\ \Sigma_{\mathbf{XX}_*}, \Sigma_{\mathbf{XX}} \end{pmatrix}\right) \tag{7.27}$$

Then, the probability of the new data $\mathbf{X}_*$ given the observed data $\mathbf{X}$ is given by (7.28):

$$p(\mathbf{X}_*|\mathbf{X}) = \mathcal{N}\left(\mu_{\mathbf{X}_*} + \mathbf{K}_{\mathbf{X}_*\mathbf{X}}\mathbf{K}_{\mathbf{XX}}^{-1}(\mathbf{X} - \mu_{\mathbf{X}}), \mathbf{K}_{\mathbf{X}_*\mathbf{X}_*} - \mathbf{K}_{\mathbf{X}_*\mathbf{X}}\mathbf{K}_{\mathbf{XX}}^{-1}\mathbf{K}_{\mathbf{XX}_*}\right) \tag{7.28}$$

The proof of (7.28) is given in Appendix [7–9].

7.8 Summary

This chapter introduces the first image classification method: Bayesian classification. Several important and interesting application of Bayesian classifier are described and demonstrated in details, including NB, word co-occurrence model, CMRM, parametric model and Gaussian process method. The key features of Bayesian classifiers can be summarized as the following

1. **Generative**. A Bayesian classifier is a typical generative model, and it assumes the distribution or model of likelihood probability is known. This likelihood probability model is typically obtained through learning from known samples.

2. **Intuitive**. Compared with many other black box-based classifiers such as SVM and ANN, Bayesian classifiers are intuitive, and results are easily interpreted by a human being. The basic idea the Bayesian method is to use our prior experience to forecast or predict new events. In this sense, we all make decision using Bayesian classifiers.

3. **Robust**. A Bayesian classifier generates a result in probabilistic form instead of deterministic form. Probabilistic prediction is more robust than deterministic prediction, e.g., a 70% chance of rain forecast is more likely to be correct than a rain/no-rain forecast.

4. **Nonlinear**. The boundary of a Bayesian classifier is nonlinear because the prediction is based on the data distributions and the distribution models can be any shape.

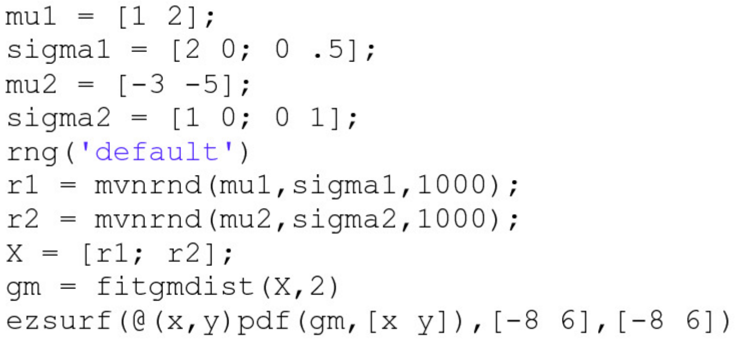
However, the downside of Bayesian classifier is that there needs large number of data samples to have a reasonable accurate estimation of data distribution.

7.9 Exercises

1. Use the example code in the following web page to generate a Gaussian mixture model: https://au.mathworks.com/help/stats/gmdistribution.html#mw_4758a58e-5bc7-4eda-b261-83521d63d1ce. First, try the `gmdistribution` function with the following code. Turn the graph to different angles and also to flat (2D) to view the model in more details. Then try different *mu* and *sigma* values to create more GMM models.

```
                                        mu = [1 2;-3- 5];
                                        sigma = cat(3,[2 .5],[1 1]);
                                        gm = gmdistribution(mu,sigma);
                                        ezsurf(@(x,y)pdf(gm,[x y]),[-10 10],[-10
10]);
```

2. Use the example code from this link: https://au.mathworks.com/help/stats/fitgmdist.html and try the `fitgmdist` function with the following code. Turn the graph to different angles and also to flat (2D) to view the model in more details. Now, try `fitgmdist` with more components and different *mu* and *sigma* values to create more complex GMM models.



```
mu1 = [1 2];
sigma1 = [2 0; 0 .5];
mu2 = [-3 -5];
sigma2 = [1 0; 0 1];
rng('default')
r1 = mvnrnd(mu1,sigma1,1000);
r2 = mvnrnd(mu2,sigma2,1000);
X = [r1; r2];
gm = fitgmdist(X,2)
ezsurf(@(x,y)pdf(gm,[x y]),[-8 6],[-8 6])
```

3. Use the code from the following web page to compute the posterior probabilities of a GMM model which you have generated from the above exercises. Explain the graph using the colors and color bar. Write a report on the GMM models, the posterior probabilities and tell how they can be used for image analysis (hints: an image or an image region is a GMM model, and a GMM model is characterized or defined by its parameters e.g. *mu* and *Sigma*). https://au.mathworks.com/help/stats/gmdistribution.posterior.html.

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8. Support Vector Machine

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To see better, go higher.

One of the key developments in recent artificial intelligence (AI) research is the SVM, which has attracted large amount of research and has produced good results in many applications. Because of the so-called kernel trick, it has made SVM one of the most effective and efficient machine learning tools in the literature. In this chapter, we attempt to do an anatomy of SVM so that readers have a good understanding of its mechanism.

SVM is basically the combination of both a linear classifier and a *k* nearest neighbor classifier (K-NN). Therefore, to understand SVM, we will first introduce the linear classifier and the K-NN classifier.

We will only focus on two-class classification problem in this chapter because any classification problem can be converted into a one-vs-all classification, which is a two-class classification problem.

8.1 Linear Classifier

The Bayesian methods in Chap. 7 are model-based, and they can give good decision if the models are accurate. However, because data distributions are usually unknown, the models can only be estimated accurately if a large number of training samples are available. This is especially true when the number of features is large, which is common for multimedia data.

An alternative approach is to assume that there exists a functional form decision boundary between each pair of classes, and the parameters of the decision boundary or discriminant function can be estimated using available training samples. A linear classifier is one of those approaches.

Suppose the data is represented as a n-dimensional feature vector $\mathbf{x} = (x_1, x_2, \ldots, x_n)$, then a linear discriminant function is formulated as:

$$f(\mathbf{x}) = w_0 + w_1x_1 + w_2x_2 + \ldots + w_nx_n \tag{8.1}$$

where x_i are the variables and w_i are the coefficients or weights. Assume $x_0 = 1$, and $f(\mathbf{x})$ can be written as

$$f(\mathbf{x}) = \sum_{j=0}^{n} w_jx_j \tag{8.2}$$

Geometrically, $f(\mathbf{x}) = 0$ is a hyperplane in n-dimensional space and $f(\mathbf{x}) = 0$ is the decision boundary between two classes. A sample data with feature vector $\mathbf{x}$ is classified into one of the classes using the following criterion.

$$\mathbf{x} \in \begin{cases} \text{class 1} & \text{if } f(\mathbf{x}) > 0 \\ \text{class 2} & \text{if } f(\mathbf{x}) < 0 \end{cases}$$

8.1.1 A Theoretical Solution

The next is to find out the parameters or the set of weights of $f(\mathbf{x})$: w_0, w_1, w_2 .... w_n, which will minimize the number of misclassified samples in a given training set.

A classical way to find the weights is to solve a set of linear equations given a set of training samples. For an n-dimensional data, there need $n + 1$ linear equations or samples to solve the $n + 1$ weights. Suppose $d_i = 1$ (or $d_i > 0$) represents class 1 and $d_i = -1$ (or $d_i < 0$)

represents class 2, and the $n + 1$ training samples are given as $(\mathbf{x}_i, d_i)$, where

$$\mathbf{x}_i = (x_{i1}, x_{i2}, \ldots, x_{in}), \quad i = 1, 2, \ldots, n + 1$$

Then, by substituting (8.2) with each of the training data $\mathbf{x}_i$, the set of weights w_i ($i = 0, 1, \ldots, n$) can be solved using the following $n + 1$ linear equations:

$$\sum_{j=0}^{n} w_j x_{ij} = d_i, \; i = 1, 2, \ldots, n + 1 \tag{8.3}$$

(8.3) can be written in matrix form:

$$\begin{bmatrix} 1, & x_{11}, & x_{12}, & \ldots\ldots, & x_{1n} \\ 1, & x_{21}, & x_{22}, & \ldots\ldots, & x_{2n} \\ & & \ldots\ldots\ldots\ldots & & \\ 1, & x_{n1}, & x_{n2}, & \ldots\ldots, & x_{nn} \\ 1, & x_{n+1,1}, & x_{n+1,2}, & \ldots\ldots, & x_{n+1,n} \end{bmatrix} \begin{bmatrix} w_0 \\ w_1 \\ w_2 \\ \ldots \\ w_n \end{bmatrix} = \begin{bmatrix} d_1 \\ d_2 \\ \ldots \\ d_n \\ d_{n+1} \end{bmatrix} \tag{8.4}$$

which in turn can be written as:

$$\mathbf{X}\mathbf{w}^T = \mathbf{d}^T$$

where $\mathbf{w}^T$ and $\mathbf{d}^T$ are the transposes of $\mathbf{w}$ and $\mathbf{d}$, and the solution of $\mathbf{w}$ is then given as (8.5):

$$\mathbf{w}^T = \mathbf{X}^{-1}\mathbf{d}^T \tag{8.5}$$

8.1.2 An Optimal Solution

The above theoretical solution is just based on $n + 1$ or part of the training samples; therefore, it is not optimal. An optimal solution is usually given by minimizing the squared errors of $f(\mathbf{x})$ on the entire training dataset of N data $(\mathbf{x}_i, d_i)$ and:

$$\mathbf{x}_i = (x_{i1}, x_{i2}, \ldots, x_{in}), \quad i = 1, 2, \ldots, N$$

That is, to minimize the following total squared error:

$$
\begin{aligned}
E &= \sum_{i=0}^{N-1} (f(\mathbf{x}_i) - d_i)^2 \\
&= \sum_{i=0}^{N-1} \left(\sum_{j=0}^{n} w_j x_{ij} - d_i \right)^2
\end{aligned}
\tag{8.6}
$$

By taking the partial derivative of E on w_k (k = 0, 1, 2, ..., n) and letting the partial derivative to be 0: $\frac{\partial E}{\partial w_k} = 0$, the following n + 1 linear equations are obtained:

$$
\sum_{i=0}^{N-1} x_{ik} \left(\sum_{j=0}^{n} w_j x_{ij} - d_i \right) = 0, \quad k = 0, 1, 2, \ldots, n \tag{8.7}
$$

which is equivalent to the following:

$$
\sum_{j=0}^{n} w_j \left(\sum_{i=0}^{N-1} x_{ik} x_{ij} \right) = \sum_{i=0}^{N-1} x_{ik} d_i, \quad k = 0, 1, 2, \ldots, n \tag{8.8}
$$

By solving the above n + 1 linear equations using the same method as solving (8.3), a set of weights (w_0, w_1, w_2 .... w_n) is obtained and an optimal hyperplane is resulted. It can be observed that compared with (8.3), in an optimal solution algorithm, x_{ij} is replaced with $\sum_{i=0}^{N-1} x_{ik} x_{ij}$, while d_i is replaced with $\sum_{i=0}^{N-1} x_{ik} d_i$. Specifically, the solution is given by:

$$
\mathbf{w}^T = \left(\mathbf{X}^T \mathbf{X} \right)^{-1} \left(\mathbf{X}^T \mathbf{d}^T \right) \tag{8.8a}
$$

where **X** is the N × (n + 1) matrix representing the N data, and **d** is a 1 × N vector representing the class values of the N data.

8.1.3 A Suboptimal Solution

Although the solution from (8.8) results in a more optimal decision boundary than that from (8.5), the solution of (8.8) would involve processing very large matrices which is computationally expensive and undesirable. This is because multimedia data usually has very high-dimensional features. An alternative approach is to use an iterative optimization algorithm to find a suboptimal solution to (8.2). Common practice is to use an error-driven weight adaption technique which is basically a trial-and-error technique. The iterative optimization procedure is given in the following.

1. Initialize the weights w_0, w_1, w_2 .... w_n with some small random values.
2. Take the next training sample $\{\mathbf{x}, d\} = \{(x_1, x_2, ..., x_n), d\}$, $d = 1$ or -1.
3. Compute $f(\mathbf{x}) = w_0 + w_1x_1 + w_2x_2 + ... + w_nx_n$
4. If $f(\mathbf{x}) \neq d$ (a misclassification), update $w_0 \leftharpoondown w_0 + cdk$ and $w_j \leftharpoondown w_j + cdx_j$, $j = 1, 2, ..., m$, where k and c are both positive constants.
5. Repeat steps 2–4 on each of the remaining training samples, until all the samples are correctly classified or the weights stop to change.

To demonstrate that the weights w_i or the hyperplane $f(\mathbf{x})$ are moving in the right directions, let f_{new} and f_{old} be the updated value and old value of $f(\mathbf{x})$, respectively. Because k, c and the feature value x_j are all positive, after the update in step 4, all the weights w_j become larger if $d = 1$ and all the weights w_j become smaller if $d = -1$. That means, if there is a misclassification, the decision function is updated according to the following rules:

$$\begin{cases} f_{\text{new}} > f_{\text{old}} & \text{if } d = 1 \\ f_{\text{new}} < f_{\text{old}} & \text{if } d = -1 \end{cases}$$

Therefore, in either case, the new hyperplane $f(\mathbf{x})$ is moving in the right direction with the updated weights, until the misclassified sample is located at the correct side of the hyperplane.

A linear classifier can only classify data which is linearly separable. However, this idea can be extended to build a nonlinear classifier. For example, we can convert a two-dimensional feature vector (x, y) in xy space to a five-dimensional feature vector $(u_1, u_2, u_3, u_4, u_5)$ in a higher-dimensional space, where $u_1 = \sqrt{2}x$, $u_2 = \sqrt{2}y$, $u_3 = x^2$, $u_4 = \sqrt{2}xy$, $u_5 = y^2$. This would be the polynomial kernel $(1 + x + y)^2$. This is the key idea behind the kernel method which will be discussed in Sect. 8.3.

8.2 K Nearest Neighbor Classification

K nearest neighbor or K-NN is a simple algorithm that stores all available cases and classifies new cases based on a decision function (e.g. a distance measure).

Given a training dataset D and a distance measure *dist*:

- $(\mathbf{x}_i, y_i)$, $i = 1, 2, \ldots, N$.
- $\mathbf{x}_i$ is a training data in R^n.
- y_i is the corresponding class of the data $\mathbf{x}_i$, and $y_i \in \{c_j, j = 1, 2, \ldots, M\}$.
- $\text{dist}(\mathbf{x}-\mathbf{x}_i) = ||\mathbf{x}-\mathbf{x}_i||$.

A new observation data $\mathbf{x}$ is classified to one of the classes y_j using the following algorithm:

1. Input the new data $\mathbf{x}$.
2. Compute the distance of $\mathbf{x}$ to all the training samples $\mathbf{x}_i$ in the dataset: $\text{dist}(\mathbf{x}-\mathbf{x}_i)$.
3. Sort $\text{dist}(\mathbf{x}-\mathbf{x}_i)$ $(i = 1, 2, \ldots, N)$ in ascending order and rank all the $\mathbf{x}_i$ accordingly: $\mathbf{x}_{r1}, \mathbf{x}_{r2}, \ldots, \mathbf{x}_{rk}, \ldots, \mathbf{x}_{rN}$.
4. For a nearest neighbor (NN) classification, classify $\mathbf{x}$ to y_{r1}.
    a. For a K-NN classification, classify $\mathbf{x}$ to the majority class y_{rp} among the top k ranked data: $\{\mathbf{x}_{r1}, \mathbf{x}_{r2}, \ldots, \mathbf{x}_{rk}\}$.

Although Euclidean (L_2) and city block distance (L_1) are typical choice for the distance measure, any other distance can be used depending on the applications. The nearest neighbor (NN or 1-NN) results in too many classes, while K-NN gives more reliable classification results. This is because the values of k have a smoothing effect that makes the classifier more resistant to outliers. However, the performance of a K-NN classifier depends on the choice of k which is usually determined empirically.

Figure 8.1 demonstrates the comparison between an NN classifier and a K-NN classifier [1]. It can be seen from the two classification results, in the case of a NN classifier (after merging), outlier data points create small islands within a class (e.g., red point within the green class) and sharp corners on the class boundaries, those islands and sharp corners likely lead to incorrect predictions, while the 5-NN classifier smooths over these outliers, which lead to better classification on the data. However, the 5-NN classifier also causes misclassifications which are characterized by the blue dots in red region and red dots in green region. There can also be confusions by the tied votes among the 5 nearest neighbors (e.g. two neighbors are red, next two neighbors are blue, and last neighbor is green).

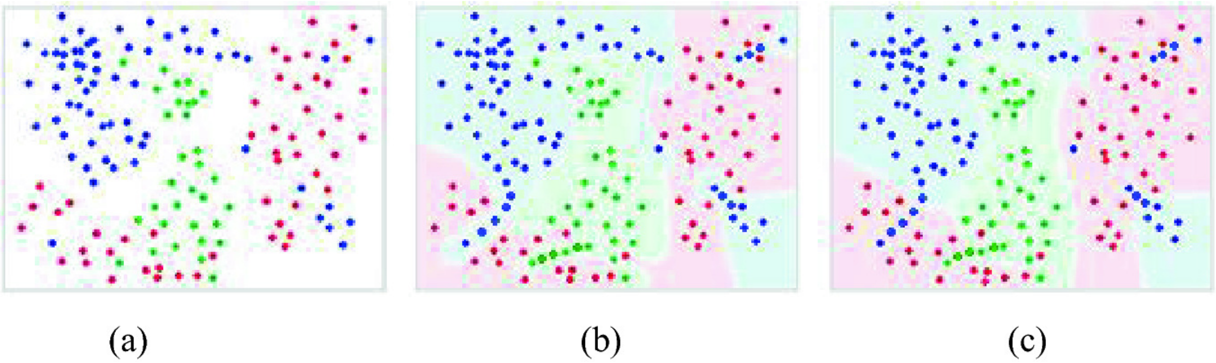

(a) (b) (c)

Fig. 8.1 Comparison between NN and K-NN. **a** The data to be classified; **b** classification result from a 1-NN classifier; **c** classification result from a 5-NN classifier

This kind of misclassification can be overcome to certain extent by using the *weighted* K-NN. The idea is to give more weight to the neighbors with shorter distance to the test data than to the far away neighbors. The commonly used weighted K-NN is the Gaussian weighted K-NN.

Unlike any other classifiers who are independent of the original training data once trained, a K-NN classifier is tied to the training data. If we analogue a classifier to a connoisseur traveling around the world to judge (classify) different kinds of antiques for people. While other types of connoisseurs only need to take a model or a tool summarizing the key characteristics of the antiques, a K-NN connoisseur will have to carry every kind of real antiques in his/her collection in order to make a new judgment. This may sound too cumbersome; however, one of the key advantages of a K-NN classifier is that it can classify data which is nonlinearly separable. This is the key idea behind the kernel-based support vector machine (SVM).

8.3 Support Vector Machine

In previous two sections, we have introduced the linear classifier and K-NN classifier, and both are keys to understand SVM.

A linear classifier is simple, and once trained, it is like a tool or a machine which can be used to tell if a data belongs to one of the classes. However, the disadvantages of a linear classifier include:

- The solution is either not optimal or computationally expensive.
- It cannot classify data which is nonlinearly separable.

A K-NN classifier is also simple and can separate data nonlinearly. However, the disadvantages of a K-NN classifier include:

- It’s difficult to choose a *k*.
- Dependence on training data.

Now that we have understood how the linear classifier and the K-NN classifier behave, we would like to build a classifier which takes the advantage of both and overcomes their disadvantages. This is SVM.

A SVM is basically a binary linear classifier, however, with two prominent goals to achieve:

- To maximize the margin which separates the two classes (optimal);

- To use only a few training data (or support vectors) to determine the hyperplane which separates the two classes (efficient).

A kernel-based SVM adds another goal to achieve:

- To be able to classify data which is nonlinearly separable.

As can be seen, once the three goals are achieved, we would truly build a machine which combines the advantages of both the linear classifier and the K-NN classifier, while overcomes their disadvantages.

To formulate SVM, we will start with the simple perceptron and the primal form of SVM. In the next, the dual form of SVM is introduced, and finally, the kernel-based SVM is described in detail.

8.3.1 The Perceptron

A perceptron is a binary linear classifier which is one of the simplest classifiers. Given an unknown data, the perceptron simply generates a linear prediction. The training process is the same as the linear classifier introduced in Sect. 8.1. The only difference is that a perceptron can do online learning, which means it can process the training data one at a time instead of having to taking the entire training dataset. Although it is simple, the perceptron is the key to understand both SVM and artificial neural network (ANN) later on.

Given a training dataset D:

- $D = \{(\mathbf{x}_i, y_i), i = 1, 2, \ldots, N\}$.
- $\mathbf{x}_i$ is a feature vector in n-dimensional space: $\mathbf{x}_i = (x_{i1}, x_{i2}, \ldots, x_{in})$.
- y_i is the corresponding class of the data $\mathbf{x}_i$, and $y_i \in \{-1, 1\}$.
- $< \mathbf{x}_i, \mathbf{x}_j >= \mathbf{x}_i \cdot \mathbf{x}_j$ is the dot product between two vectors.

A perceptron is a binary linear classifier which is formulated as follows:

1. $f(\mathbf{x}) = <\mathbf{w}, \mathbf{x}> + b$.

2. Let $w_0 = b$ and $x_0 = 1$, then the above can be simply written as $f(\mathbf{x}) = <\mathbf{w}, \mathbf{x}>$

3. $h(\mathbf{x}) = sign\ (f(\mathbf{x})) = y_i\ (f(\mathbf{x}))$

```
4. Take the next training data $(\mathbf{x}_i, y_i) \in D$
5. if $h(\mathbf{x}_i) \geq 0, \mathbf{w}_{k+1} \leftarrow \mathbf{w}_k$
6. if $h(\mathbf{x}_i) < 0$
       then $\mathbf{w}_{k+1} \leftarrow \mathbf{w}_k + \eta y_i \mathbf{x}_i, \eta > 0$
7. Repeat from 4.
```

8.3.2 SVM—The Primal Form

8.3.2.1 The Margin Between Two Classes

Continue from the perceptron discussion and its training data assumption.

The perceptron gives us a hyperplane to separate the two classes of data; however, there are an infinite number of hyperplanes between two classes of data as shown in Fig. 8.2. The one resulted from the perceptron is just one of them, and it's nothing optimal. Although an optimal hyperplane was given in Sect. 8.1, it's optimal only in terms of minimizing the total error, and it's still far from the optimal hyperplane we *perceive*.

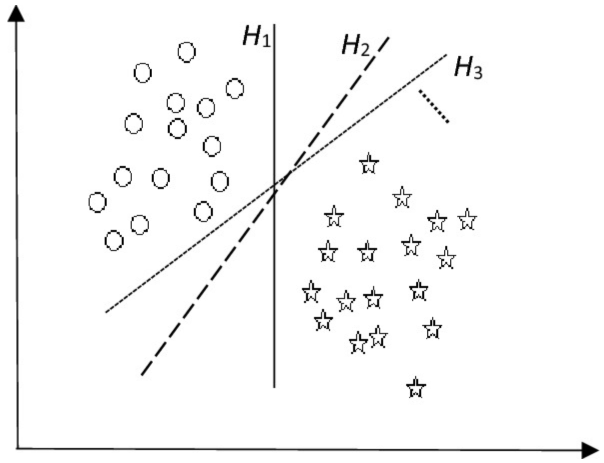


Fig. 8.2 Hyperplanes between two classes of data

The optimal or the best hyperplane we *perceive* is the one separating the two classes with the maximal margin as shown in

Fig. 8.3. That is the hyperplane we are going to find out.

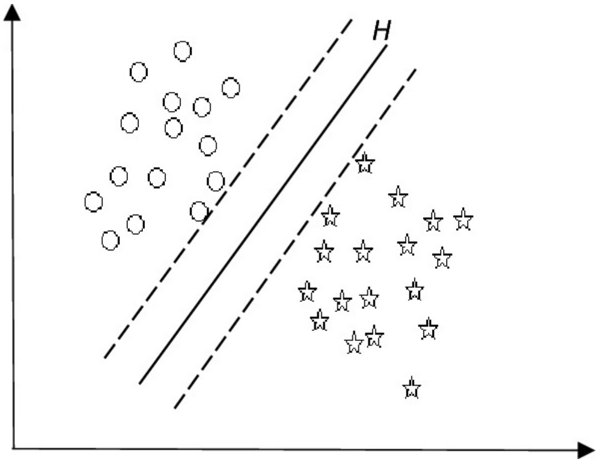


Fig. 8.3 Optimal hyperplane *H* between two classes of data

Assume the two subspaces corresponding to the two classes of data are, respectively,

$$
\begin{aligned}
< \mathbf{w}, \mathbf{x} > +b \geq 1 \quad & \text{for } y_i = +1 \\
< \mathbf{w}, \mathbf{x} > +b \leq -1 \quad & \text{for } y_i = -1
\end{aligned}
$$

The above two inequalities can be combined into one:

$$y_i(< \mathbf{w}, \mathbf{x} > +b) - 1 \geq 0 \tag{8.9}$$

The boundaries between the two subspaces are hyperplanes H_1 and H_2, respectively:

$$H_1: \quad < \mathbf{w}, \mathbf{x} > +b - 1 = 0 \tag{8.10}$$

$$H_2: \quad < \mathbf{w}, \mathbf{x} > +b + 1 = 0 \tag{8.11}$$

and the hyperplane between H_1 and H_2 is given as H_0:

$$H_0: \quad < \mathbf{w}, \mathbf{x} > +b = 0 \tag{8.12}$$

The two classes of data and the three hyperplanes separating them are shown in Fig. 8.4.

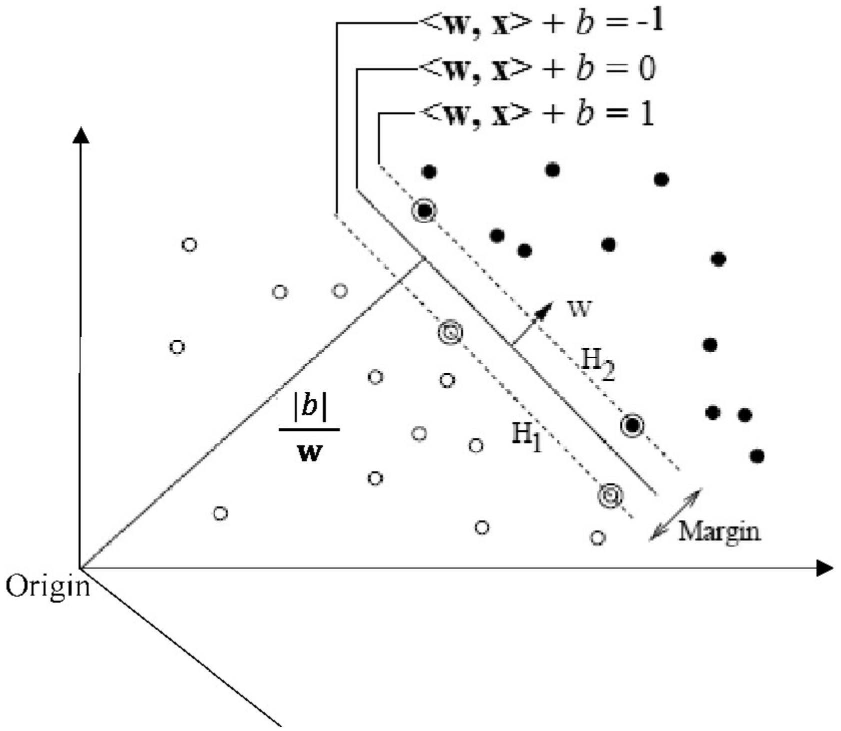


Fig. 8.4 Two classes of data and the hyperplanes separating them

Our purpose is not only to find H_0 but also to maximize the distance between H_1 and H_2, which is the margin between the two classes of data. How to work out the distance between H_1 and H_2? Here is how it works out.

- Remember in a 2D space, a hyperplane is just a line which is expressed as: $ax + by + c = 0$. The constant c is called the intercept, and $|c|$ is associated with the distance from the origin to the line.
- This is also true in higher-dimensional space. For example, in a 3D space, a plane is given as $Ax + By + Cz + D = 0$, and $|D|$ is associated with the distance from the origin to the plane, so on so forth.
- Therefore, the distance between H_1 and H_2 is equal to the difference between the distance of each of them to the origin.

Specifically, based on the theory of geometry, the distance of a point (x_0, y_0, z_0) to a plane in 3D space: $Ax + By + Cz + D = 0$, is given as follows:

$$\frac{|Ax_0 + By_0 + Cz_0 + D|}{\sqrt{A^2 + B^2 + C^2}} \tag{8.13}$$

Because this is also true for higher-dimensional space, accordingly, the distance from H_0 to the origin (0, 0, ..., 0) in n-dimensional space is given as:

$$\frac{|b|}{||\mathbf{w}||} \tag{8.14}$$

where $||\mathbf{w}||$ is the magnitude or length of vector **w**, and the distance

from H_1 and H_2 to the origin (0, 0, ..., 0) in n-dimensional space is given by the following two, respectively:

$$\frac{|b+1|}{||\mathbf{w}||} \quad \text{and} \quad \frac{|b-1|}{||\mathbf{w}||} \tag{8.15}$$

Therefore, by calculating the difference between the two terms of (8.15), the margin between the two hyperplanes H_1 and H_2 is obtained as:

$$\frac{2}{||\mathbf{w}||} \tag{8.16}$$

The data points which lie on H_1 and H_2 are called *support vectors* (marked by circles in Fig. 8.3), which are both necessary and sufficient to define the boundary hyperplanes.

8.3.2.2 Margin Maximization

Therefore, based on (8.16), to maximize the distance between the two subspaces is equivalent to the following optimization problem:

$$\text{Minimize: } f(\mathbf{w}) = \frac{1}{2}||\mathbf{w}||^2 = \frac{1}{2} < \mathbf{w}, \mathbf{w} > \tag{8.17}$$

$$\text{Subject to: } g_i(\mathbf{w}, b) = y_i(< \mathbf{w}, \mathbf{x}_i > +b) - 1 \geq 0, i = 1, 2, \ldots, N \tag{8.18}$$

The above is a constrained optimization problem, and there are a few important facts to be pointed out [2]:

- b is one of the weights to be found because if we let $x_0 = 1$, then $w_0 = b$.

- (8.17) is a paraboloid in n-dimensional space.
- A paraboloid has a single global minimum at the bottom.
- (8.18) is a hyperplane in n-dimensional space.
- The solution to this constrained optimization problem is at the tangent point of the paraboloid and the hyperplane.
- At the tangent point, the normal vectors or gradient vectors of both the paraboloid and the hyperplane are parallel.
- That is, $\nabla f = \alpha_i \nabla g_i$, ($i = 1, 2, \ldots, N$), where ∇ is the gradient and α_i is a constant.

Based on the above analysis, the optimization problem of (8.17) and (8.18) is equivalent to combining them into the following *Lagrange function* and solve $\nabla L = 0$ or $\partial_{\mathbf{w},b} L = 0$:

$$L(\mathbf{w}, b, \alpha_i) = f(\mathbf{w}) - \sum_i \alpha_i g_i(\mathbf{w}, b) \tag{8.19}$$

$$\begin{aligned} L(\mathbf{w}, b, \alpha_i) &= \frac{1}{2}|\mathbf{w}|^2 - \Sigma_i \alpha_i \left[y_i (< \mathbf{w}, \mathbf{x}_i > +b) - 1 \right] \\ &= \frac{1}{2}\mathbf{w} \cdot \mathbf{w} - \Sigma_i \alpha_i y_i (\mathbf{w} \cdot \mathbf{x}_i + b) + \Sigma_i \alpha_i \end{aligned} \tag{8.20}$$

8.3.2.3 The Primal Form of SVM

From (8.20), we can obtain the *primal form* of the SVM:

$$\text{Minimize: } L(\mathbf{w}, b, \alpha_i) = \frac{1}{2}\mathbf{w} \cdot \mathbf{w} - \Sigma_i \alpha_i y_i (\mathbf{w} \cdot \mathbf{x}_i + b) + \Sigma_i \alpha_i \tag{8.21}$$

$$\text{Subject to: } \alpha_i \geq 0, i = 1, 2, \ldots, N$$

8.3.3 The Dual Form of SVM

Although the primal form (8.21) lets us to find the weights **w** and a hyperplane which separates the two classes of data with the maximum margin, the optimization is too expensive. Because we have to optimize two sets of parameters at the same time: **w** and α_i, this is very undesirable. In the next, we want to make it more efficient.

Since (8.21) is a quadratic function, based on mathematics, at the global minima of the quadratic function, the gradient or the partial derivatives of $L(\mathbf{w}, b, \alpha_i)$ are 0. Therefore, we have

$$\nabla L(\mathbf{w}, b, \alpha_i) = \nabla f(\mathbf{w}) - \nabla [\sum_i \alpha_i g_i(\mathbf{w}, b)] = 0 \tag{8.22}$$

Now let

$$\frac{\partial L}{\partial \mathbf{w}} = 0 \quad \text{and} \quad \frac{\partial L}{b} = 0$$

This leads to

$$\mathbf{w} = \Sigma_i \alpha_i y_i \mathbf{x}_i \quad \text{and} \quad \Sigma_i \alpha_i y_i = 0 \tag{8.23}$$

Substituting the primal form (8.21) with (8.23) leads to the following *dual form* of the SVM:

$$\text{Maximize: } L_D = \Sigma_i \alpha_i - \frac{1}{2} \Sigma_{\text{ij}} \alpha_i \alpha_j y_i y_j < \mathbf{x}_i, \mathbf{x}_j > \tag{8.24}$$

$$\text{Subject to: } \alpha_i \geq 0 \quad \text{and} \quad \Sigma_i \alpha_i y_i = 0$$

To see why it has changed from minimization in the primal form to maximization in the dual form, let's have a good look at (8.24). The value of L_D is determined by the following three cases [2]:

- If the two features $\mathbf{x}_i$, $\mathbf{x}_j$ are completely dissimilar, ($\mathbf{x}_i$, $\mathbf{x}_j$ are from different classes and are very different), their dot product $<\mathbf{x}_i, \mathbf{x}_j> = 0$. That means, *features from different classes and are far away from the boundaries between two classes don't contribute to* L_D
- If the two features $\mathbf{x}_i$, $\mathbf{x}_j$ are completely alike and from the same class, $<\mathbf{x}_i, \mathbf{x}_j> \approx 1$ and $y_i\, y_j = 1$. Therefore, $\alpha_i\, \alpha_j\, y_i\, y_j <\mathbf{x}_i, \mathbf{x}_j>$ would be positive and this would decrease the L_D. That means, L_D *downgrades similar features in the same class but far away from the boundaries between two classes*
- If the two features $\mathbf{x}_i$, $\mathbf{x}_j$ are completely alike but from the different class, $<\mathbf{x}_i, \mathbf{x}_j> \approx 1$ but $y_i\, y_j = -1$. Therefore, $\alpha_i\, \alpha_j\, y_i\, y_j <\mathbf{x}_i, \mathbf{x}_j>$ would be

negative, and this would increase L_D or maximize it. That means, L_D *is maximized with similar features from different classes* or L_D *is maximized with features on the opposite boundaries of two classes.*

To summarize the above analysis, by *maximizing* L_D, the dual-form SVM

1. Emphasizes the feature vectors on the opposite boundaries between two classes;
2. Ignores or suppresses those feature vectors far away from the boundaries between two classes.

This is exactly what we want, because in terms of finding the hyperplanes separating the two classes with maximum margin, only those vectors on or close to the boundaries between the two classes matter most. Those feature vectors are called *support vectors*, and the classifier defined by support vectors is called a *support vector machine*.

8.3.3.1 The Dual-Form Perceptron

Because L_D is determined by the small number of support vectors on the boundaries between the two classes, not surprisingly, most of the α_i would be zero. Once α_i, $i = 1, 2, \ldots, N$ are solved, the weights for the hyperplane separating the two classes of data with the maximum margin are given as follows:

$$\mathbf{w} = \Sigma_i \alpha_i y_i \mathbf{x}_i \tag{8.25}$$

Therefore, the weight of the SVM hyperplane is just a linear combination of the training data, and this is consistent with the weight updating methods used in the linear and perceptron classifiers introduced earlier.

A set of α_i can be estimated using the *dual-form* perceptron:

1. $$\begin{aligned} f(\mathbf{x}) &= < \mathbf{w}, \mathbf{x} > +b \\ &= \sum_i a_i y_i < \mathbf{x}_i, \mathbf{x} > +b \end{aligned}$$

2. Take the next training data $(\mathbf{x}_j, y_j) \in D$

3. *If* $y_j\ (\Sigma_i\ \alpha_i\ y_i\!<\!\mathbf{x}_i, \mathbf{x}_j\!> + b) \geq 0$
   then $\alpha_{i+1} \leftarrow \alpha_i$

4. *If* $y_j\ (\Sigma_i\ \alpha_i\ y_i\!<\!\mathbf{x}_i, \mathbf{x}_j\!> + b) < 0$
   then $\alpha_{i+1} \leftarrow \alpha_i + \eta, \eta > 0$

5. *Repeat from step* 2.

8.3.4 Kernel-Based SVM

8.3.4.1 The Dual-Form SVM Versus NN Classifier

With the dual-form SVM (8.24), we have successfully reduced the primal form optimization problem to optimizing just one set of parameters: α_i, $i = 1, 2, \ldots, N$. This is much more efficient than (8.21). However, this is just a small part of the story about SVM, and the more important part of the story is the transform of SVM optimization from testing $<\mathbf{w}, \mathbf{x}_i>$ to testing $<\mathbf{x}_i, \mathbf{x}_j>$. This is explained in the following.

- An n-dimensional data $\mathbf{x}$ is a feature vector in space, and geometrically, the dot product is defined as follows:

$$< \mathbf{x}_i, \mathbf{x}_j >= \|\mathbf{x}_i\| \left\|\mathbf{x}_j\right\| \cos\theta \tag{8.26}$$

  where θ is the angle between the two feature vectors $\mathbf{x}_i$ and $\mathbf{x}_j$

- In practice, the magnitudes of all feature vectors are normalized to unit or 1 so that they can be fairly matched.
- Therefore, the dot production of two feature vectors is just $cos\theta$.
- Because all feature values are positive, θ is between 0° and 90°.
- For two feature vectors at the same direction or $\theta = 0°$ (identical), the dot product is 1: $\cos\theta = 1$.
- For two feature vectors at vertical angle or $\theta = 90°$ (completely different), the dot product is 0: $\cos\theta = 0$.

- For two feature vectors at an angle $0^\circ < \theta < 90^\circ$ (between similar to different), the dot product is between (0, 1): $0 < \cos\theta < 1$.
- Therefore, the dot product $cos\theta$ actually measures the similarity between the two feature vectors, or *the dot product is just the cosine distance between the two feature vectors*.

Equipped with this key finding, now let's go back to (8.24):

$$\text{Maximize} \quad L_D = \Sigma_i \alpha_i - \frac{1}{2} \Sigma_{ij} \alpha_i \alpha_j y_i y_j < \mathbf{x}_i, \mathbf{x}_j >$$

It is equivalent to

$$\text{Minimize} \quad \Sigma_{ij} \alpha_i \alpha_j y_i y_j < \mathbf{x}_i, \mathbf{x}_j > \tag{8.27}$$

Because $<\mathbf{x}_i, \mathbf{x}_j>$ is just the distance between $\mathbf{x}_i$ and $\mathbf{x}_j$, by recalling what has been discussed in the K-NN section, we can see that (8.27) is just the *weighted nearest neighbor* classification.

Now, if we look at the dual-form perceptron at the end of Sect. 8.3.3, the connection between SVM and K-NN is even clearer. The dual-form classifier is given as (8.28):

$$f(\mathbf{x}) = \sum_i a_i y_i < \mathbf{x}_i, \mathbf{x} > +b \tag{8.28}$$

The classification of each training data $\mathbf{x}_j$ is done by testing

$$y_j(\sum_i a_i y_i < \mathbf{x}_i, \mathbf{x}_j > +b) \geq 0, \; j = 1, 2, \ldots, N \tag{8.29}$$

Again, this is just a *weighted nearest neighbor classifier*.

This is a significant development, because, by using the dual form, we not only make the SVM more efficient but also make it a *nonlinear classifier*.

8.3.4.2 Kernel Definition

These are some of the key points obtained from the above:

- The dot product is a kind of distance.
- The dual-form SVM is a kind of weighted nearest neighbor classifier.
- The weighted nearest neighbor classifier is a nonlinear classifier.

Now that we understand how an important role the dot product plays in the dual-form SVM, we can extend this idea to any function that behaves like a dot product.

It turns out that the dot product of data points can be generalized as *kernelling*. Any function $K(\mathbf{x})$ which has the following property can be regarded as a *kernel*:

$$K(\mathbf{x}_1, \mathbf{x}_2) = <\Phi(\mathbf{x}_1), \Phi(\mathbf{x}_2)> \tag{8.30}$$

where $\Phi(\mathbf{x})$ is a function transforming feature vector $\mathbf{x}$ in one space R^m to another higher-dimensional space R^n $(n > m)$. From the definition, a kernel behaves like a dot product, and it takes two feature vectors as input and maps the two vectors to a scalar or a real value. The difference of a kernel from a dot product is that a kernel does the dot product at a higher-dimensional space, called the Hilbert space. We will explain the benefit of doing this.

Not surprisingly, with this definition, the dot product itself is a kernel, because

$$K(\mathbf{x}, \mathbf{y}) = <\mathbf{x}, \mathbf{y}> = <\Phi(\mathbf{x}), \Phi(\mathbf{y})> \tag{8.31}$$

where $\Phi(\mathbf{x}) = \mathbf{x}$.

Given a kernel, the kernel-based SVM can now be written as:

$$f(\mathbf{x}) = \sum_i a_i y_i K < \mathbf{x}_i, \mathbf{x} > +b \tag{8.32}$$

The questions now are:

1. Are there any other kernel functions than the dot product?

2. How useful is a kernel?

The answer to the first question is yes, there are many such kinds of kernel functions. Common kernel functions used in multimedia data classification include the following:

1. Quadratic kernel

$$K(\mathbf{x}, \mathbf{y}) = <\mathbf{x}, \mathbf{y}>^2 \text{ and } [1 + <\mathbf{x}, \mathbf{y}>]^2 \tag{8.33}$$

2. Polynomial kernel

$$K(\mathbf{x}, \mathbf{z}) =< \mathbf{x}, \mathbf{y} >^d \text{ and } [1+ < \mathbf{x}, \mathbf{y} >]^d, d > 2 \quad (8.34)$$

3. Radial basis function (RBF) kernel

$$K(\mathbf{x}, \mathbf{y}) = e^{-\gamma \|\mathbf{x}-\mathbf{y}\|^2}, \quad \gamma > 0 \qquad (8.35)$$

To demonstrate these functions having the kernel property of (8.30), let's assume **x** and **y** are in R^2 and $\mathbf{x} = (x_1, x_2)$, $\mathbf{y} = (y_1, y_2)$.

For $<\mathbf{x}, \mathbf{y}>^2$:

$$\begin{aligned} < \mathbf{x}, \mathbf{y} >^2 &= [(x_1, x_2) \cdot (y_1, y_2)]^2 = (x_1 y_1 + x_2 y_2)^2 \\ &= x_1^2 y_1^2 + x_2^2 y_2^2 + 2 x_1 x_2 y_1 y_2 \\ &=< (x_1^2, \sqrt{2} x_1 x_2, x_2^2), (y_1^2, \sqrt{2} y_1 y_2, y_2^2) > \end{aligned} \qquad (8.36)$$

or

$$\begin{aligned} &=< (x_1^2, x_1 x_2, x_2 x_1, x_2^2), (y_1^2, y_1 y_2, y_2 y_1, y_2^2) > \\ &=< \Phi(\mathbf{x}), \Phi(\mathbf{y}) > \end{aligned} \qquad (8.37)$$

where $\Phi(\mathbf{x}) = (x_1^2, \sqrt{2} x_1 x_2, x_2^2)$ or $(x_1^2, x_1 x_2, x_2 x_1, x_2^2)$ is a function which maps a 2D feature vector to a 3D or 4D feature vector. Therefore, $<\mathbf{x}, \mathbf{y}>^2$ is a kernel, and so is $<\mathbf{x}, \mathbf{y}>^d$ when $d > 2$.

For $(1 + \mathbf{x} \cdot \mathbf{y})^2$, we have:

$$\begin{aligned} (1 + \mathbf{x} \cdot \mathbf{y})^2 &= [1 + (x_1, x_2) \cdot (y_1, y_2)]^2 \\ &= (1 + x_1 y_1 + x_2 y_2)^2 \\ &= 1 + 2 x_1 y_1 + 2 x_2 y_2 + 2 x_1 x_2 y_1 y_2 + x_1^2 y_1^2 + x_2^2 y_2^2 \\ &=< (1, \sqrt{2} x_1, \sqrt{2} x_2, x_1^2, \sqrt{2} x_1 x_2, x_2^2), (1, \sqrt{2} y_1, \sqrt{2} y_2, y_1^2, \sqrt{2} y_1 y_2, y_2^2) > \\ &=< \Phi(\mathbf{x}), \Phi(\mathbf{y}) > \end{aligned} \qquad (8.38)$$

where $\Phi(\mathbf{x}) = (1,\ \sqrt{2}x_1,\ \sqrt{2}x_2, x_1^2,\ \sqrt{2}x_1x_2, x_2^2)$ is a function mapping a 2D feature vector to a 6-dimensional feature vector. Therefore, $(1 + \mathbf{x} \cdot \mathbf{y})^2$ is also a kernel, so is $(1 + \mathbf{x} \cdot \mathbf{y})^{\mathrm{d}}$ for $d > 2$.

In general, a quadratic kernel $<\mathbf{x}, \mathbf{y}>^2$ transforms an n-dimensional vector $\mathbf{x} = (x_1, x_2, \ldots, x_n)$ to vector in $n(n + 1)/2$-dimensional space:

$$\Phi\colon \mathbf{x} \rightarrow (x_1^2, x_2^2, \ldots, x_n^2, x_1x_2, x_1x_3, \ldots, x_1x_n, x_2x_3, \ldots, x_2x_n, \ldots, x_{n-1}x_n) \tag{8.39}$$

For RBF $e^{-\gamma\|\mathbf{x}-\mathbf{z}\|^2}$, again assume $\mathbf{x}$ and $\mathbf{z}$ are in 2D, since:

$$\begin{aligned} \|\mathbf{x} - \mathbf{z}\|^2 &= (x_1 - z_1)^2 + \left(x_2 - z^2\right)^2 \\ &= x_1^2 + z_1^2 - 2x_1z_1 + x_2^2 + z_2^2 - 2x_2z_2 \end{aligned}$$

Without loss of generality, let $\gamma = ½$, then we have:

$$\begin{aligned} e^{-\gamma\|\mathbf{x}-\mathbf{z}\|^2} &= e^{-\frac{1}{2}\left(x_1^2+z_1^2-2x_1z_1+x_2^2+z_2^2-2x_2z_2\right)} \\ &= e^{-\frac{1}{2}\left(x_1^2+x_2^2\right)}e^{-\frac{1}{2}\left(z_1^2+z_2^2\right)}e^{(x_1z_1+x_2z_2)} \\ &= e^{-\frac{1}{2}\|\mathbf{x}\|^2}e^{-\frac{1}{2}\|\mathbf{z}\|^2}e^{\langle\mathbf{x},\mathbf{z}\rangle} \\ &= Ce^{\langle\mathbf{x},\mathbf{z}\rangle} \\ &= C\sum_{n=0}^{\infty}\frac{\langle\mathbf{x},\mathbf{z}\rangle^n}{n!} \qquad \text{(Taylor expansion of } e^x\text{)} \\ &= C\sum_{n=0}^{\infty}\frac{K_{\mathrm{poly}(n)}(\mathbf{x},\mathbf{z})}{n!} \end{aligned} \tag{8.40}$$

where $C = e^{-\frac{1}{2}\|\mathbf{x}\|^2}e^{-\frac{1}{2}\|\mathbf{z}\|^2}$ is a constant because feature vector is normalized to unit length, and $K_{poly(n)}(\mathbf{x}, \mathbf{z})$ is a polynomial kernel [3].

Therefore, the RBF is a kernel because the sum of kernels is also kernel (see the following). (8.40) shows that the RBF maps a vector into a space with infinite dimensions.

8.3.4.3 Building New Kernels

It can be shown that the following rules are true:

1. The sum of two kernels is also a kernel

$$K(\mathbf{x}, \mathbf{y}) = K_1(\mathbf{x}, \mathbf{y}) + K_2(\mathbf{x}, \mathbf{y}) \qquad (8.41)$$

2. A scalar times a kernel is also a kernel

$$K(\mathbf{x}, \mathbf{y}) = aK_1(\mathbf{x}, \mathbf{y}) \qquad (8.42)$$

3. The product of two kernels is also a kernel

$$K(\mathbf{x}, \mathbf{y}) = K_1(\mathbf{x}, \mathbf{y}) \times K_2(\mathbf{x}, \mathbf{y}) \qquad (8.43)$$

Therefore, by using these rules and existing kernels, we may build more kernels for different applications.

8.3.4.4 The Kernel Trick

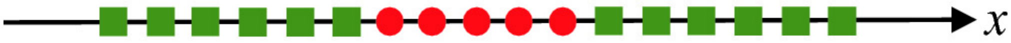
Now that we have defined the kernels and understood their behaviors, the next is to answer the *second question* we mentioned earlier. That is, why kernels or why we transform a feature vector to a higher-dimensional space? It appears the dual-form SVM is good enough because it not only gives us a SVM but also let us do nonlinear classification. So what’s the benefit of using kernels?

There are two reasons to use a kernel instead of just the dot product.

- One is to transform nonlinear data in lower-dimensional space to linear data in higher-dimensional space so that they can be separated linearly using the SVM.
- The other is to have more and better choices of distance measurement than the dot product, so as to improve the performance of a SVM.

To demonstrate how a kernel can transform nonlinear data into linear data, we will use the quadratic kernels as examples.

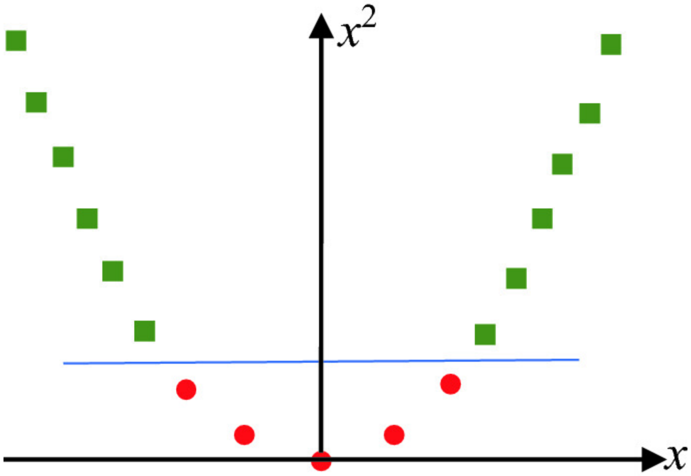
Consider the following 1D binary data (red and green dots) which is a nonlinear data because it cannot be separated by a point or a line.



Now map each of the samples using the following function:

$$\Phi : x \rightarrow \left\{x, x^2\right\} \tag{8.44}$$

Φ is a quadratic mapping, and it transforms a 1D line into a 2D parabola:



By transforming the 1D data into a 2D space, now the data in 2D space can be separated using a line (blue) or linearly separable. This is exactly the first reason of using kernel. This phenomenon can also be demonstrated using a 2D nonlinear data (Fig. 8.5) [4]. By using the following mapping function to map the 2D data on the left of Fig. 8.5 to a paraboloid in 3D space, the data can now be separated using a 2D plane and is linearly separable:

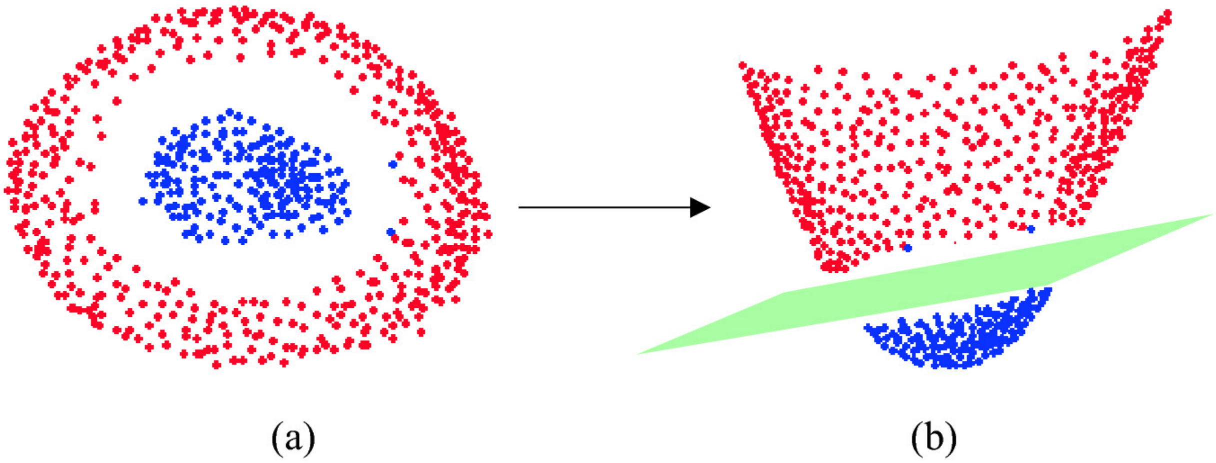


Fig. 8.5 Mapping of nonlinear data to linear data in higher-dimensional space. **a** An original nonlinear data in 2D space; **b** transformed data in 3D space using a quadratic mapping function φ

$$\Phi\colon (x_1, x_2) \to (x_1^2,\ \sqrt{2}x_1x_2, x_2^2) \tag{8.45}$$

Because the dot product is kind of distance measure, therefore, all kernels behave like a distance measure. Just like a good distance measure is crucial to a classifier, the choice of a good kernel can affect a classifier significantly. This is the reason why a kernel-based SVM is always better than a SVM just using the simple dot product.

Although the use of kernel gives us the advantage to do nonlinear classification, the explicit mapping from a lower-dimensional space to a higher-dimensional space is undesirable and can be expensive in terms of computation, given the fact that a feature vector usually has high dimension. Furthermore, data representation using very high dimension in Hilbert space is inefficient too.

Fortunately, the mapping doesn't need to be done explicitly. So long it's a kernel, and it *implicitly* maps a data to one in another space which is linearly separable. Put the other way, a kernel is just a dot product (*implicit*) regardless the space where the dot product is done, and according to (8.32), a kernel SVM is just a weighted nearest neighbor classifier by which a data can always be separated nonlinearly. Therefore, all we need to do for a kernel SVM is just to replace the dot product with a kernel. This is called the *kernel trick*.

To further improve the efficiency, in practice, an $N \times N$ kernel (or Gram) matrix is pre-computed for a dataset of N elements before the actual learning, so that there is no need to recompute the dot products at every iteration of the optimization. A kernel matrix K has the following properties:

- K is a positive definite matrix.
- $K(i, j) = K(\mathbf{x}_i, \mathbf{x}_j) = <\Phi(\mathbf{x}_i), \Phi(\mathbf{x}_j)>$ (implicit dot product in higher dimension space).
- K is symmetric, or $K(i, j) = K(j, i)$.
- $K(i, j)$ measures the similarity between *ith* and *jth* training samples in feature space.

$K =$

$K(\mathbf{x}_1, \mathbf{x}_1)$	$K(\mathbf{x}_1, \mathbf{x}_2)$	$K(\mathbf{x}_1, \mathbf{x}_3)$	…….	$K(\mathbf{x}_1, \mathbf{x}_N)$
$K(\mathbf{x}_2, \mathbf{x}_1)$	$K(\mathbf{x}_2, \mathbf{x}_2)$	$K(\mathbf{x}_2, \mathbf{x}_3)$	…….	$K(\mathbf{x}_2, \mathbf{x}_N)$
$K(\mathbf{x}_3, \mathbf{x}_1)$	$K(\mathbf{x}_3, \mathbf{x}_2)$	$K(\mathbf{x}_3, \mathbf{x}_3)$	…….	$K(\mathbf{x}_3, \mathbf{x}_N)$
…….	…….	…….	…….	…….
$K(\mathbf{x}_N, \mathbf{x}_1)$	$K(\mathbf{x}_N, \mathbf{x}_2)$	$K(\mathbf{x}_N, \mathbf{x}_3)$	…….	$K(\mathbf{x}_N, \mathbf{x}_N)$

8.3.5 The Pyramid Match Kernel

A well-designed kernel is crucial to a SVM classifier. Conventional kernel design is independent of feature itself. However, the selection of a kernel for a particular type of features is difficult because there is no natural connection between a feature and a kernel. Consequently, the selection of kernel for a SVM classifier is often arbitrary or empirical at best. The pyramid match kernel or PMK [5] is a method to design a kernel which matches the specific type of image features.

The idea is to extract a pyramid histogram feature at different level of resolutions and build a kernel using a weighted sum of histogram intersections. The idea of the PMK is described in detail in the following.

- Start with image X itself as level 0 and the total number of levels is L.
- Divide image into grids at different levels of resolutions. The grid at level l has a total of $2^l \times 2^l = 4^l$ cells, with 2^l cells along each dimension.
- A histogram is computed for each block at each level of resolutions.
- Histograms at each level l are given a different weight.
- The weighted histograms from all levels are concatenated as the pyramid histogram of the image.
- A kernel of weighted histogram intersection is built for the SVM.

$$K(X, Y) = \sum_{l=1}^{L} \alpha_l k^l (X_m, Y_m) \tag{8.46}$$

where X_m and Y_m are two weighted pyramid histograms and k is the histogram intersection.

- The idea is illustrated in Fig. 8.6 [5].

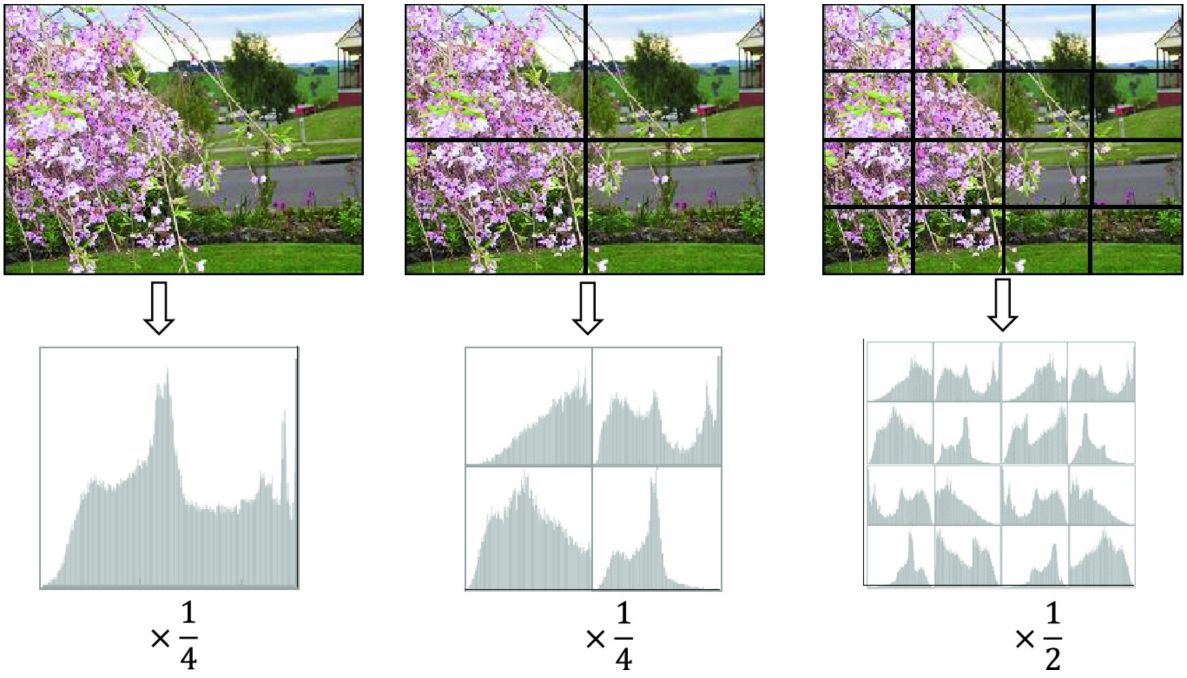


Fig. 8.6 Computation of pyramid match kernel. An image is divided into 3 levels of grids. At each level of the grid, a histogram is computed for each block of the grid. Histograms at each level are given a weight, and the weighted histograms are then concatenated as a feature vector

Let X^l and Y^l stand for the histograms of X and Y at level l, then the number of matches at this level is given by the histogram intersection

$$k^l = \sum_{i=1}^{4^l} \min[X^l(i), Y^l(i)] \tag{8.47}$$

where $l = 0, 1, 2, \ldots, L$. k^l at lower levels represent global features, while k^l at higher levels represent local features. Since global features can cause more confusion than local features, global features should be given less weights than local features. Therefore, the weight given to level l is set to $1/2^{L-l}$, which is inversely proportional to the block width at that level. Since the total weights must sum to 1, the combined matching result between two images is given in (8.48).

$$K(X, Y) = \frac{1}{2^L}k^0 + \sum_{l=1}^{L} \frac{1}{2^{L-l+1}}k^l \tag{8.48}$$

The next is to prove (8.48) is a kernel. Because a linear combination of kernels is also a kernel, we just need to prove each histogram intersection k^l is a kernel.

Let X_m and Y_m be the histograms of two images or image blocks X and Y. Each image has N pixels. We can then represent X_m and Y_m as two $N \times m$-dimensional binary vectors [6].

$$X_m = (\overbrace{1, 1, \ldots, 1}^{x_1}, \underbrace{0, 0, \ldots, 0}_{N - x_1}; \overbrace{1, 1, \ldots, 1}^{x_2}, \underbrace{0, 0, \ldots, 0}_{N - x_2}; \ldots; \overbrace{1, 1, \ldots, 1}^{x_m}, \underbrace{0, 0, \ldots, 0}_{N - x_m}) \tag{8.49}$$

$$Y_m = (\overbrace{1, 1, \ldots, 1}^{y_1}, \underbrace{0, 0, \ldots, 0}_{N - y_1}; \overbrace{1, 1, \ldots, 1}^{y_2}, \underbrace{0, 0, \ldots, 0}_{N - y_2}; \ldots; \overbrace{1, 1, \ldots, 1}^{y_m}, \underbrace{0, 0, \ldots, 0}_{N - y_m}) \tag{8.50}$$

With the above representation, the histogram intersection of X_m and Y_m is given as the dot product of the two histograms:

$$k(X_m, Y_m) = X_m \cdot Y_m \tag{8.51}$$

Therefore, k^l is a kernel and as a result, $K(X, Y)$ in (8.48) is also a kernel.

A histogram is a statistical feature, and it captures the feature distribution in an image or an image block. Histogram intersection tells how much area two distributions share; the more area they share, the more similar the two distributions are. Figure 8.7 shows an example of histogram intersection. The shared region is about 33% of the two histograms; therefore, the similarity between the two histograms is about 33%.

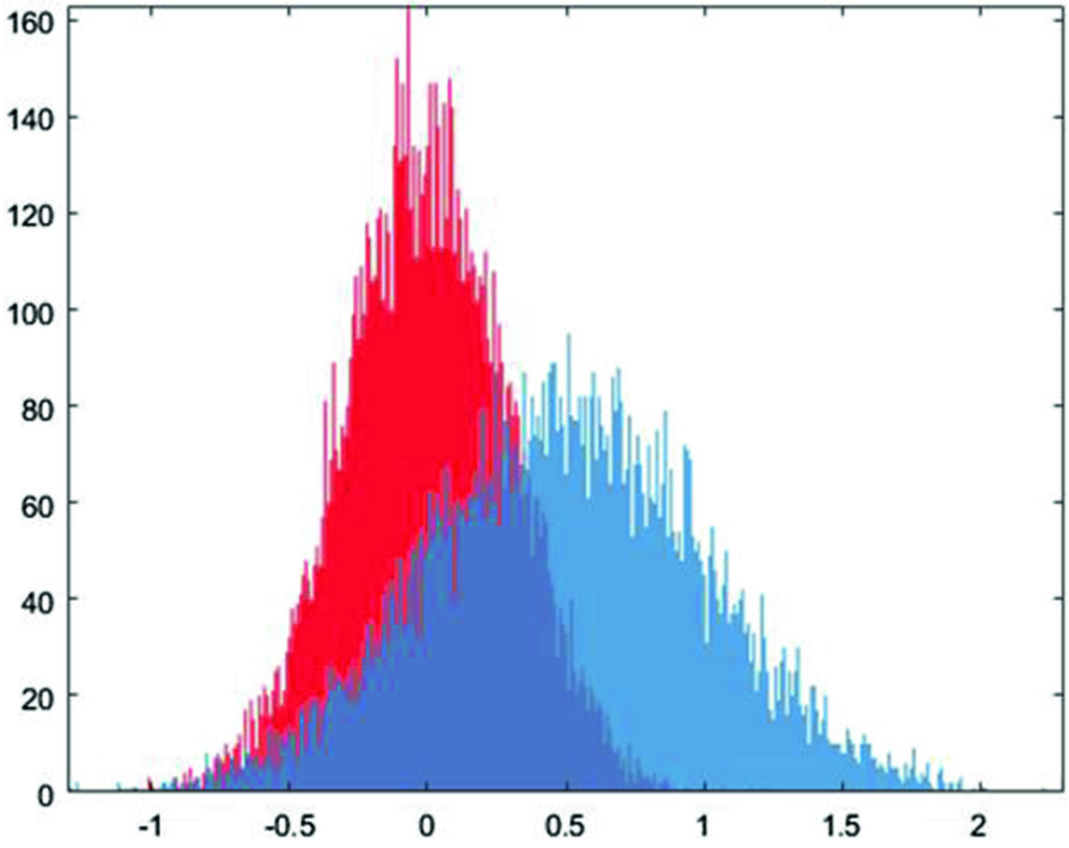


Fig. 8.7 Histogram intersection of two normal distributions

8.3.6 Discussions

Kernel-based support vector machine is essentially a training-based nearest neighbor classifier. The use of dot product transforms the support vector machine into a nonlinear nearest neighbor classifier. Traditional nearest neighbor has two limitations, the determining of k and it does not support training. However, if the training set is sufficiently large, both limitations can be overcome. First, the *k* can be determined empirically. The second limitation can be overcome by determining the class boundary with a piecewise linear approximation. For example, the class boundary of the following data can be approximated by 5 hyperplanes, which can then be used to classify new data (Fig. 8.8).

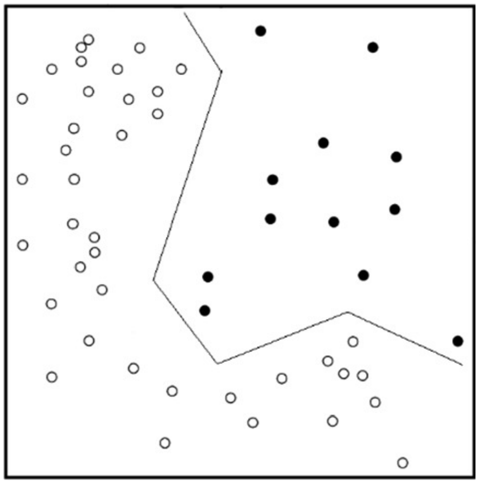


Fig. 8.8 Approximation of class boundary using piecewise hyperplanes

Although the piecewise linear boundary given by the K-NN is not optimal as the boundary provided by the kernel-based SVM, in terms of classification, the effectiveness of the two classifiers can be comparable. However, it would not be as efficient as SVM.

8.4 Fusion of SVMs

8.4.1 Fusion of Binary SVMs

An SVM is essentially a binary classifier. However, automatic image classification and annotation need a multiclass classifier. The most common approach is to train a separate SVM for each concept *c*, and each SVM generates a decision value $d_c(\mathbf{x})$. During the testing phase, the decisions from all classifiers are fused to obtain the final class label of a test image. Figure 8.9 demonstrates this two-level fusion process [7, 8]. The first level consists of multiple binary classifiers, and the second level fuses the decisions from the first-level classifiers.

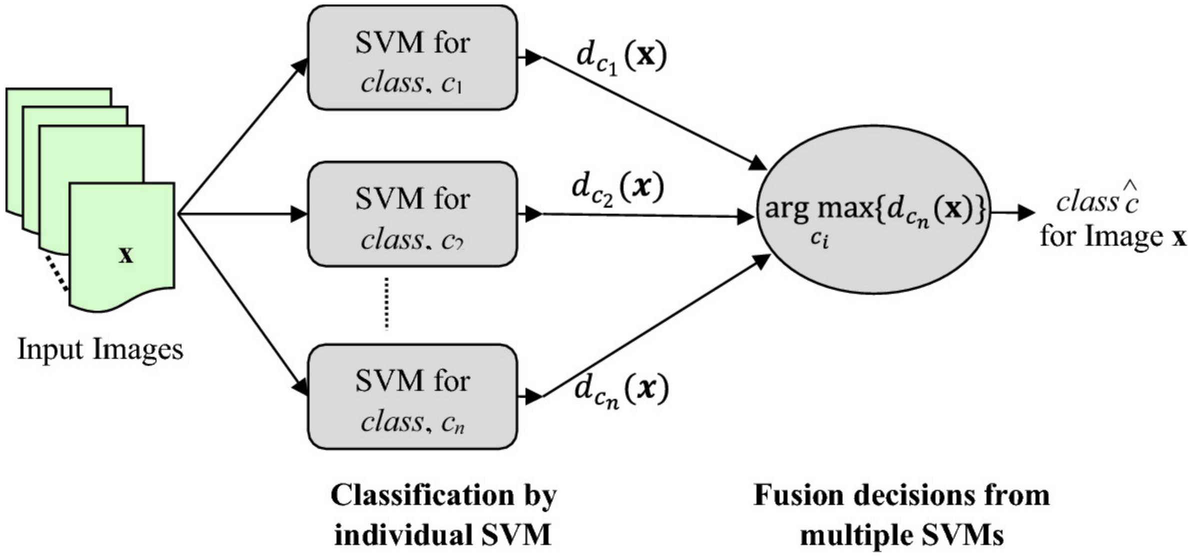

Input Images
x
SVM for class, c_1
SVM for class, c_2
SVM for class, c_n
$d_{c_1}(\mathbf{x})$
$d_{c_2}(\mathbf{x})$
$d_{c_n}(\mathbf{x})$
$\arg\max_{c_i}\{d_{c_n}(\mathbf{x})\}$
class $\hat{c}$ for Image $\mathbf{x}$
Classification by individual SVM
Fusion decisions from multiple SVMs

Fig. 8.9 A fusion of binary SVM classifiers

8.4.2 Multilevel Fusion of SVMs

The above approach can be regarded as a base-level fusion, and it works well for small number of concepts. The quality of classification degrades with the increase of the number of concepts due to the increase of the noise and class imbalance in the training data. To be more robust, *multiple sets* of base-level fusion of SVMs can be merged to make a more powerful fusion as shown in Fig. 8.10 [7, 8]. Each set of SVMs in level 1 and level 2 is similar to the base-level fusion shown in Fig. 8.9 and independently classifies an input image, and the final decision is fused from the decisions of all the individual sets at level 3.

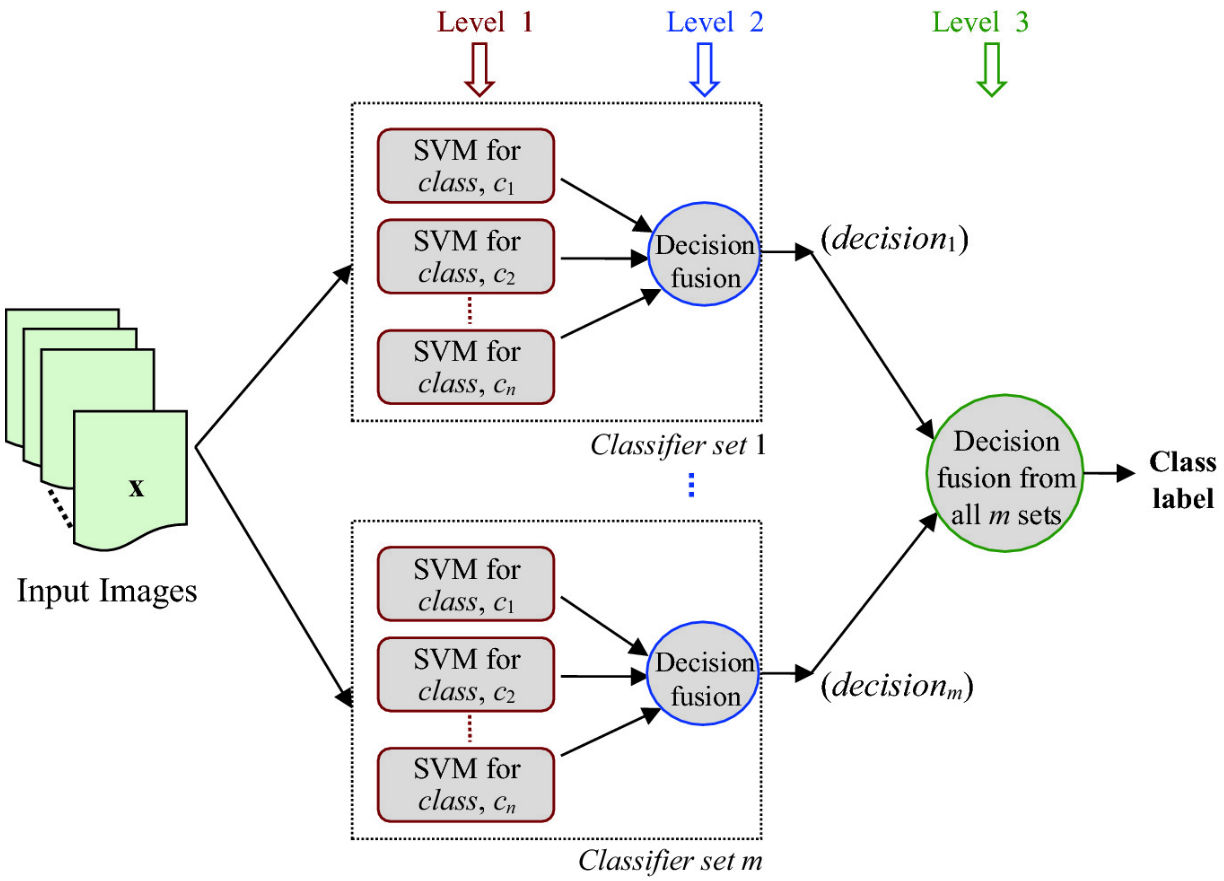

Level 1
Level 2
Level 3
SVM for class, c_1
SVM for class, c_2
SVM for class, c_n
Decision fusion
($decision_1$)
Classifier set 1
x
Input Images
Decision fusion from all m sets
Class label
($decision_m$)
Classifier set m

Fig. 8.10 A 3-level fusion of SVMs

The key advantage of using multiple sets of SVMs is to learn a more accurate and robust classifier using different types of SVMs, such as classification of SVMs, regression SVMs and SVMs with/without soft margins.

8.4.3 Fusion of SVMs with Different Features

Fusion of classifiers can also be done with combination of different types of features. For example, both global and local features can be used to train two different sets of SVMs at level 1 as shown in Fig. 8.11 [7, 8]. The results from the two sets of SVMs are then be fused in two steps. First, decisions of each concept made by each set of SVM are fused at level 2. Next, the final decision is made using a maximization at level 3.

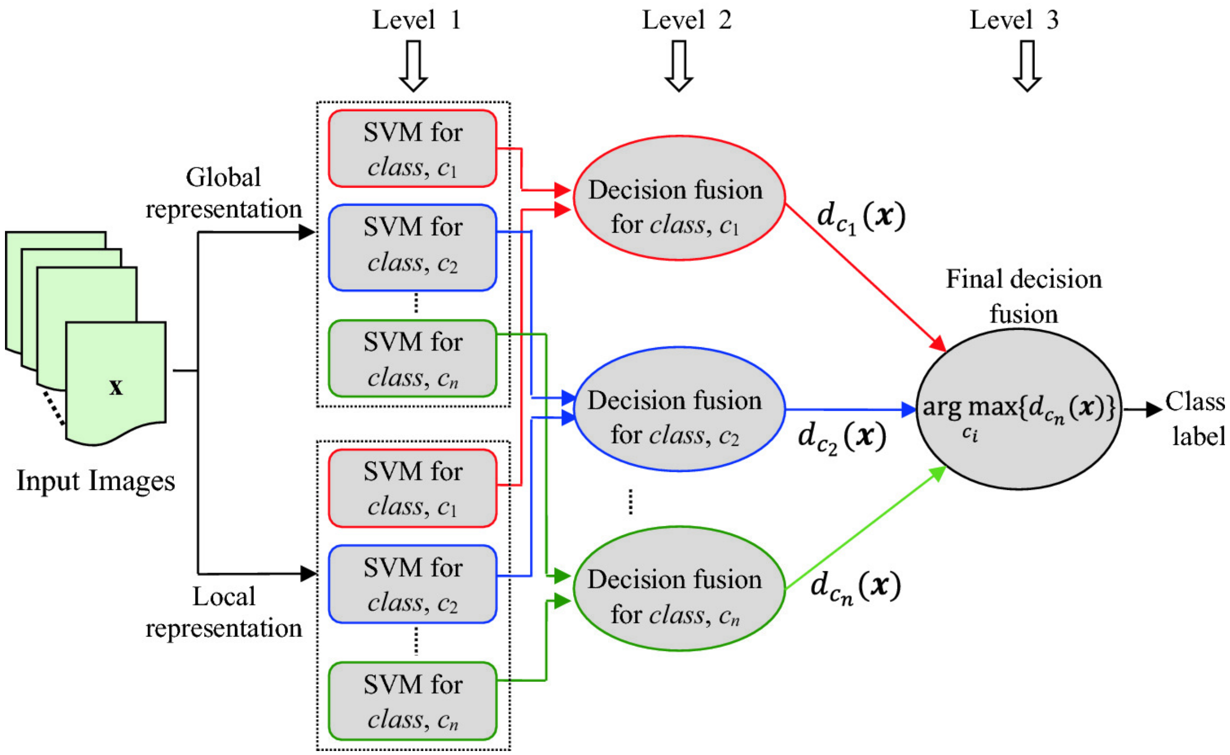

Level 1
Level 2
Level 3
Global representation
Local representation
Input Images
x
SVM for class, c_1
SVM for class, c_2
SVM for class, c_n
SVM for class, c_1
SVM for class, c_2
SVM for class, c_n
Decision fusion for class, c_1
Decision fusion for class, c_2
Decision fusion for class, c_n
$d_{c_1}(\boldsymbol{x})$
$d_{c_2}(\boldsymbol{x})$
$d_{c_n}(\boldsymbol{x})$
Final decision fusion
$\arg\max_{c_i}\{d_{c_n}(\boldsymbol{x})\}$
Class label

Fig. 8.11 A 3-level class-by-class fusion of SVMs with both global and local features

Although the fusion methods discussed in this section are shown as fusion of SVMs, they can also be applied to fusion of different types of classifiers such as Bayesian, ANN and DT.

8.5 Summary

SVM is basically a supervised linear classifier which divides a dataset into two classes with a hyperplane in data space. However, different from an ordinary linear classifier, it offers an optimal hyperplane which separates two classes of data with maximum margin between them. The data points that make the hyperplane are called the support vectors. SVM works by repeat guessing with candidate hyperplanes until the optimal hyperplane is found.

The biggest progress of SVM is the kernel-based SVM which achieves nonlinearity without the use of networking like ANN. Nonlinearity of SVM is achieved through transforming data into higher space so that they can be separated linearly. Due to the kernel trick, this transformation is even unnecessary so long as the distance is a kernel. This makes SVM very efficient compared with ANN.

However, SVM is essentially a binary classifier or non-probabilistic classifier. This makes it less robust than other probabilistic classifiers such as Bayesian classifiers and DT. In addition, a multiclass SVM needs to be achieved through fusion or assembly.

8.6 Exercises

1. Experiment on the *perceptron* algorithm. Download the dataset from the following Web site: http://networkrepository.com/pima-indians-diabetes.php. Now, run the following Matlab code and examine the `data` variable (double click it) in the Workspace. Next, study every variable in the Workspace, comment or describe every line of the code and compare the code with the perceptron algorithm in Sect. 8.3.1. Change the `epochs` to 1, 10 and 100, and see what happens to the `mis_class` variable. Find a different binary dataset (two-class data) and run the code again to see the new classification result. Write a short report to record your findings.

```
clear all
clc
tic;
data = load ('pima-indians-diabetes.csv');
x = data(:, 1:8);
y = data(:, end);
[N, n] = size(x);
p = 0;
for i=1:N
    if y(i)==0
        y(i) = -1;
        p = p+1;
    end
end
w0 = rand(8, 1);
epochs = 1000;
eta = 0.05;
w = w0;
iter = 0;
mis_class = N;
while(mis_class>0)&&(iter<epochs)
    iter = iter+1;
    mis_class = 0;
    w1 = w0; %zeros(1, n);
    for i=1:N
        if((x(i, :)*w)*y(i)<0)
            mis_class = mis_class + 1;
            w1 = w1 - eta*(y(i)*x(i, :));
        end
    end
    w = w - eta*w1';
end
toc
```

2. Matrix solutions on *linear classifier*. This exercise is based on the code from the above. First, load the dataset of Exercise 1 to Matlab Workspace. Next, select `n + 1` data from the dataset and use Matlab matrix inverse function `inv()` to compute the weight vector `w` of Eq. (8.5). Finally, write a short piece of code (by revising and simplifying the code in Exercise 1) to do the classification of the dataset using the weight vector `w`. Repeat the above steps for Eq. (8.8a), but this time you need to use the entire dataset instead of just `n + 1` data. Write a short report to compare both of your new results with the classification result from Exercise 1.

3. *Linear SVM classifier*. Open your Matlab editor, visit the following Matlab Web site: https://au.mathworks.com/help/stats/fitcsvm.

html#bt8v_23-1, and run the code of the first example 'Train SVM Classifier.' You can copy and run the code line by line or block by block in Matlab command line. Or you can copy the entire code of the example, save it as a Matlab m file, and run it. Once you've run the entire code of the example, now do the following:

- Examine the `meas` (data or features) and `species` (classes) variables in Workspace.
- Examine the `X` and `y` variables, and compare them with the `meas` and `species`, respectively. The removal of the two features from the `meas` and one class from the `species` is to visualize the data in 2D space.
- Examine the `SVMModel` variable in Workspace, especially the `KernelParameters`, `IsSupportVector` and the `SupportVectors` parameters.
- Observe the support vectors on the scatter diagram. Draw a line between two support vectors so that the classification error is minimum.
- Once you've understood how SVM works, move to the second example 'Train and Cross-Validate SVM Classifier.'

4. *Nonlinear SVM classifier*. Open your Matlab editor, visit the following Matlab Web site: https://au.mathworks.com/help/stats/support-vector-machines-for-binary-classification.html, and run the code of the first example 'Train SVM Classifiers Using a Gaussian Kernel.' Try different kernels such as `'polynomial'` or a custom kernel and compare the cross-validation results.

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9. Artificial Neural Network

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Law of nature is The Way.

9.1 Introduction

When comes to learning and classifications, no other tool is more efficient and powerful than human brains. Therefore, there is sufficient motivation to design a machine learning tool which simulates human brains. This is further encouraged by the recent research findings on human brain from both cognitive science and biology. It is believed that a human brain is consisted of 10 s of billions of neurons interconnected into a sophisticated network. The neurons in a brain are organized into functional units or regions, such as regions for visual, auditory, motion, reasoning and speech. An individual neuron is shown in Fig. 9.1.

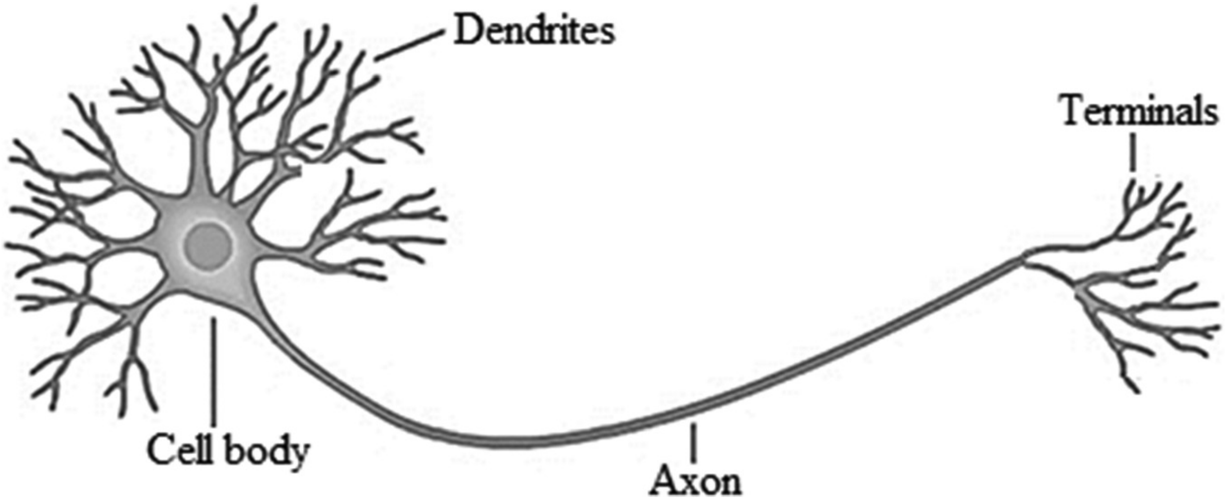

Fig. 9.1 A neuron of human brain

It is found that a neuron receives inputs from its dendrites, processes them in the cell body and transmits the output signal to other neurons through its axon. The inputs the neuron received can be either *excitory* or *inhibitory*. When there are more excitory inputs than inhibitory inputs, the neuron is activated and a signal is transmitted out through the axon; otherwise, no signal is generated.

Then neurons in many regions of a human brain are further organized into layers to create a layered network. Neurons from one layer usually receives inputs from neurons in an adjacent layer. Connections between layers are mostly in one direction, moving from low-level layer sensors like eyes or ears to higher coordination and reasoning layer [1].

With these understandings of human brains and neurons, it is possible to design artificial neurons and an artificial neural network or ANN.

9.2 Artificial Neurons

The design of an artificial neural network starts with the modeling of artificial neurons. From the above understandings, a neuron is basically an unit which receives inputs and generates an output. Specifically, a biological neuron consists of three components: the inputs (dendrites), an activation or processing unit (cell body) and an output (axon). Electronically, these three components can be respectively represented as a set of inputs x_i, a weighted sum of the inputs Σ and a threshold of the weighted sum. The alignment of an electronic neuron and a biological neuron is shown in Fig. 9.2.

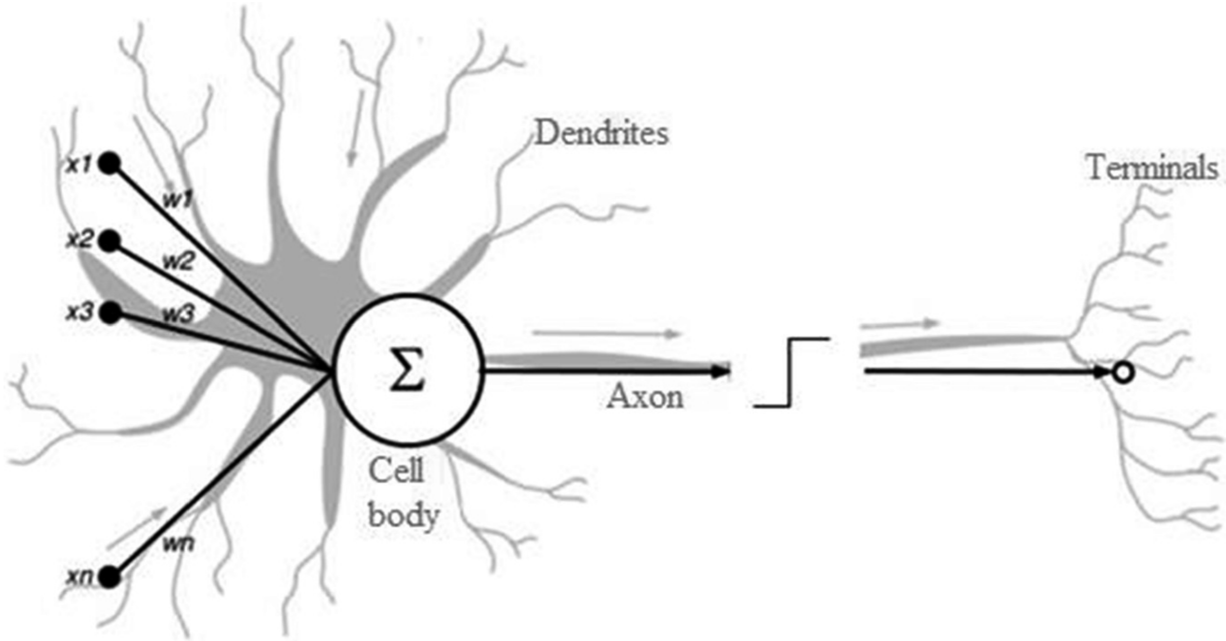
x1
x2
x3
xn
w1
w2
w3
wn
Σ
Dendrites
Cell body
Axon
Terminals

Fig. 9.2 Alignment of an artificial neuron with a biologic neuron

The weighted sum and the thresholding are usually merged into a single activation unit, and the axon is replaced with an output signal. Therefore, the simplified artificial neuron is shown in Fig. 9.3.

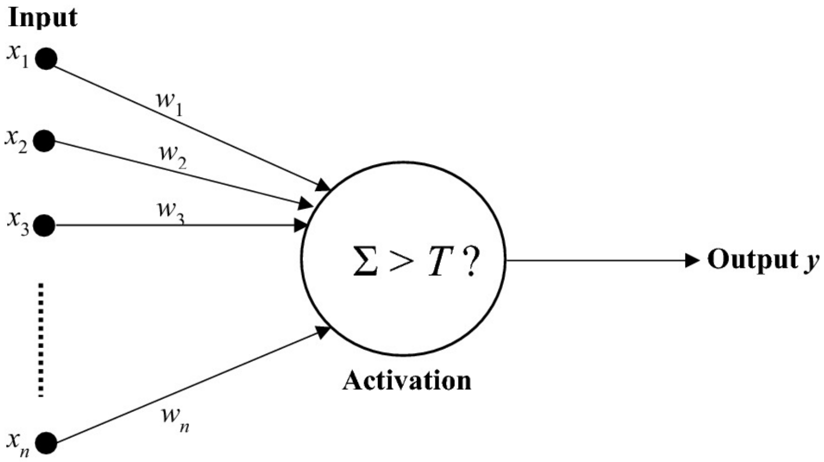
Input
x_1
x_2
x_3
x_n
w_1
w_2
w_3
w_n
$\Sigma > T\,?$
Activation
Output y

Fig. 9.3 Modellng of an artificial neuron

It turns out that an artificial neuron is just a binary linear classifier. Given an input $\mathbf{x} = (x_1, x_2, \ldots, x_n)$, a weighted sum Σ is calculated and compared with a threshold T:

$$\Sigma = w_1x_1 + w_2x_2 + \ldots + w_nx_n > T \tag{9.1}$$

If $\Sigma > T$, the neuron is activated and an output signal y is sent out. In other words, the activation of the neuron or output y is based on the following rule:

$$y = \begin{cases} 1 & \Sigma > T \\ 0 & \Sigma < T \end{cases} \tag{9.2}$$

It is more convenient to combine both Σ and T and rewrite (9.1) as:

$$\begin{aligned} D = \Sigma - T &= w_1x_1 + w_2x_2 + \ldots + w_nx_n - T \\ &= -T + w_1x_1 + w_2x_2 + \ldots + w_nx_n \end{aligned} \tag{9.3}$$

For notation purpose, let $w_0x_0 = -T$ which represents a constant and $x_0 =$ 1, then (9.3) becomes:

$$D = w_0x_0 + w_1x_1 + w_2x_2 + \ldots + w_nx_n \tag{9.4}$$

And (9.2) becomes:

$$y = \begin{cases} 1 & D > 0 \\ 0 & D < 0 \end{cases} \tag{9.5}$$

We can use this artificial neuron to do many simple linear classifications. One of them is to simulate the logic gates, such as the AND, OR, NAND and NOR.

9.2.1 An AND Neuron

Let's start with the AND gate; the AND function is given in Table 9.1.

Table 9.1 AND Gate

Input		**Output**	**Sum**
x_1	x_2		
0	0	0	0
0	1	0	1
1	0	0	1
1	1	1	2

Now if we set the activation or threshold value as $T = 1.5$ (or any value between 1 and 2), only input (1, 1) will be activated; this is exactly what we want. Therefore, the classifier for the AND function is given as:

$$y = -1.5 + x_1 + x_2 \tag{9.6}$$

In space, the classifier of (9.6) is represented by the following hyperplane which is a line in this case:

$$-1.5 + x_1 + x_2 = 0 \tag{9.7}$$

The AND data and the linear classifier is shown in Fig. 9.4. The neuron which implements the AND function is shown in Fig. 9.5 [1].

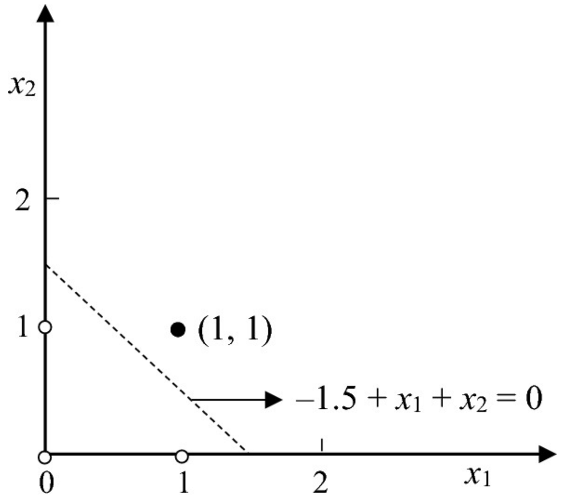

Fig. 9.4 The data of AND can be separated by a single line $-1.5 + x_1 + x_2 = 0$

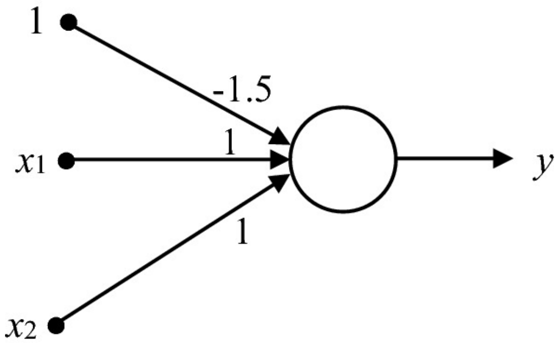

Fig. 9.5 Neuron which implements the AND function

9.2.2 An OR Neuron

Similarly, the classifier of an OR function and the neuron that implements the OR function are shown in Figs. 9.6 and 9.7, respectively.

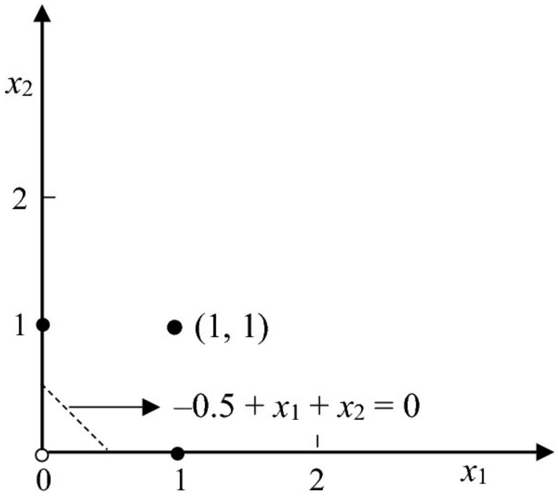

Fig. 9.6 Data of OR can be separated by a single line $-0.5 + x_1 + x_2 = 0$

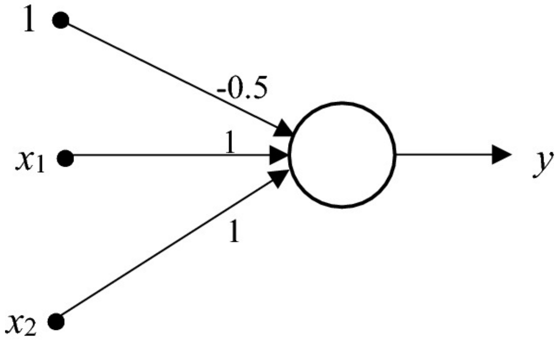

Fig. 9.7 Neuron which implements the OR function

An artificial neuron is called a node in an artificial neural network and is usually represented by a circle.

9.3 Perceptron

The neuron we designed above can do binary and linear classification; however, both the weights and the threshold are predetermined by a human designer. A biological neuron of a human brain on the other hand can learn from new instances and memorize. It would be desirable that an artificial neuron can also learn and memorize. This is done by feeding the neuron with a set of known data or pre-labeled data and learn the weights by using certain criterion or algorithm such as minimizing the total error.

From (9.4), the decision function of a neuron is given as:

$$Y = w_0 + w_1x_1 + w_2x_2 + \ldots + w_nx_n \tag{9.8}$$

To train the neuron,

- A training set $S = \{(\mathbf{x}_q, y_q), q = 1, 2, \ldots, N\}$ is collected,
- Where y_q is the desired output of qth sample feature vector $\mathbf{x}_q = (x_{q1}, x_{q2}, \ldots, x_{qn})$,
- The training is then to minimize the squared error or MSE:

$$E = E(w_1, w_2, \ldots, w_n) = \frac{1}{2}\sum_{q=1}^{N}\left(Y_q - y_q\right)^2 \tag{9.9}$$

- Where $Y_q = w_0 + w_1x_{q1} + w_2x_{q2} + \ldots + w_nx_{qn}$.

The minimization follows the *steepest descent* direction which is given by the gradient vector of

$$\left(-\frac{\partial E}{\partial w_0}, \ -\frac{\partial E}{\partial w_1}, \ -\frac{\partial E}{\partial w_2}, \ \ldots, \ -\frac{\partial E}{\partial w_n}\right) \tag{9.10}$$

If a sample is misclassified and the actual output Y is different from the correct output y, we would want to change the weights so that E is minimized. Therefore, the *steepest descent* algorithm to minimize E is given by the following algorithm:

1. Choose an initial weight set of $w_0, w_1, w_2, \ldots w_n$ and a positive constant c.

2. For $i = 0, 1, 2, \ldots, n$, compute the partial derivatives of $\partial E/\partial w_i$ and let $w_i = w_i - c(\partial E/\partial w_i)$.

3. Repeat step 2 until $w_0, w_1, w_2, \ldots w_n$ stop to change.

By combining (9.9) and (9.10), the partial derivatives $\partial E/\partial w_i$ in the above algorithm is given by

$$\frac{\partial E}{\partial w_i} = \left(Y_q - y_q\right)x_{qi}, \quad i = 0, 1, 2, \ldots, n \tag{9.11}$$

Therefore, the MSE learning algorithm of a *perceptron* is given as:

1. Choose an initial weight set of $w_0, w_1, w_2, \ldots w_n$ and a positive constant c.

2. For each of samples $q = 1, 2, \ldots, N$, compute $Y_q = \sum_{i=0}^{n} w_i x_{qi}$.

3. Let $w_i = w_i - c(Y_q - y_q)x_{qi}$ for $i = 0, 1, 2, \ldots, n$.

4. Repeat steps 2 and 3 until $w_0, w_1, w_2, \ldots w_n$ stop to change.

9.4 Nonlinear Neural Network

The perceptron is essentially a two-layer neural network with an input layer and an output layer, and it can be trained to classify any linear data which can be separated by a hyperplane. However, for nonlinear data such as XOR (Fig. 9.8) and other data with convex data regions (Fig. 9.9), they cannot be separated by a single hyperplane in space, and consequently, they cannot be classified by a perceptron.

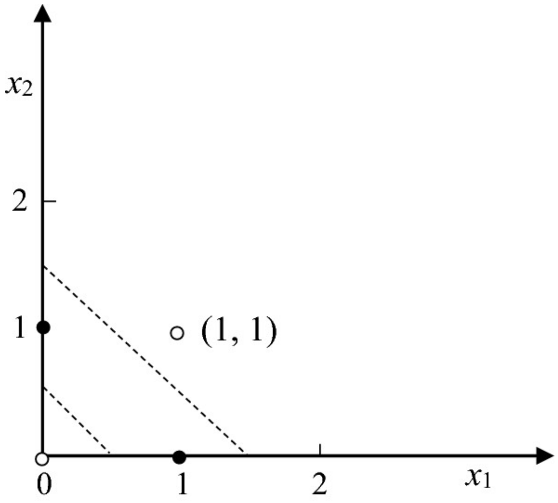

Fig. 9.8 Outputs of an XOR cannot be separated by a single line in 2D space

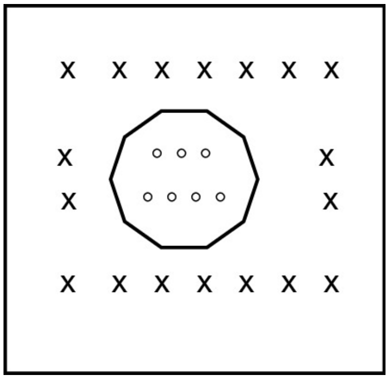

Fig. 9.9 Convex data region in the center cannot be separated by a single line in 2D space

Although a convex data region in space (a region is convex if any two data points can be connected by a line segment inside the region) cannot be separated by a single hyperplane, its boundary can be approximated by the intersection of a finite number of hyperplanes. For example, the XOR data in Fig. 9.8 can be separated by the following two half planes in 2D space:

$$-0.5 + x_1 + x_2 > 0 \quad \text{and} \quad -1.5 + x_1 + x_2 < 0 \tag{9.12}$$

The two neurons represent the two half planes in (9.12) and are given by

$$-0.5 + x_1 + x_2 > 0 \quad \text{and} \quad 1.5 - x_1 - x_2 > 0 \tag{9.13}$$

Now, by AND(ing) (Fig. 9.5) the two neurons of (9.13) with a third neuron or node, a neural network with a middle layer or hidden layer is created which can separate the XOR outputs. The neural network with hidden layer is shown in Fig. 9.10 [1].

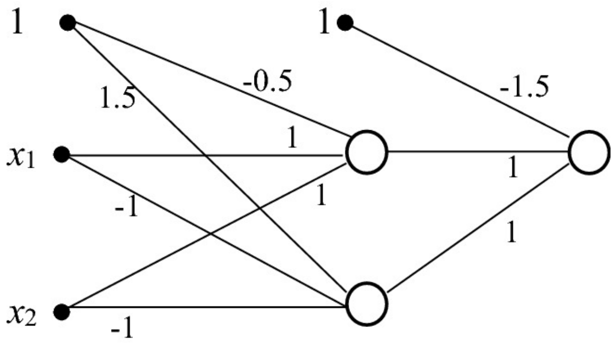

Fig. 9.10 Three-layer neural network to implement XOR. The two linear classifiers at the hidden layer are ANDed at the third layer

This idea of three-layer neural network can be easily extended to classify any generic convex nonlinear data like the one shown in Fig. 9.9. All we need now is more nodes in the second layer or middle layer (Fig. 9.11). Usually, a small number of nodes in the middle layer are sufficient to separate a convex region; however, more middle-layer nodes produce a smoother region boundary.

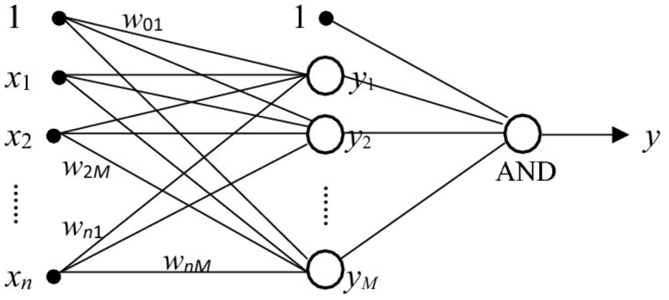

Fig. 9.11 Three-layer neural network with a hidden layer which can classify generic convex nonlinear data

By extending the above idea of classifying *convex* nonlinear data using neural network with a hidden layer, it is also possible to classify *non-convex* data using neural network. This is because a *non-convex* region can always be approximated by the union of a finite number of convex regions.

Therefore, it is possible to create a number of convex nodes in the third layer using the method discussed above and combine those convex nodes in the third layer using a logic OR in the fourth layer.

For example, the non-convex data region (black dots) in Fig. 9.12 can be approximated by three convex data regions, which can then be classified using a four-layer neural network shown in Fig. 9.13.

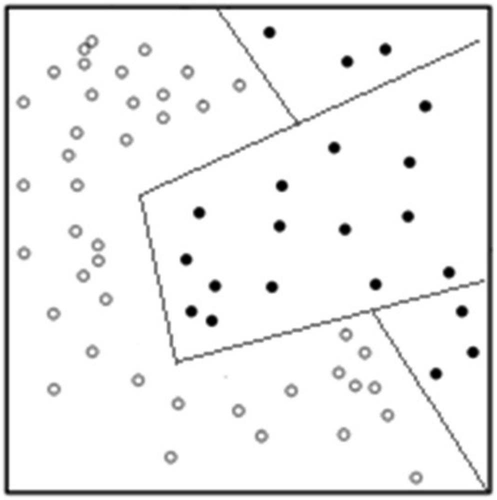

Fig. 9.12 Non-convex data region (black dots) is approximated by three convex regions

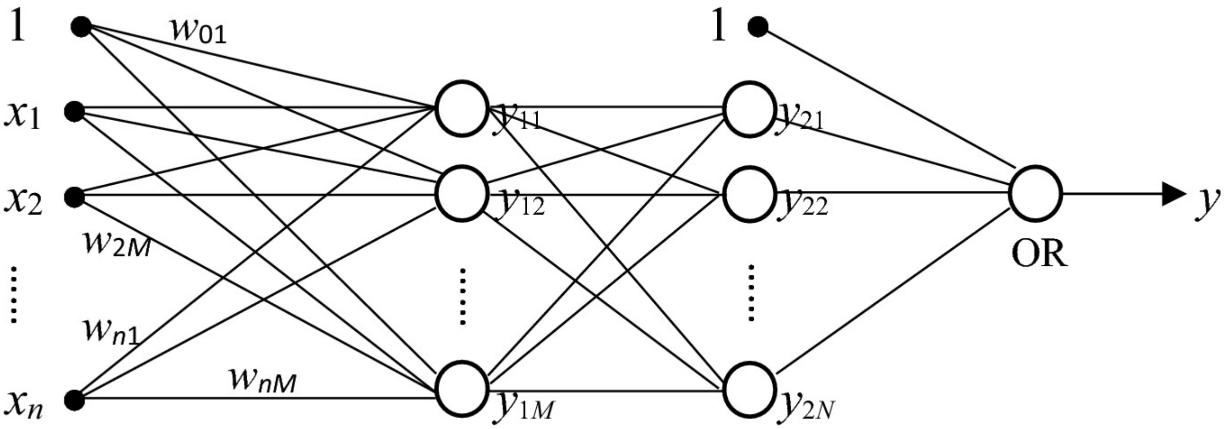

Fig. 9.13 Four-layer neural network which can classify any nonlinear data

This indicates that any *nonlinear* data can be classified by a four-layer neural network.

9.5 Activation and Inhibition

It should be noted that the activation or threshold function is crucial to a neural network because it is shown that any neural network without thresholding is equivalent to a two-layer network which cannot separate nonlinear data. However, the binary threshold function is not desirable because it is not continuous. This non-continuity can cause the network to take a very long time to converge or even not converge. This is because the gradients from the MSE are differential values and are small, so the changes of the weights are also small. As the result, the small changes to the weights is usually not enough to pass the threshold or generate an output signal.

9.5.1 Sigmoid Activation

It is desirable to have a continuous activation function which changes continuously from 0 to 1 instead of jumping from 0 to 1. Among the many proposed continuous activation functions, the most widely used is the *sigmoid function*. The S-shaped *sigmoid function* is defined as (9.14), and the shape of the function is shown in Fig. 9.14.

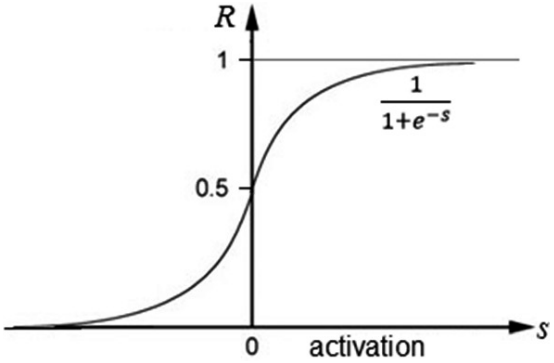

Fig. 9.14 Sigmoid function

The $R(s)$ function guarantees an output signal while preserves the thresholding functionality of an activation function.

$$R\left(s\right)=\frac{1}{1+e^{-s}} \tag{9.14}$$

The $R(s)$ function has the following important properties:

1. $\lim\limits_{s\to-\infty} R\left(s\right)=0$

2. $\lim_{s \to \infty} R(s) = 1$

3. $R(0) = 1/2$

4. $\frac{dR}{ds} = R(1 - R)$(9.15)

This final property has a convenient use in the following backpropagation algorithm. $R(1–R)$ is close to 0 at both ends of region (0, 1).

9.5.2 Shunting Inhibition

It is known that a biological neuron can be either *excitatory* or *inhibitory*. An inhibitory signal prevents impulse from arising in the receiving neuron. This inhibitory phenomenon can be represented mathematically as reducing the excitatory potential by division. This is called *shunting inhibitory* or SI. The idea is to learn a dual set of weights D_j and divided the original output of a neuron with the dual output adjusted by a decay factor. An SI neuron is illustrated in Fig. 9.15 [2].

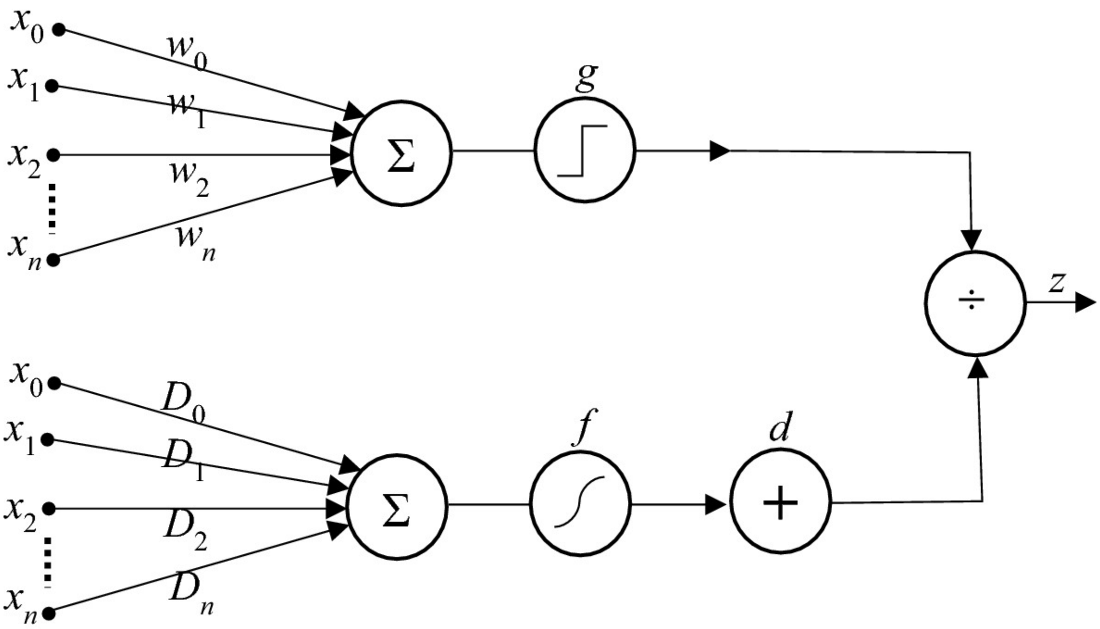

Fig. 9.15 Shunting inhibitory neuron

Mathematically, the output from a SI neuron is given by (9.16) [2].

$$z = \frac{g\left(\sum_{j=1}^{n} w_j x_j + b\right)}{d + f\left(\sum_{j=1}^{n} D_j x_j + a\right)} \tag{9.16}$$

where

- z is the output of the shunting neuron.
- x_j is the jth input.
- C_j and D_j are the connection weights of the jth input.
- $a = w_0 x_0$ and $b = D_0 x_0$ are biases.
- d is the passive decay rate.
- f and g are activation functions.
- n is the number of inputs from the previous layer.
- $d + f\left(\sum_{j=1}^{n} D_j x_j + a\right) > 0\cdot$

An ANN designed with SI neurons is called an SIANN. The key to an SI neural network is to use a different activation functions f and g in a layer so that only the strongest neurons are activated. Experiments show that when f and g are hyperbolic tangent function and exponential function respectively, the network has better convergence.

9.6 The Backpropagation Neural Network

9.6.1 The BP Network and Error Function

One of humans' great learning skills is learning from mistakes or errors; this is because the mistakes/errors provide important feedback to improve the original learning process. Unfortunately, the conventional ANN described above does not provide this function. However, this function can be simulated in a neural network by using the backpropagation algorithm. The idea is to add another process so that the outputs in the final layer are used as feedback to the previous layer to update the weights, and repeat this feedback until the input layer.

Therefore, a *backpropagation neural network* or a BP-ANN consists two major processes: (1) a conventional feed-forward process which computes outputs at each layer starting from the input layer and (2) a backpropagation process where the weights are updated at each layer starting from the output layer, in attempt to improve the classification accuracy.

In order to formulate the backpropagation algorithm, the following notations are defined.

- k denotes the kth layer of a network: $k = 0, 1, 2, \ldots, K$. Layer 0 is the input, and layer K is the output.
- M_k denotes the number of nodes at layer k, $k = 1, 2, \ldots, K$.
- $\mathbf{x} = (x_1, x_2, \ldots, x_n)$ stands for a training sample data.
- w_{ij}^k stands for the weight of connection between node i at layer $k-1$ and node j at layer k, $k = 1, 2, \ldots, K$.
- $net_j^k = \sum_{i=0}^{M_{k-1}} w_{ij}^k y_i^{k-1}$ stands for the output or the weighted sum of jth node of layer k, $j = 0, 1, 2, \ldots M_k$, $k = 1, 2, \ldots, K$.
- $y_j^k = R\left(net_j^k\right)$ stands for the activated or thresholded output from the jth node of layer k, $j = 0, 1, 2, \ldots M_k$, $k = 1, 2, \ldots, K$.

The notations are shown in the following backpropagation neural network.

The BP-ANN uses the same MSE and steepest gradient descent optimization as in the conventional ANN described earlier from (9.9) to (9.11). Assume t_j is the true output of node j at the final layer; then the total squared error of the BP network in Fig. 9.16 is given by (9.17).

$$E = \frac{1}{2}\sum_{j=1}^{M_K}\left(y_j^K - t_j\right)^2 \tag{9.17}$$

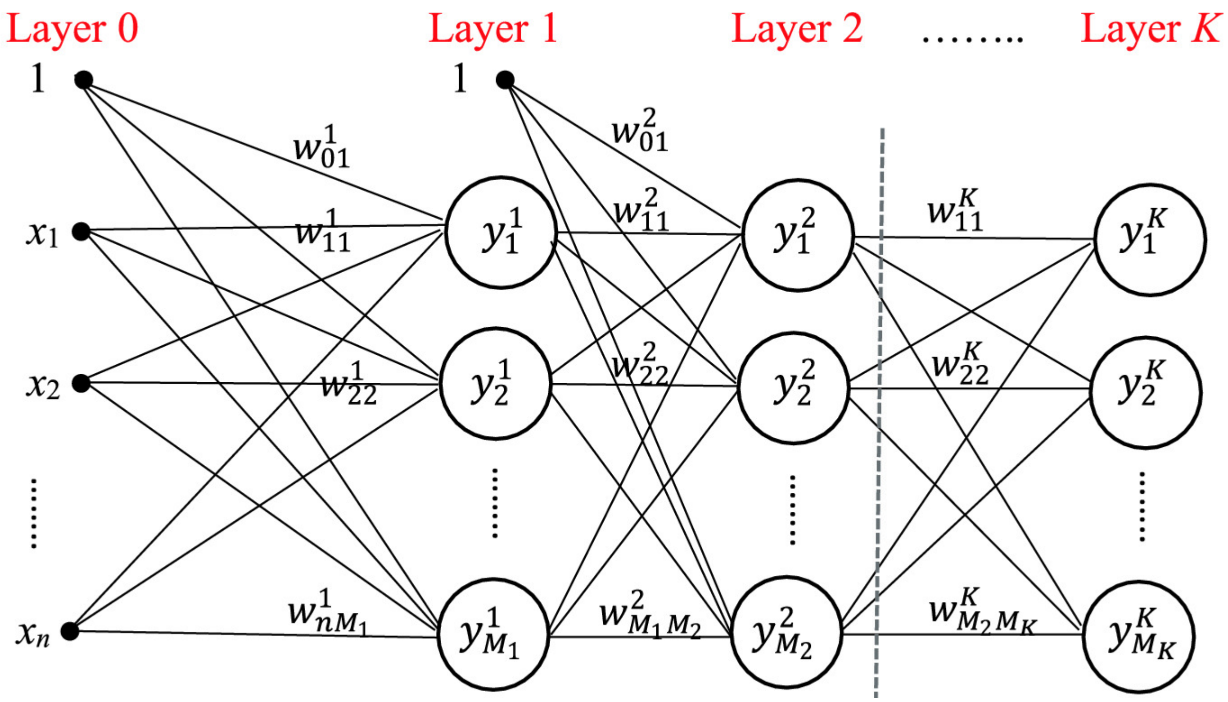
Layer 0
Layer 1
Layer 2
……..
Layer K
1
1
x_1
x_2
x_n
w^1_{01}
w^1_{11}
w^1_{22}
$w^1_{nM_1}$
w^2_{01}
w^2_{11}
w^2_{22}
$w^2_{M_1M_2}$
w^K_{11}
w^K_{22}
$w^K_{M_2M_K}$
y^1_1
y^1_2
$y^1_{M_1}$
y^2_1
y^2_2
$y^2_{M_2}$
y^K_1
y^K_2
$y^K_{M_K}$

Fig. 9.16 K-layer backpropagation neural network

The backpropagation algorithm starts from estimating and updating the weights of the final layer K; then propagates the same estimating and updating procedure back to layer $K-1$, $K-2$, …, until layer 1.

9.6.2 Layer *K* Weight Estimation and Updating

- The weights of layer K are given by w^K_{ij}, $i = 1, 2, \ldots, M_{K-1}$; $j = 1, 2, \ldots, M_K$;
- To estimate w^K_{ij}, we compute the partial derivatives $\frac{\partial E}{\partial w^K_{ij}}$;
- We will make use the 4th property of $R(s)$ in (9.15) for the following computations;
- Remember every y^k_j is a $R(s)$ function: $y^k_j = R\left(net^k_j\right)$;
- Fig. 9.15 shows the connection with weight w^K_{ij} (red line) in a BP network.

Therefore, the computation of $\frac{\partial E}{\partial w^K_{ij}}$ is simple, because among the M_K terms in (9.17), only the jth term $(y^K_j - t_j)^2$ is related to w^K_{ij}, while all the other terms are irrelevant because they are not connected to node i in layer $K-1$. Therefore, we have the following:

$$\begin{aligned}\frac{\partial E}{\partial w_{ij}^K} &= \frac{\partial E}{\partial y_j^K}\frac{\partial y_j^K}{\partial w_{ij}^K} \\ &= \left(y_j^K - t_j\right)\frac{\partial y_j^K}{\partial w_{ij}^K} \\ &= \left(y_j^K - t_j\right)\frac{\partial y_j^K}{\partial net_j^K}\frac{\partial net_j^K}{\partial w_{ij}^K} \\ &= \left(y_j^K - t_j\right)y_j^K\left(1 - y_j^K\right)y_i^{K-1} \\ &= \delta_j^K y_i^{K-1}\end{aligned} \tag{9.18}$$

where

$$\delta_j^K = y_j^K\left(1 - y_j^K\right)\left(y_j^K - t_j\right) \tag{9.19}$$

Therefore, the weights of layer K are updated according to (9.20)

$$w_{ij}^K \leftarrow w_{ij}^K - c\frac{\partial E}{\partial w_{ij}^K} = w_{ij}^K - c\delta_j^K y_i^{K-1} \tag{9.20}$$

where c is a positive constant. δ_j^K is equivalent to a *network sensor*, and it measures if the signal of a connection should be raised or suppressed. This can be explained by (9.19) and (9.20):

- w_{ij}^K is increased (raised) if $\delta_j^K < 0$ (when $y_j^K < t_j$).
- w_{ij}^K is decreased (supressed) if $\delta_j^K > 0$ (when $y_j^K > t_j$).
- w_{ij}^K changes little if δ_j^K is close to 0 (when y_j^K is close to t_j, 0 or 1), indicating converging.
- w_{ij}^K changes most significantly if y_j^K is very different from t_j.

9.6.3 Layer *K*−1 Weight Estimation and Updating

- The weights of layer $K-1$ are given by w_{mi}^{K-1}, $m = 1, 2, \ldots, M_{K-2}$; $i = 1, 2, \ldots, M_{K-1}$.

- To estimate w_{mi}^{K-1}, we compute the partial derivatives $\frac{\partial E}{\partial w_{mi}^{K-1}}$.
- The computation of partial derivative $\frac{\partial E}{\partial w_{mi}^{K-1}}$ at layer $K-1$ is more complicated than layer K.
- This is because w_{mi}^{K-1} connects to node i (at layer $K-1$), which is then connected to all nodes at layer K.
- The connections which are relevant to w_{mi}^{K-1} are shown in Fig. 9.16 (red lines) (Fig. 9.17)

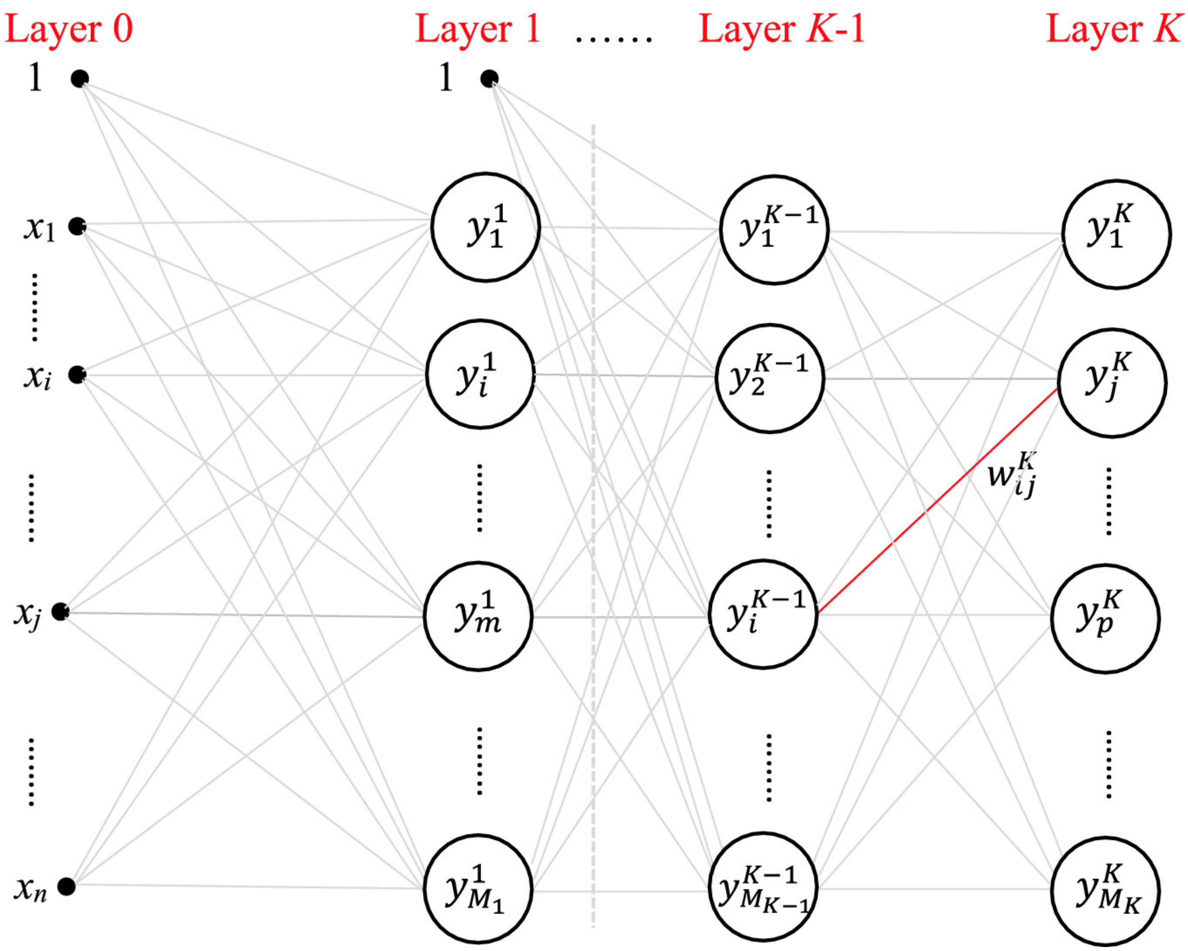
Layer 0
Layer 1
……
Layer K-1
Layer K
1
1
x_1
x_i
x_j
x_n
y_1^1
y_i^1
y_m^1
$y_{M_1}^1$
y_1^{K-1}
y_2^{K-1}
y_i^{K-1}
$y_{M_{K-1}}^{K-1}$
y_1^K
y_j^K
w_{ij}^K
y_p^K
$y_{M_K}^K$

Fig. 9.17 Illustration of a connection between node *i* in layer *K*−1 and node *j* in layer *K* in a *K*-layer BP neural network

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- Therefore, every of the M_K terms in (9.17) is now related to the computation of $\frac{\partial E}{\partial w_{mi}^{K-1}}$ (Fig. 9.18).

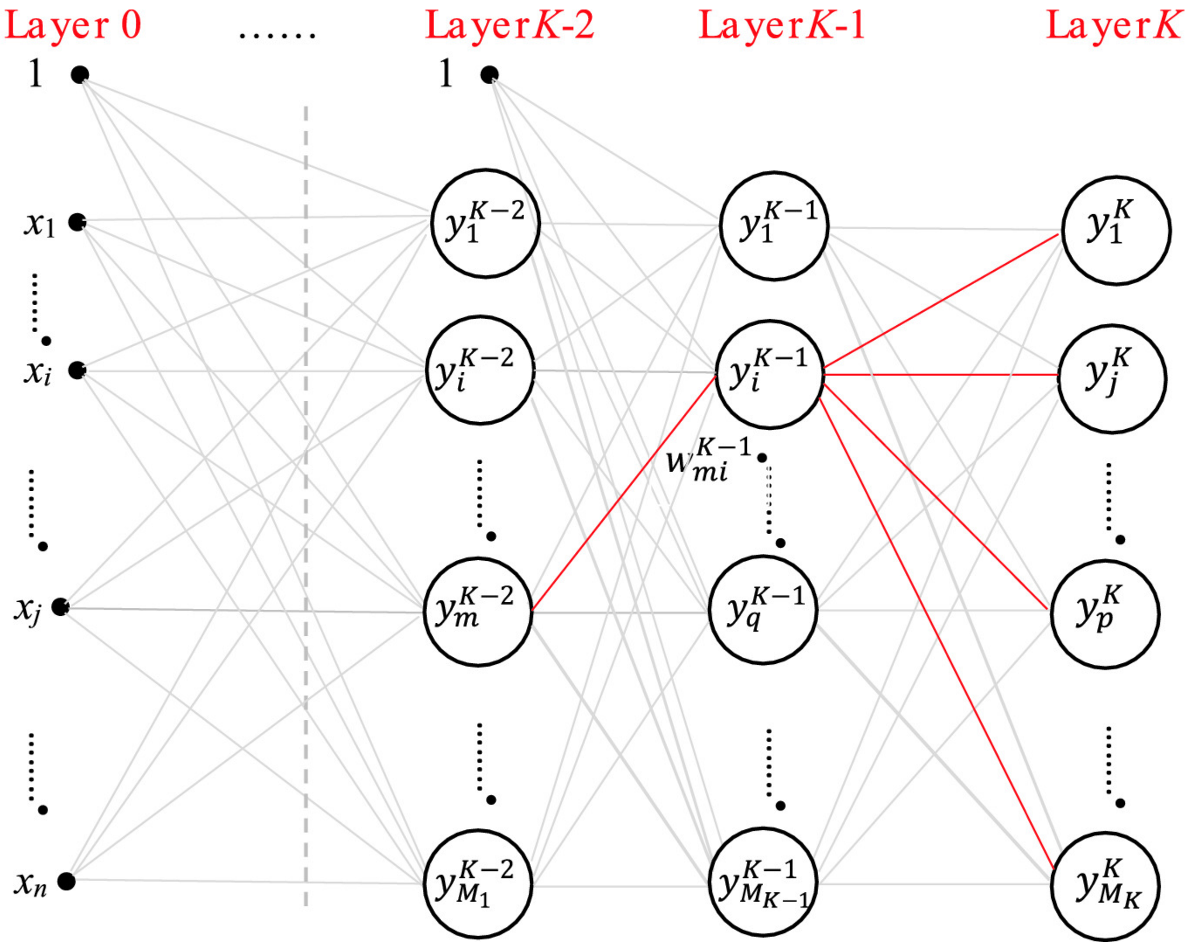

Layer 0
……
Layer K-2
Layer K-1
Layer K
1
x_1
x_i
x_j
x_n
1
y_1^{K-2}
y_i^{K-2}
y_m^{K-2}
$y_{M_1}^{K-2}$
y_1^{K-1}
y_i^{K-1}
w_{mi}^{K-1}
y_q^{K-1}
$y_{M_{K-1}}^{K-1}$
y_1^K
y_j^K
y_p^K
$y_{M_K}^K$

Fig. 9.18 Illustration of all connections relevant to w_{mi}^{K-1} in a K-layer BP neural network. Relevant connections are shown in red lines

Therefore, by using $y_j^k = R(net_j^k)$ and $dR(s)/ds = R(s)[1 - R(s)]$, the computation of $\frac{\partial E}{\partial w_{mi}^{K-1}}$ is given by the sum of chaining derivatives:

$$\begin{aligned}
\frac{\partial E}{\partial w_{mi}^{K-1}} &= \frac{1}{2}\sum_{j=1}^{M_K}\left(\frac{\partial\left(y_j^K - t_j\right)^2}{y_j^K}\frac{\partial y_j^K}{\partial net_j^K}\frac{\partial net_j^K}{\partial y_i^{K-1}}\frac{\partial y_i^{K-1}}{\partial net_i^{K-1}}\frac{\partial net_i^{K-1}}{\partial w_{mi}^{K-1}}\right)\\
&= \left[\sum_{j=1}^{M_K}\left(y_j^K - t_j\right)y_j^K\left(1 - y_j^K\right)w_{ij}^K\right]y_i^{K-1}\left(1 - y_i^{K-1}\right)y_i^{K-2}\\
&\overset{(9.19)}{\Rightarrow}[y_i^{K-1}\left(1 - y_i^{K-1}\right)\sum_{j=1}^{M_K}\delta_j^K w_{ij}^K]y_i^{K-2}\\
&= \delta_i^{K-1}y_i^{K-2}
\end{aligned} \tag{9.21}$$

where

$$\delta_i^{K-1} = y_i^{K-1}(1 - y_i^{K-1})\sum_{j=1}^{M_K}\delta_j^K w_{ij}^K \tag{9.22}$$

By repeating (9.21), it can be shown that for *any hidden layer k*, δ_i^k is given by (9.23).

$$\delta_i^k = y_i^k(1 - y_i^k)\sum_{j=1}^{M_{k+1}}\delta_j^{k+1}w_{ij}^{k+1} \tag{9.23}$$

Eq. (9.23) indicates that a network sensor at layer *k* depends on the combined network sensors at next layer *k* + 1. In other words, during the backpropagation, the weighted sum of network sensors at layer *k* + 1 has been propagated (through $dR(s)/ds$) to each network sensor at previous layer *k*. This kind of propagation is similar to the feed-forward process where the weighted sum of network values (or signals) at layer *k* is propagated (through $R(s)$) to each connection at next layer *k* + 1.

The difference between the two rounds of propagation is that different propagation functions are used. In the feed-forward process, the propagation function is just the activation function $R(s)$ itself; while in the backpropagation process, the propagation function is the gradient of the activation function: $dR(s)/ds$.

9.6.4 The BP Algorithm

Now that we have computed the gradients or partial derivatives of the error function E, the BP algorithm is designed as the following [1]:

1. Initialize all the weights w_{ij}^k (for all i, j, k) on the network and the constant c with some small random values.

2. Input a new training data: $\mathbf{x} = (x_1, x_2, \ldots, x_n)$ from a set of N training data.

3. *Feed-forward step*. Compute the outputs at each layer starting from the input layer:

$$y_j^k = R\left(\sum_{i=0}^{M_{k-1}} w_{ij}^k y_i^{k-1}\right) \qquad j = 1, 2, \ldots M_k; \quad k = 1, 2, \ldots, K.$$

4. *Back-propagation step*. Compute the network sensors at each layer starting from the output layer:

$$\delta_j^K = y_j^K(1 - y_j^K)\left(y_j^K - t_j\right) \qquad \text{(for layer } K\text{)}$$

$$\text{and} \quad \delta_i^k = y_i^k(1 - y_i^k) \sum_{j=1}^{M_{k+1}} \delta_j^{k+1} w_{ij}^{k+1} \quad (\text{for } k = K - 1, \mathrm{K} - 2, \ldots, 2, 1)$$

.

5. Update weights on the network by: $w_{ij}^k \leftarrow w_{ij}^k - c\delta_j^k y_i^{k-1}$ for all i, j, k.

6. Repeat steps 2 and 5 until all the weights w_{ij}^k stop to change or stop to change significantly.

Because the BP algorithm is a steepest gradient descent algorithm, choosing the initial values for w_{ij}^k and the constant c is crucial to the performance of a network. If the initial values of w_{ij}^k are too far from the global minima, the algorithm may converge to a local minimum. Consequently, the result class boundaries are not accurate. If the initial value of the constant c is either too small or too big, the converging progress can be very slow. In practice, several rounds of guessing the initial values of both the weights and c may be required to achieve a desirable performance.

9.7 Convolutional Neural Network

An ordinary ANN does not take raw data as input; instead, it takes features as input and classify the data into classes based on their features. The features are computed through a separated feature extraction process (hand crafted) and are given as an n-dimensional feature vector. The reason behind this separation of feature extraction and classification is that the data dimension is usually very larger, typically from tens of thousands to millions. Direct connection of raw data to an ANN would make the network too complex and too expensive to compute with traditional computing power. Besides, the various data dimensions are also a design issue for such a combined ANN.

Nowadays, with the rapid increase of computation power, it is possible to combine both the feature extraction and the classification processes into a single neural network. The idea is to integrate a feature extraction network in front of an ordinary ANN. Because the feature extraction is typically done through the convolution of local filters upon an image, an ANN with feature extraction functionality is called a *convolutional neural network*, or CNN for short.

9.7.1 CNN Architecture

The architecture of a CNN can be best demonstrated using the LeNet [3] in Fig. 9.19. Basically, a CNN consists of a *convolution network* in front and a *fully connected MLP* (multilayer perceptron, an ordinary ANN) at the backend.

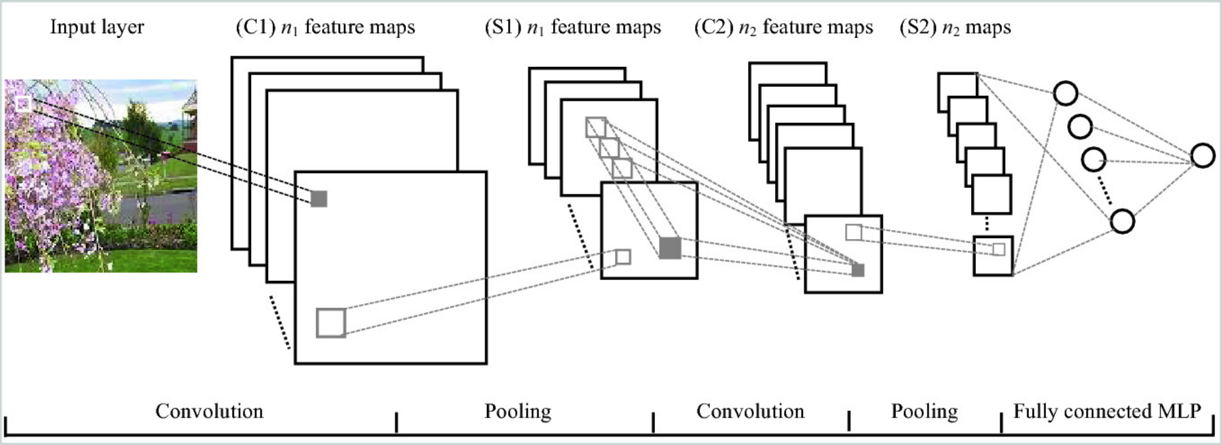


Fig. 9.19 Architecture of a CNN

Because each hidden unit in the convolutional network is only connected to a local neighborhood (e.g., a clock) in the input image instead of every pixel, it is also called a *locally connected* network. In contrast, in an ordinary ANN, each element of an input data is connected to each hidden unit in the network, so it is called *fully connected* network.

The convolutional network is a repeat process of *convolution* and *pooling* as shown in Fig. 9.19 [3]. Depending on the dimension of the input data, the repetitions can occur for a number of rounds. In the following, we describe the CNN architecture in details.

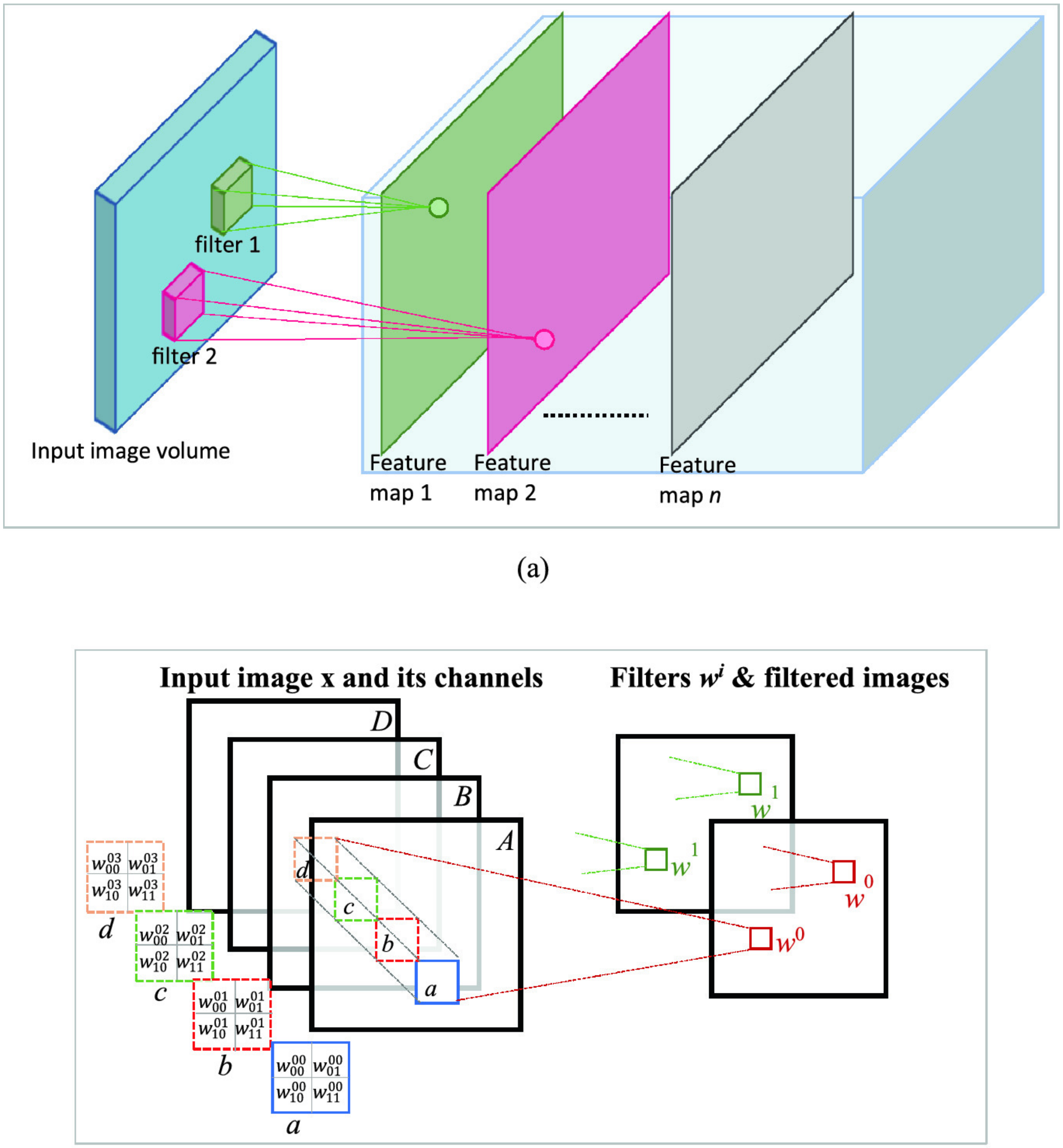
9.7.2 Input Layer

- The input data are a set of training images $\mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_n$.
- Each image $\mathbf{x}$ is a C-dimensional volume $M \times M \times C$, where M is the height and width of the image and C is the number of channels.
- For the convenience of formulation, the height and width of the images are assumed to be the same.
- Typically, the input is a RGB color image $\mathbf{x} = \mathbf{x}[i, j, k]$ and $C = 3$.
- For a gray-level image, $C = 1$.

9.7.3 Convolution Layer 1 (C1)

In a CNN, the convolution is a high-dimensional volume convolution.

- Specifically, the convolution is done by shifting a high-dimensional *volume filter* W: $N \times N \times S$ across the image as shown in Fig. 9.20a, where N is the height and width of the windowed filter and S is the number of channels of the filter.


filter 1
filter 2
Input image volume
Feature map 1
Feature map 2
Feature map n
Input image x and its channels
Filters w^i & filtered images
D
C
B
A
d
c
b
a
w00^03 w01^03 w10^03 w11^03
w00^02 w01^02 w10^02 w11^02
w00^01 w01^01 w10^01 w11^01
w00^00 w01^00 w10^00 w11^00
w^1
w^1
w^0
w^0

(a)

(b)

Fig. 9.20 Volume convolution. **a** Demonstration of volume filter and high-dimensional convolution; **b** Demonstration of high-dimensional convolution $\mathbf{x} * w^0$ which can be done using a series of 2D convolutions. Each of the filter channels *a*, *b*, *c* and *d* is convoluted with each of the corresponding image channels *A*, *B*, *C* and *D*

- S can be either the same as the number of image channels C or different.
- It can be shown that a high-dimensional volume filter consists of S number of 2D filters w with size of $N \times N$.
- In practice, the convolution is done by convoluting each channel of the high-dimensional volume filter with each channel of the input image.

- Each of these 2D filters w is meant to capture a particular type of edges, shapes or textures from the input image.
- Fig. 9.20b demonstrates how a volume convolution is done by a series of 2*D convolution*
- In Fig. 9.20b, the input data is an image $\mathbf{x}$ with four channels A, B, C and D.
- There are two high-dimensional volume filters w^0 and w^1 on the right-hand side; each of the volume filters consists of four channels a, b, c and d which are shown at the bottom left of Fig. 9.20 [3].
- The convolution between $\mathbf{x}$ and w^0 ($\mathbf{x}*w^0$) is done by convoluting each of the filter channels a, b, c and d across each of the corresponding image channels A, B, C and D.
- The convolution of image $\mathbf{x}$ with filter w^1: $\mathbf{x}*w^1$ is done the same way.
- Therefore, understanding 2D convolution is the key to understand high-dimensional volume convolution.

9.7.3.1 2D Convolution

- A 2D convolution is done by sliding an $N \times N$ window w across the image $\mathbf{x}$ row by row and column by column, assuming the window slides one pixel per time and there is no padding for the moment.
- The 2D convolution of $\mathbf{x} * w$ is given by (9.24), and an example of a 2D convolution is shown in Fig. 9.21 [4].

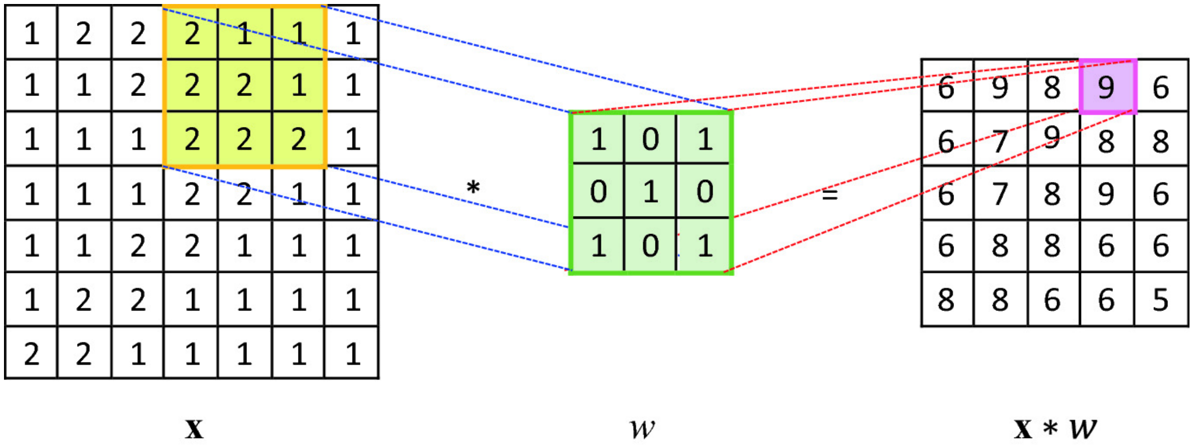


Fig. 9.21 2D convolution. An image $\mathbf{x}$ is convoluted with a filter window w and the result of the convolution is given by $\mathbf{x}\ *w$ at the right-hand side

$$X_{mn} = (\mathbf{x} * w)_{mn} = \sum_{j=0}^{N-1} \sum_{i=0}^{N-1} w[i, j] \cdot \mathbf{x}[m - i, n - j] \tag{9.24}$$

9.7.3.2 Stride and Padding

- The dimensions of the convoluted image depend on two parameters: *stride* and *padding*.
- The *stride* determines the number of pixels the filter window shifts per time, and the *padding* determines if and what the input image should be padded when the filter window is at the image boundary, e.g., 0 padding.
- If the stride value is 1 and the padding is yes, the dimensions of the convoluted image are the same as the input image.
- In Fig. 9.21, the stride is 1 and there is no padding; therefore, the convoluted image loses two pixels at both ends of each row and column.

9.7.3.3 Bias

- In a CNN, the values in a filter w are regarded as the weights for the connections between the filter and the network.
- These weights are to be learned during the training of the network.
- Therefore, a bias b is added to compensate for the estimation error.

$$X'_{mn} = (\mathbf{x} * w)_{mn} + b = b + \sum_{j=0}^{N-1} \sum_{i=0}^{N-1} w\left[i, j\right] \cdot \mathbf{x}\left[m - i, n - j\right] \tag{9.25}$$

9.7.3.4 Volume Convolution in Layer C1

- Each of the S channels of the *volume filter* is first convoluted with each corresponding channel of the input image x.
- The S filtered channels are then combined to create a 2D feature map or image f_{mn}.

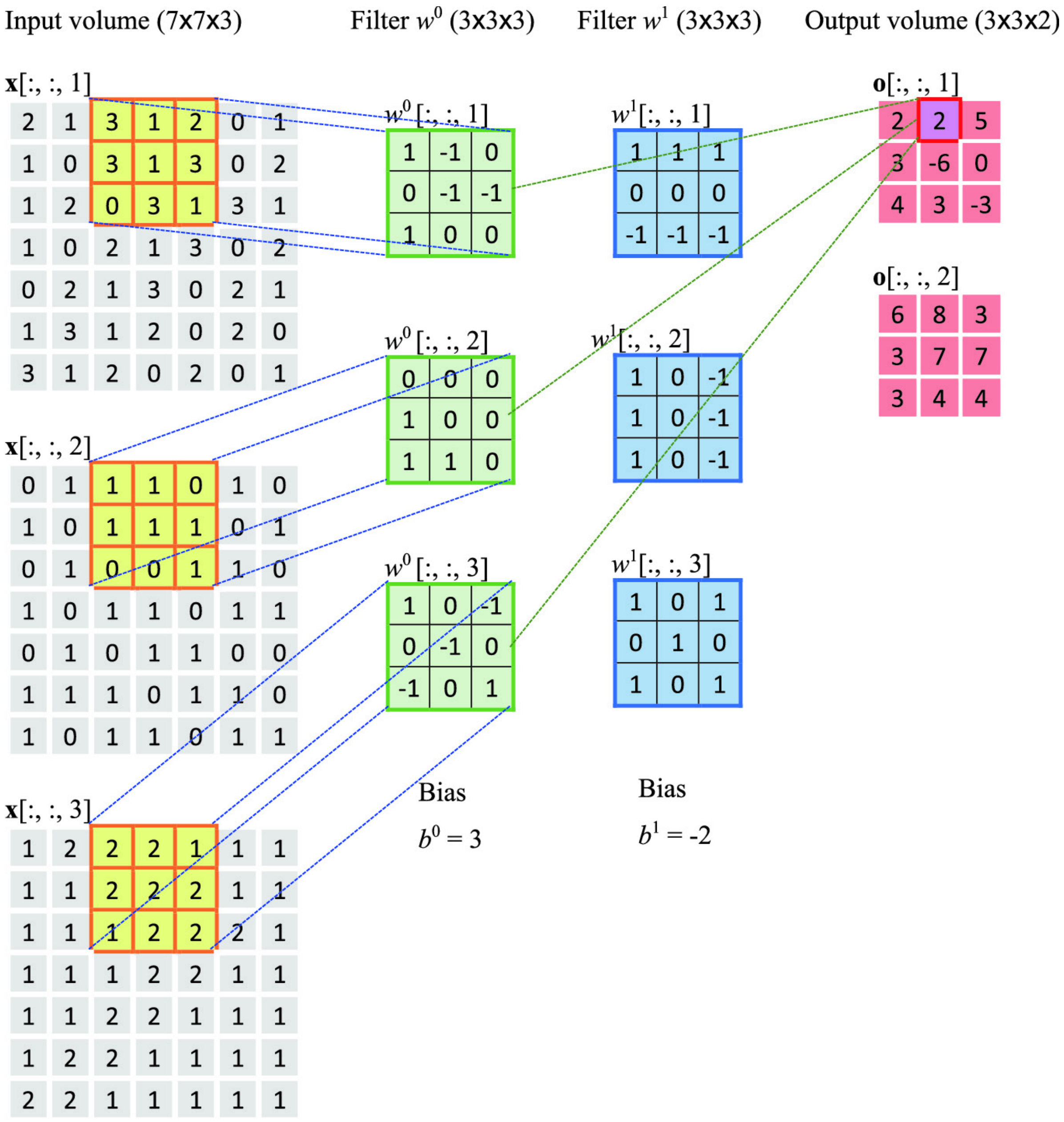
$$\begin{aligned} f_{mn} &= \sum_{k=1}^{S} (\mathbf{x} * w\left[:, :, k\right])_{mn} + b \\ &= b + \sum_{k=1}^{S} \sum_{j=0}^{N-1} \sum_{i=0}^{N-1} w\left[i, j, k\right] \cdot \mathbf{x}\left[m - i, n - j, k\right] \end{aligned} \tag{9.26}$$

9.7.3.5 *Depth of the Feature Map Volume*

- Multiple *volume filters* are used in a convolution layer to create a volume of feature maps.
- Each of the volume filters captures a particular type of image features.
- The number of volume filters R is called the *depth* of the feature map volume.
- The *rth* feature map is given by (9.27), $r = 0, 1, \ldots, R-1$.

$$f_{mn}^{r} = b + \sum_{k=1}^{S} \sum_{j=0}^{N-1} \sum_{i=0}^{N-1} w^{r}\left[i, j, k\right] \cdot \mathbf{x}\left[m-i, n-j, k\right] \tag{9.27}$$

- Fig. 9.22 shows how two volume filters w^0 and w^1 are used in layer C1 to create the two feature maps (light red) at the right most hand side [5].



$\mathbf{x}[:,:,1]$

2	1	3	1	2	0	1
1	0	3	1	3	0	2
1	2	0	3	1	3	1
1	0	2	1	3	0	2
0	2	1	3	0	2	1
1	3	1	2	0	2	0
3	1	2	0	2	0	1

$\mathbf{x}[:,:,2]$

0	1	1	1	0	1	0
1	0	1	1	1	0	1
0	1	0	0	1	1	0
1	0	1	1	0	1	1
0	1	0	1	1	0	0
1	1	1	0	1	1	0
1	0	1	1	0	1	1

$\mathbf{x}[:,:,3]$

1	2	2	2	1	1	1
1	1	2	2	2	1	1
1	1	1	2	2	2	1
1	1	1	2	2	1	1
1	1	2	2	1	1	1
1	2	2	1	1	1	1
2	2	1	1	1	1	1

$w^0[:,:,1]$

1	-1	0
0	-1	-1
1	0	0

$w^0[:,:,2]$

0	0	0
1	0	0
1	1	0

$w^0[:,:,3]$

1	0	-1
0	-1	0
-1	0	1

$w^1[:,:,1]$

1	1	1
0	0	0
-1	-1	-1

$w^1[:,:,2]$

1	0	-1
1	0	-1
1	0	-1

$w^1[:,:,3]$

1	0	1
0	1	0
1	0	1

$\mathbf{o}[:,:,1]$

2	2	5
3	-6	0
4	3	-3

$\mathbf{o}[:,:,2]$

6	8	3
3	7	7
3	4	4

Fig. 9.22 Input image is convoluted with two volume filters w^0 and w^1. The two result feature maps are at the right most hand side (light red). The *stride* value is 2, and there is no padding

- In the figure, the input image **x** is a color image with R, G and B channels, and each of the two volume filters also has three channels. The figure demonstrates the convolution of the three channels (*green*) of the first filter with a block (*yellow*) in image **x**. The convolutional output of the yellow block of image **x** is shown as the *pink* pixel in the first output image on the right most hand side of the figure.
- Although the input **x** is a 7 × 7 image, due to the stride value of the convolution is 2, the filtered output is just a 3 × 3 image. Therefore, in order

to output a filtered image with the same size as the input image, we not only need to set the *stride* value as 1 but also need to *pad* the image with half the filter size.

9.7.3.6 ReLU Activation

- The output from a volume filter or the feature map is essentially the weighted sum of the input layer.
- As in an ordinary neural network, it needs to pass an activation function.
- It has been found that in a convolution layer, the *max* (0, x) function is more effective than a sigmoid function for the activation.
- *max* (0, x) is basically a rectified linear function because it simply rectifies or refracts the negative half of $y = x$ to 0.
- Therefore, it is often called a *rectifier* and a node activated by the rectifier is also called a *rectified linear unit* or ReLU.
- So, we have

$$ReLU\,(x) = \max\,(0, x) \tag{9.28}$$

- The output from node r of layer C1 is finally given as (9.29)

$$y_{mn}^{r} = ReLU(f_{mn}^{r}) \tag{9.29}$$

- The ReLU activation is usually implemented as a separate layer after the convolution layer.

9.7.3.7 Batch Normalization

In a CNN, learning rate or convergence speed is a major issue. Due the convolution, the range of output values of the filters in each layer varies widely. In other words, the convolution has changed the original distribution of the input data, breaking the *independent* and *identically distributed* or i.i.d. assumption on input data. Worse still, each layer has to adapt to distribution drift from lower layers in order to revise its own weights. This makes the learning very inefficient and convergence very slow, especially for layers with *sigmoid* or *tanh* activation. This phenomenon is called the *internal covariance shift* or the change of data distribution from the input data distribution. In order to overcome this undesirable effect, a batch normalization procedure is introduced before the activation layer in attempt to keep the mean and variance of the input data fixed, so that layers learn themselves more or less independent with each other. The basic idea is to normalize the input data of all layers in the network to have 0 mean and unit variance. In practice, the normalization is done to the input data or data to be activated dimension by dimension and batch by batch. Let's take a particular activation x (a single dimension of the input data); for example, there are m values from a mini-batch: $B = \{x_1, x_2, \ldots, x_m\}$. The algorithm of the batch normalization of x is given as the following [6]:

Input: Values of x from a mini-batch $B = \{x_1, x_2, \ldots, x_m\}$

Parameters to be learned: γ, β

Output: Batch normalised values $\{y_i = BN_{\gamma,\beta}(x_i)\}$

$$\mu_B \leftarrow \frac{1}{m}\sum_{i=1}^{m} x_i \qquad //mini-batch\ mean$$

$$\sigma_B^2 \leftarrow \frac{1}{m}\sum_{i=1}^{m}(x_i - \mu_B)^2 \qquad //mini-batch\ variance$$

$$\hat{x}_i \leftarrow \frac{x_i - \mu_B}{\sqrt{\sigma_B^2 + \varepsilon}} \qquad //sample\ normalisation$$

$$BN_{\gamma,\beta}(x_i) = y_i \leftarrow \gamma\hat{x}_i + \beta \qquad //batch\ normalisation$$

For convolution layers, the normalization is done by jointly normalizing all the activations in a mini-batch over all locations. Specifically, the pair of parameters γ and β are learnt per feature map instead of per activation [6].

By batch normalization, the values of input features to each layer are normalized into the same range, and this reduces the oscillations of gradient descent when it approaches the minimum point and consequently makes it converging faster. Another benefit of batch normalization is that it adds minor noise to each layer due to each training sample is mixed with other samples in a mini-batch, and this reduces the effect of overfitting. In practice, lower dropout rate is needed for a network with batch normalization.

9.7.4 Pooling or Subsampling Layer 1 (S1)

The feature maps output from layer C1 usually have the same dimension as the input image. Their dimensions are too high to be connected to an ANN. Besides, the feature maps represent the finest details of the input image, these features are not as reliable. Therefore, it's tempting to down sample the feature maps so that features at a coarser level can be extracted. This is done by passing each feature map through a 2 × 2 subsampling function. Several types of subsampling functions can be used, such as *max*( ), *average*( ), L_2 *norm* or *spectral transform* such as DWT and DCT.

For example, if the *max* function is used, the subsampling is called a *max pooling*. Figure 9.23 demonstrates a *max pooling* which reduces a 4 × 4 feature map to a 2 × 2 feature map.

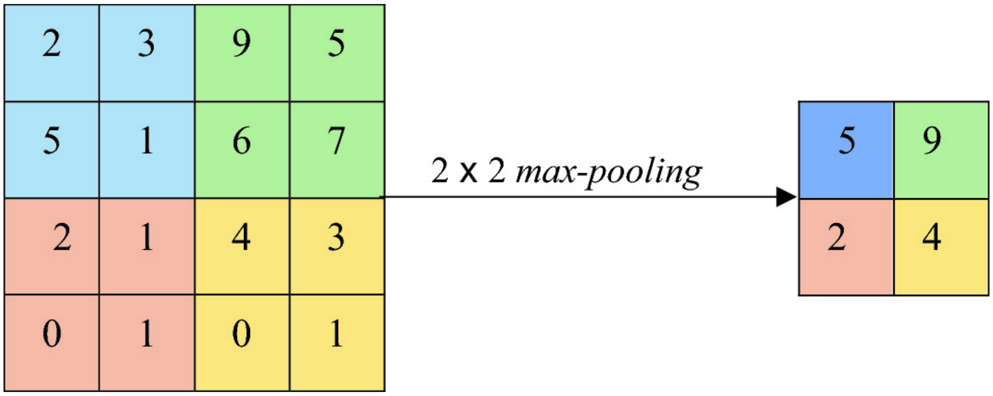


Fig. 9.23 Illustration of a max pooling. The maximum value of each quarter block of the left image is computed as the output value of the max pooling image at the right-hand side

9.7.5 Convolution Layer 2 (C2)

The outputs from the pooling layer 1 (S1) are subsampled feature maps from layer C1. New features can be computed from those feature maps by doing another round of convolution using new volume filters. The convolution procedure is the same as that in layer C1 except each volume filter in layer C2 uses different combination of feature maps from layer S1.

For example, in Fig. 9.24, the two volume filters w^0 and w^1 are convoluted with different channels or feature maps output from layer S1. While filter w^0 is convoluted with feature maps A-D, filter w^1 is convoluted with feature maps C-F.

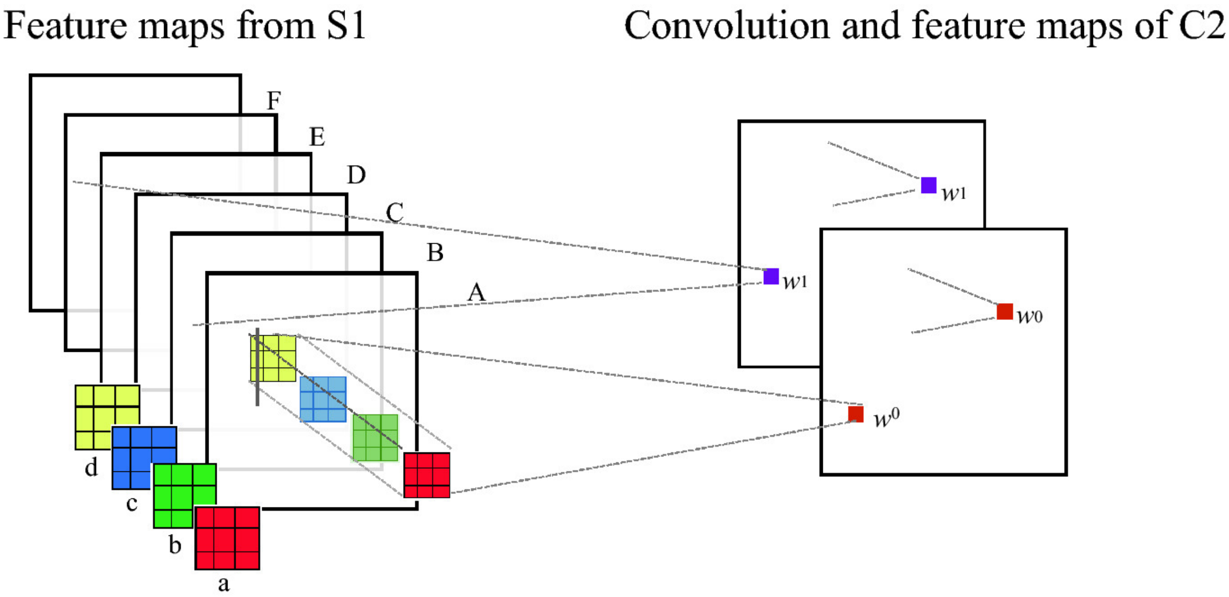


Fig. 9.24 Volume convolution in layer C2. Volume filter w^0 is convoluted with feature maps A-D, while volume filter w^1 is convoluted with feature maps C-F

If the depth of S1 is R, the total number of combinations of R channels is given as:

$$\sum_{k=1}^{R} \binom{R}{k} = 2^R - 1 \tag{9.30}$$

where k is the number of channels in a filter in layer C2.

The convolution and pooling can be repeated for a number of rounds depending on the size of the input data. The feature maps from the final pooling layer are flattened to create a 1D feature vector, and this feature vector is fed into the fully connected ANN at the backend of a CNN.

9.7.6 Hyperparameters

The performance of a CNN depends on the selection of the following hyperparameters. These parameters may be data dependant and need to be determined empirically.

- *Filter size*. The window size of the volume filter.
- *Stride*. The number of pixels per shift by the filter window at each layer.
- *Padding*. Whether padding will be used at the boundary of an input image and a feature map. What type of padding will be used, e.g., zero padding or wrap around padding.
- *Depths*. The number of channels or filters at each convolution layer.

- *Dropout-rates*. The percentage of neurons to be dropped out from each of the hidden layers at each iteration to prevent overfitting and cope with missing data.
- *Epochs*. The number of times the training algorithm will iterate over the entire training set before terminating.
- *Pooling size and function*. The size of a pooling function and the type of pooling function such as *max*( ), *average*( ) or L_2 *norm,* etc.
- *Activation function*. The function use to generate a threshold output at each layer, such as *ReLU*( ), *sigmoid* and *tanh*( ).
- The number of neurons in the fully connected layer of ANN.

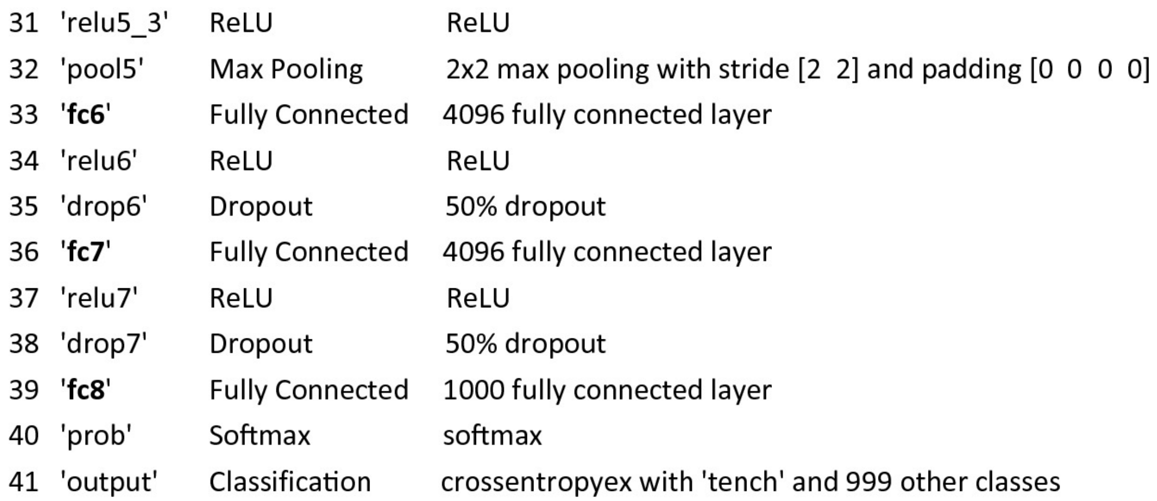
9.8 Implementation of CNN

To demonstrate a CNN in action, we show a high-performance CNN implementation by Oxford's Visual Geometry Group or VGGNet [7]. It has won the runner up of the 2014 ImageNet Large Scale Visual Recognition Challenge (ILSVRC) [Image-Net.org]. ImageNet is the largest hand-annotated visual dataset, and it holds image recognition competitions every year among researchers around the world. Compared with other high-performance CNN models, VGGNet is known for its simplicity because it is a *series network*.

9.8.1 CNN Architecture

The architecture of VGGNet is shown in the following list which is obtained by using Matlab code: net = vgg16; net.Layers. The 16 core layers are highlighted using bold font and are organized into five blocks: conv1–conv5. Therefore, it is often referred to as VGG16. It is a typical stacked convolution + pooling layers followed by fully connected ANN. The purpose of the softmax layer is to convert any vector of real numbers into a vector of probabilities, which correspond to the likelihoods that an input image is a member of a particular class.

01	'input'	Image Input	224x224x3 images with 'zerocenter' normalization
02	'**conv1_1**'	Convolution	64 3x3x3 convolutions with stride [1 1] and padding [1 1 1 1]
03	'relu1_1'	ReLU	ReLU
04	'**conv1_2**'	Convolution	64 3x3x64 convolutions with stride [1 1] and padding [1 1 1 1]
05	'relu1_2'	ReLU	ReLU
06	'pool1'	Max Pooling	2x2 max pooling with stride [2 2] and padding [0 0 0 0]
07	'**conv2_1**'	Convolution	128 3x3x64 convolutions with stride [1 1] and padding [1 1 1 1]
08	'relu2_1'	ReLU	ReLU
09	'**conv2_2**'	Convolution	128 3x3x128 convolutions with stride [1 1] and padding [1 1 1 1]
10	'relu2_2'	ReLU	ReLU
11	'pool2'	Max Pooling	2x2 max pooling with stride [2 2] and padding [0 0 0 0]
12	'**conv3_1**'	Convolution	256 3x3x128 convolutions with stride [1 1] and padding [1 1 1 1]
13	'relu3_1'	ReLU	ReLU
14	'**conv3_2**'	Convolution	256 3x3x256 convolutions with stride [1 1] and padding [1 1 1 1]
15	'relu3_2'	ReLU	ReLU
16	'**conv3_3**'	Convolution	256 3x3x256 convolutions with stride [1 1] and padding [1 1 1 1]
17	'relu3_3'	ReLU	ReLU
18	'pool3'	Max Pooling	2x2 max pooling with stride [2 2] and padding [0 0 0 0]
19	'**conv4_1**'	Convolution	512 3x3x256 convolutions with stride [1 1] and padding [1 1 1 1]
20	'relu4_1'	ReLU	ReLU
21	'**conv4_2**'	Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
22	'relu4_2'	ReLU	ReLU
23	'**conv4_3**'	Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
24	'relu4_3'	ReLU	ReLU
25	'pool4'	Max Pooling	2x2 max pooling with stride [2 2] and padding [0 0 0 0]
26	'**conv5_1**'	Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
27	'relu5_1'	ReLU	ReLU
28	'**conv5_2**'	Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]
29	'relu5_2'	ReLU	ReLU
30	'**conv5_3**'	Convolution	512 3x3x512 convolutions with stride [1 1] and padding [1 1 1 1]



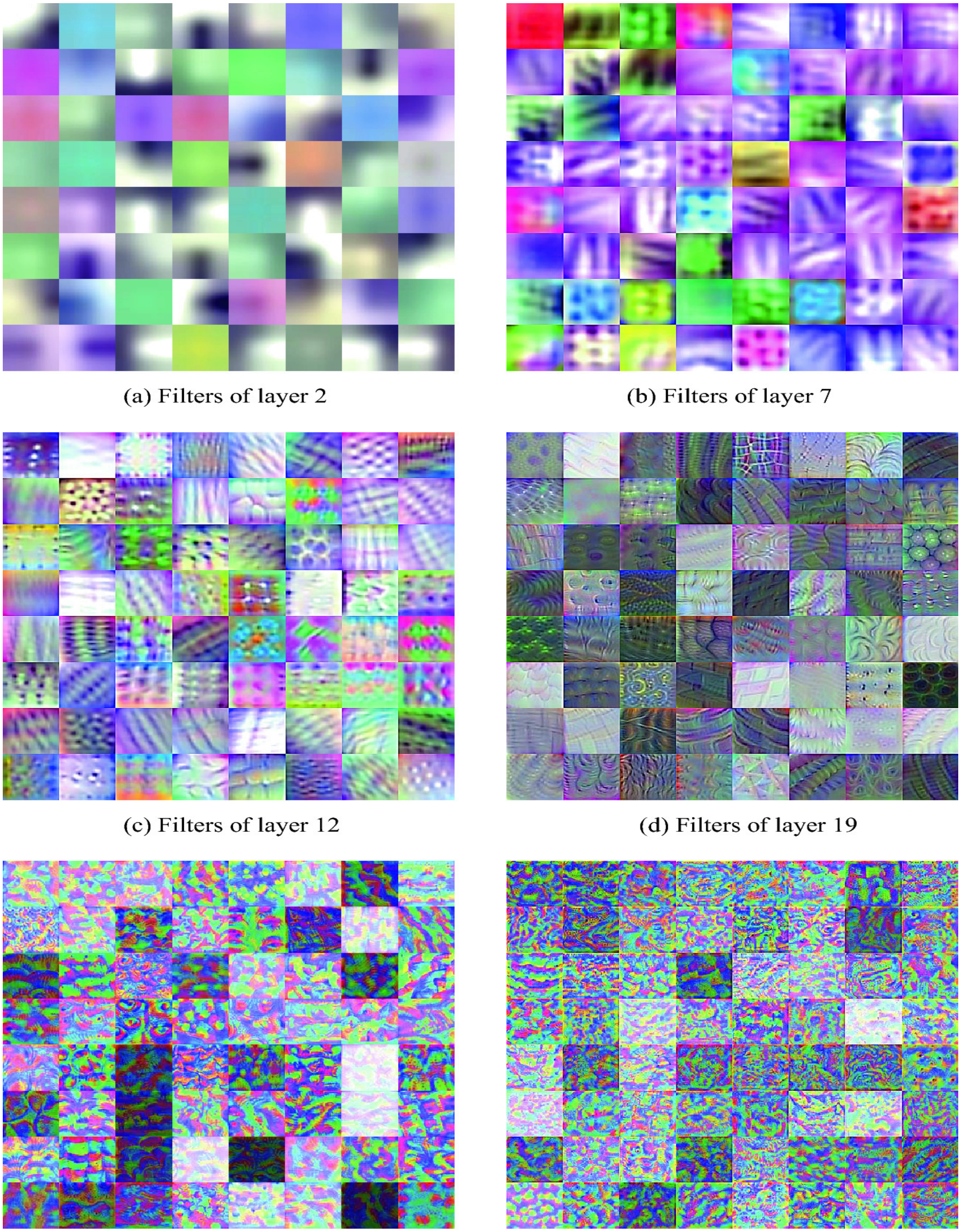
31	'relu5_3'	ReLU	ReLU
32	'pool5'	Max Pooling	2x2 max pooling with stride [2 2] and padding [0 0 0 0]
33	'**fc6**'	Fully Connected	4096 fully connected layer
34	'relu6'	ReLU	ReLU
35	'drop6'	Dropout	50% dropout
36	'**fc7**'	Fully Connected	4096 fully connected layer
37	'relu7'	ReLU	ReLU
38	'drop7'	Dropout	50% dropout
39	'**fc8**'	Fully Connected	1000 fully connected layer
40	'prob'	Softmax	softmax
41	'output'	Classification	crossentropyex with 'tench' and 999 other classes

VGGNet shows that the depth of the network is a critical component for good performance. The number of filters (depth) increase from 64 to 512 as it goes deeper into the network. The consecutive use of 3 × 3 convolutions has the effect of causing more nonlinearity as more than one ReLU functions have been applied at each stage of convolutions.

Another advantage of using consecutive convolutions is the increasing size of the receptive field. This is because two consecutive 3 × 3 convolutions have the effective receptive field of a single 5 × 5 convolution, while three stacked 3 × 3 convolutions have the receptive field of a single 7 × 7 one [7].

9.8.2 Filters of the Convolution Layers

To validate a CNN, it’s valuable to inspect and examine the internal structure of the network. Figure 9.25 shows the first 64 pre-trained filters from 6 of the 16 layers of VGG16 net. It can be observed that the filters typically capture the blobs, edges, regularity, directionality and other features of an image. Filters in early layers (layers 2 and 7) typically focus on pixels, blobs and edges, and as the network goes deeper, the filters become coarser, where low-level features are organized into shapes and parts of objects.



(a) Filters of layer 2

(b) Filters of layer 7

(c) Filters of layer 12

(d) Filters of layer 19

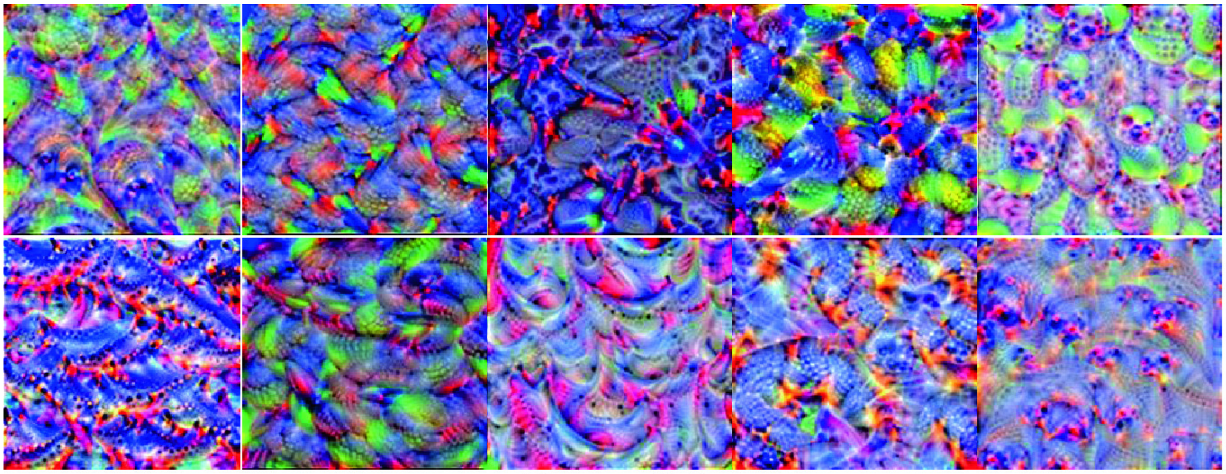
(e) Filters of layer 26

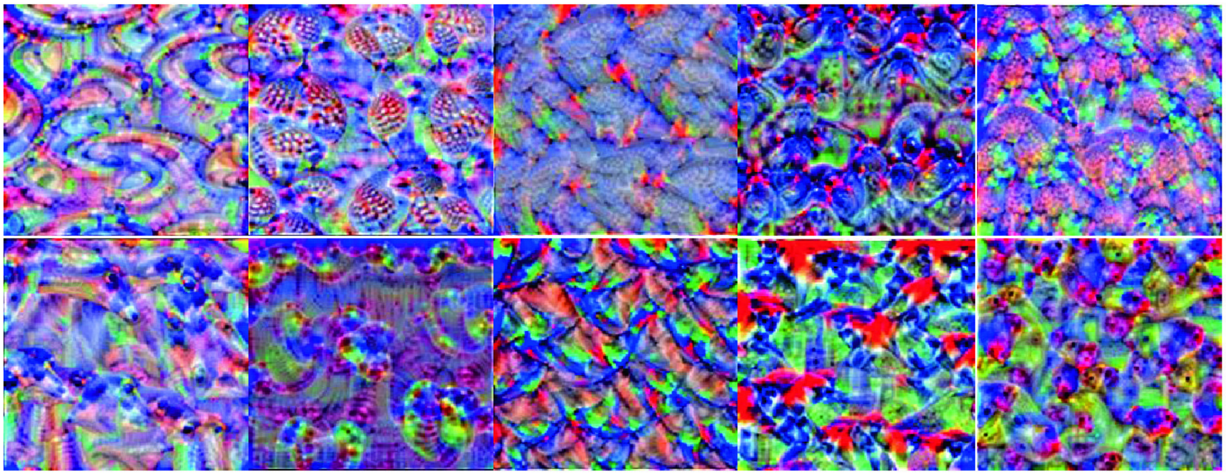
(f) Filters of layer 30

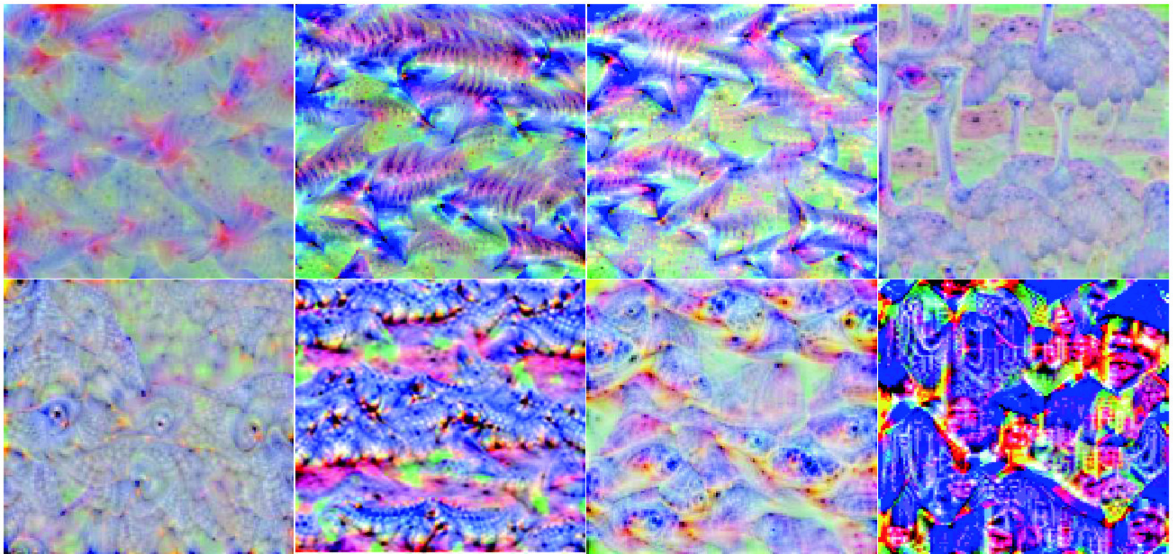
Fig. 9.25 Pre-trained filters of 6 of the 13 VGG16 convolution layers

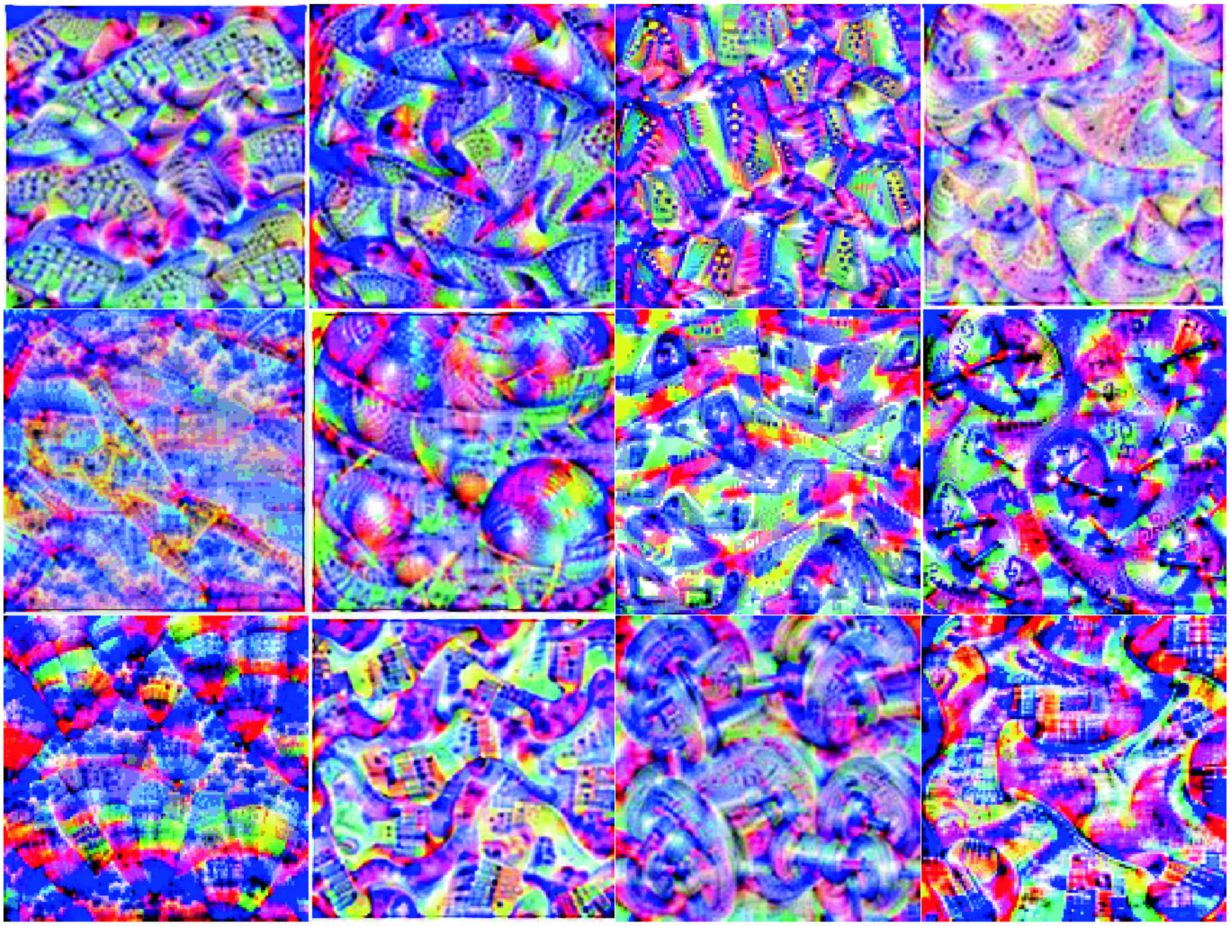
9.8.3 Filters of the Fully Connected Layers

If the convolution layers try to capture the texture and shape features from images, the fully connected layers attempt to organize the features into objects. Figure 9.26a, b shows the first 10 channels of layer ‘fc6’ (layer 33) and ‘fc7’ (layer 36), respectively. This phenomenon of learning objects is more obvious in the final fully connected layer where the class names are known (using Matlab code: net.Layers(end).Classes). Figure 9.26c shows 20 channels from ‘fc8’ (layer 39) with class names as follows: goldfish, tiger shark, hammerhead shark, ostrich, great gray owl, African crocodile, mud turtle, academic gown computer keyboard, cowboy boot, accordion, cowboy hat, crane (machine), crash helmet, ambulance, analog clock, balloon, dining table, dumbbell, acoustic guitar.


(a) Layer ‘fc6’


(b) Layer ‘fc7’





(c) Layer ‘fc8’

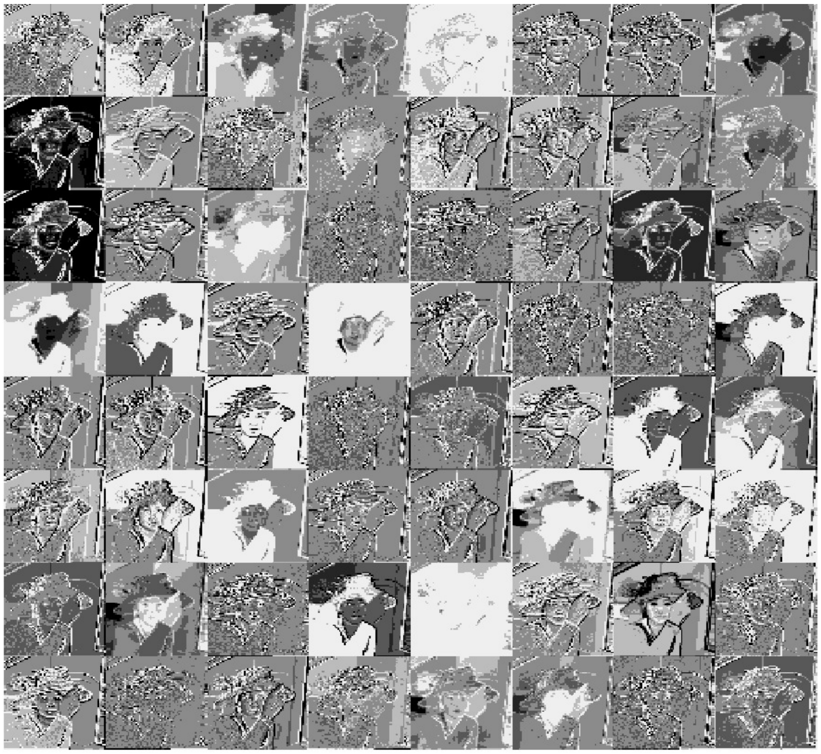
Fig. 9.26 Filters of the fully connected layers

It can be observed from Fig. 9.26c that the signature patterns and shapes of these objects are well captured. More interestingly, the filters have learnt multiple copies of the same objet to adapt to changes.

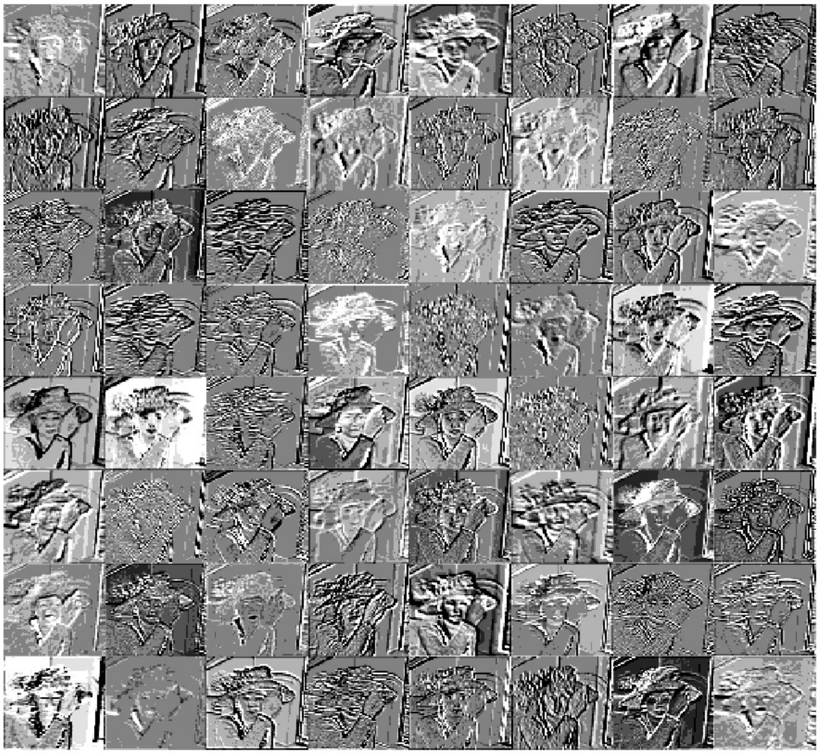
9.8.4 Feature Maps of Convolution Layers

To further understand the implementation of a CNN, it is more revealing to examine the convolution process by using a real input image. A CNN is basically a combination of two components: *convolution layers* and *fully connected layers*. The convolution layers are responsible for feature extraction, and the fully connected layers are responsible for the classification. The convolution component is the main powerhouse of a CNN model. Given an input image, the different filters in the convolution layers detect features such as edges, blobs and regions, which represent eyes, ears, legs, feather, leaves, water, sand, windows, and wheels. The CNN doesn’t know if they are eyes, ears, legs, etc. It learns to detect them as features by memorizing a lot of them in the input images. The fully connected layers learn how to use these features to classify the images into different classes.

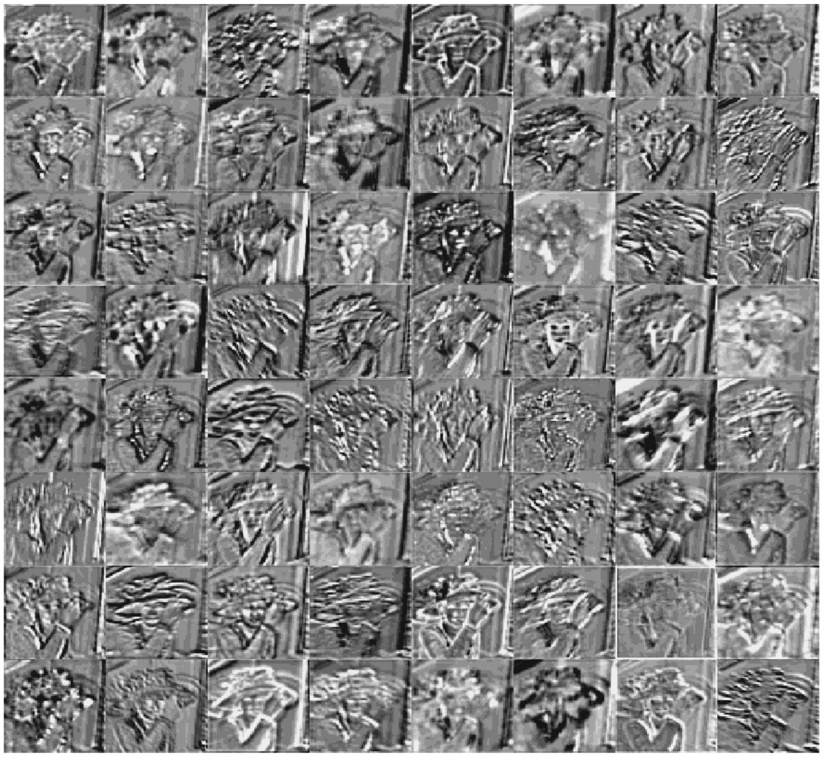
One important thing to note is that due to the nature of consecutive convolution and pooling, the features leant from the CNN is evolutional or hierarchical. In other words, the CNN is a learning process from fine features to coarse features. The convolution layers learn such fine to coarse features by building on top of each other. The first layers detect edges, the next layers combine them to detect shapes, and the following layers merge shape information to infer objects such as eyes, ears and legs. Figure 9.27 demonstrates this evolutional process by showing the first 64 feature maps from each of the four blocks of the lady image in Fig. 3.2: conv1_2, conv2_2, conv3_3, conv4_3 and conv5_1. It can be observed that the prominent features (hat, face) in the image are well captured by the filters. It's interesting to find that each filter captures different aspects of the image such as the surface and outline of the hat, the face, eyes, clothe, hand and background. It can also be seen from the figure that the features from the first block of layers (conv1_1) are sparse and show the fine details/edges of the image, and as the network goes deeper, the features become coarser and coarser due to pooling, until the final block of layers where only the most prominent features (e.g., eyes, mouth) in the input image survive.



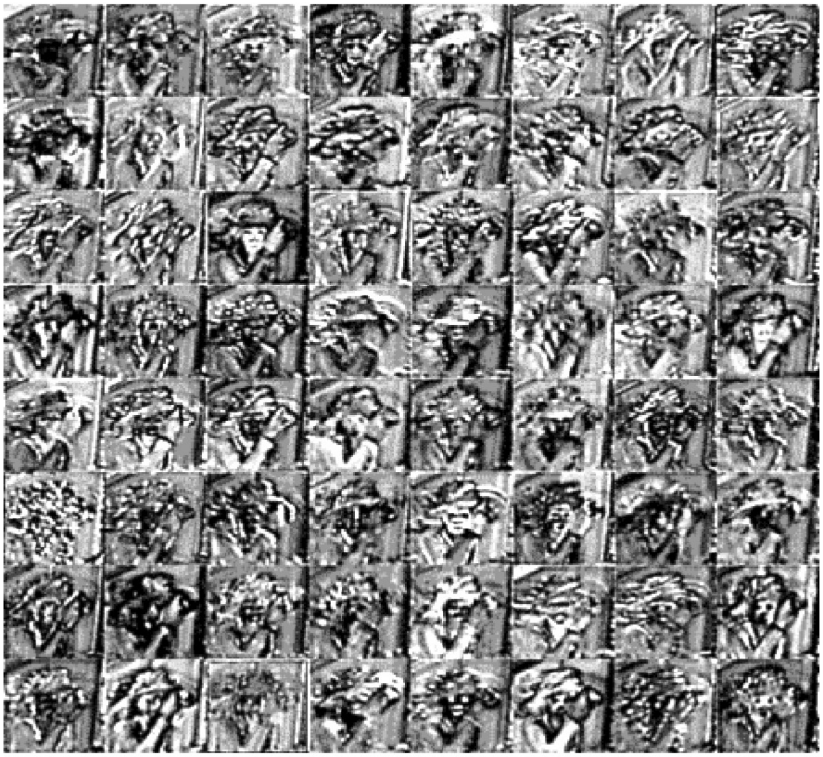
(a) conv1_2



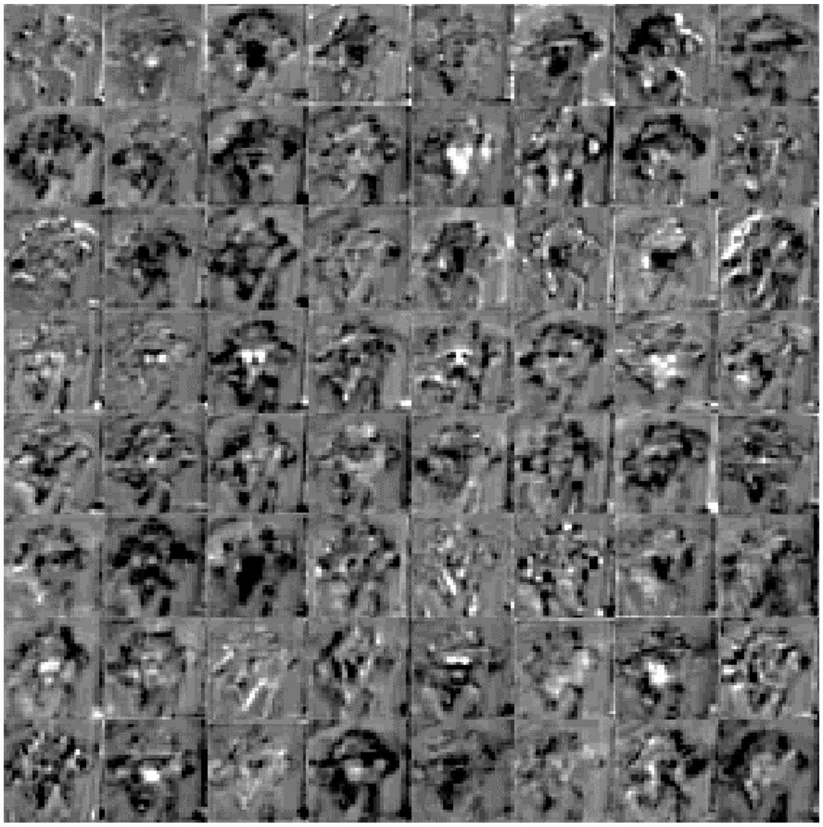
(b) conv2_2



(c) conv3_3



(d) conv4_3



(e) conv5_1

Fig. 9.27 Feature maps from different convolution layers of VGG16

Figure 9.28 uses heat maps of the channels from each of the blocks to demonstrate how the prominent features of a face image have been tracked by the network. It can be seen that the eyes of the face are well tracked by the network, and as the network goes deeper, the face pattern becomes coarser and coarser until it's completely blurred.

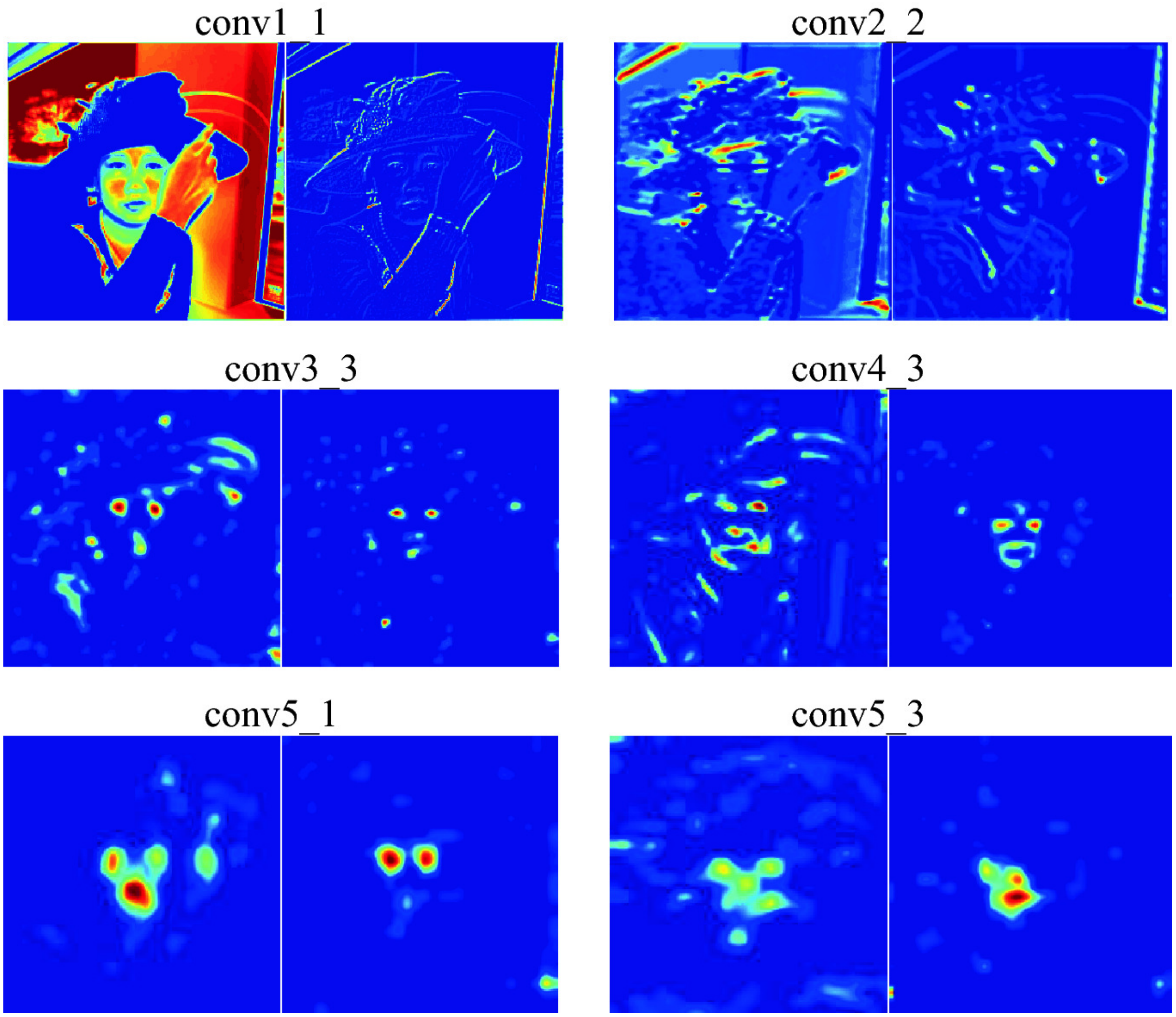


Fig. 9.28 Channels from each of the five blocks of VGG16 net

Although conventional feature extraction methods can also extract similar kind of coarse features for classification, a CNN model can combine many types of such kind of coarse features to form a set of more powerful features which lead to more accurate classification.

Overfitting is a common problem on image classification because usually there are too few training samples, resulting in a model with poor generalization performance. One solution to overfitting is to use *data augmentation*. Data augmentation is a method to generate more training data from the current training set. It is an artificial way to boost the size of the training set, reducing overfitting.

Data augmentation is typically done by data transformations and processing, such as rotation, shifting, resizing, adding noiseand contrast change. It should be noted that data augmentation is only performed on the training data, not on the validation or test set.

9.8.5 Matlab Implementation

Matlab's Deep Learning Toolbox™ has a number of built-in networks which are pre-trained on ImageNet, including ResNet-50, AlexNet, GoogleNet, VGG-16 and VGG-19. In this section, we show how to use VGG-16 for image classification [8]. The Matlab program at the end of this section provides a step-by-step implementation of a CNN.

- It first loads the network into memory, display its structure and a convolution layer. Users can choose a different network and a different layer to display.
- It then loads the images into memory, divides them into training and testing sets and normalizes the images into required size.
- Next, it extracts the training features from the network by using the `activations` function which takes the input images, passes them through the network, collects the features at the fully connected layer and stores them in a cell array or matrix. Because the network has been pre-trained, the feature extraction only requires a single pass through the net.
- It then uses the extracted features of the training set to train a SVM classifier.
- Finally, the trained SVM is used to predict the label of a new image from the testing set.

Training images needs to be first categorized and organized into subfolders. The name of each subfolder represents the label of the image category, e.g., *bird*, *people*, *tiger,* etc. For example, if your images are under the folder of 'C:\...\imgCategories', and the images have been organized into subfolders: 'cat1', 'cat2', ..., 'cat*n*' under imgCategories, you may simply copy the full folder path of your images from the address bar of the Windows File Explorer and assign it to a variable using Matlab function `fullfile`: myFolder = fullfile ('C:\...\imgCategories').

The following code can be run line by line or block by block in Matlab command line, or you may save the entire code into a *m* file such as *exampleCNN.m* and run it in Matlab IDE using the 'Run' button at the top.

```
% Load the Pretrained VGG-16 network

   net = vgg16();

   net.Layers;  %inspect the network architecture

% Extract and Display Feature Maps

   % Extract the filters for convolutional layer 1: conv1_1
   filter1 = net.Layers(2).Weights;
   filter1 = mat2gray(filter1);
   filter1 = imresize(filter1,5);
   figure
   montage(filter1)
   title('First convolutional layer filters')

% Prepare Training and Testing Image Sets

   % Loading images into an imageDataStore Object, e.g., load images from folder:
   C:\...\imgCategories

   myFolder = fullfile('C:\...\imgCategories');

   categories = {'cat1', 'cat2',…, 'catn'};

   imstore = imageDatastore(fullfile(myFolder, categories), 'LabelSource',
   'foldernames');

   % Split the dataset into training set (30%) and testing set (70%)
   [trainingSet, testingSet] = splitEachLabel(imstore, 0.3, 'randomize');

   % Normalise Dataset images to required size and RGB format
   imSize = net.Layers(1).InputSize;
   normTrainingSet = augmentedImageDatastore(imSize, trainingSet,
   'ColorPreprocessing', 'gray2rgb');
   normTestingSet = augmentedImageDatastore(imSize, testingSet,
   'ColorPreprocessing', 'gray2rgb');

   % Extract features from the last fully connected layer
   fcFeature = 'fc8';
   trainingFeatures = activations(net, normTrainingSet, fcFeature, ...
           'MiniBatchSize', 32, 'OutputAs', 'columns');

% Train a Multiclass SVM Classifier Using the Extracted Features

   % Get training labels from the trainingSet
   trainingLabels = trainingSet.Labels;
   classifier = fitcecoc(trainingFeatures, trainingLabels, ...
    'Learners', 'Linear', 'Coding', 'onevsall', 'ObservationsIn', 'columns');

% Test the SVM Classifier on New Images

   newImage = imread(fullfile(myFolder, 'cat1', 'image001.jpg'));

   % Normalise the new images.
   normImage = augmentedImageDatastore(imSize, newImage, 'ColorPreprocessing',
   'gray2rgb');

   % Extract image features using the CNN
   imFeatures = activations(net, normImage, fcFeature, 'OutputAs', 'columns');

   % Make a prediction using the classifier
   label = predict(classifier, imFeatures, 'ObservationsIn', 'columns')
```

9.9 Summary

ANN is a powerful nonlinear classifier by layering a number of linear classifiers. However, the usage of ANN in the past has been hindered by two aspects. First, it does not appear to have the transparency as in other machine learning tools such as the Bayesian classifier, DT and SVM. It is often regarded as a black box-type classifier. Second, it suffers from high computation curse due to the complex optimization involves the combination of multiple layers and a large number of nodes. However, these issues have been overcome since the introduction of CNN and more powerful computing hardware and software. Furthermore, CNN has also extended the traditional ANN from network and computing (fully connected layers) to including sensors (the convolution layers). This means that CNN is a simulation of a complete human visual system. The downside of a CNN though is the high number of parameters which need to be determined empirically.

The introduction of CNN is a significant development to ANN and machine learning as a whole. This is because the convolution layers can be independent of the ANN, and they can be connected to any other machine learning tools such as the Bayesian classifier, DT and SVM. With the Matlab Deep Learning Toolbox and other powerful tools, the internal structure and learning process of a CNN can now be studied at the same transparent level as other machine learning tools. Because of the transparency, the computation and learning process can now be controlled using a step-by-step approach. Due to the development of CNN, ImageNet and the ever increasing computation power, the future of image data mining has become much brighter.

9.10 Exercises

1. Build a simple ANN. Visit the following website: https://au.mathworks.com/matlabcentral/fileexchange/22010-a-very-simple-and-intuitive-neural-network-implementation and download both the *neural.m* and *mendez.m* into your Matlab working folder. Clear the Matlab workplace with a command ‘`clear`’ and use ‘`clc`’ command to clean the command window whenever necessary.
   - Make sure you understand that the *mendez.m* is to make two lists:
     - Attributes[ ] is the list of feature vectors $\mathbf{x}_i$
     - Classifications[ ] is the list of classes t_i

  - Each row of [Attributes, Classifications] makes a training sample ($\mathbf{x}_i$, t_i).
- Next, go through the code of *neural.m* line by line, make sure you understand the meaning of each variable and they match the BP algorithm in Sect. 9.6.4. Figure out the dimensions of each variable and note them down. (Tips: W and U are the weights of the second layer and last layer respectively; '*' is the linear algebraic product of two matrices while '.*' is the elementwise multiplication of two matrices).
- Next, remove the first code line '`function m=neural()`' from the *neural.m* file and add an 'end' as the very last line of code in the file. Run the *neural.m* file by clicking the 'Run' button.
- Now, examine each of the variables in the Workspace of Matlab and do the dimensions of each of the variable match those in your notes?
- Try different values of *n* and epochs to see what would happen.
- Try a different data file to examine the code and results again.

2. Learn the fundamentals of convolution theories. Visit the following website to download the file *practical-cnn-2017a.tar.gz* with both code and data (under the TOC): https://www.robots.ox.ac.uk/~vgg/practicals/cnn/index.html. Unpack the zip file to a Matlab working folder. Open the '*exercise*1.*m*' file in Matlab.

- Clear the Matlab workplace with a command '`clear`' and use '`clc`' command to clean the command window whenever necessary.
- Change '`w = randn(5,5,3,10,'single')`' to '`w = randn(5,5,3,12,'single')`'.
- Can you visualize the 12 4D filters `w` in a 3D diagram? Tip: align the 5 × 5 × 3 volumes in rows.
- Set a break point at line 14 by clicking the 'Breakpoint' button at the menu bar.
- Run the exercise1.m file by clicking the 'Run' button, the running program stops at the red break point.
- Press the 'Step' button besides the 'Continue' button once at a time.
- At each step of running, study the values and dimensions of each output variable at the Matlab Workspace, relate them to the convolution theories discussed in Sect. 9.7. Make sure the dimensions match your understanding.
- At each step of the running, observe the output results with full screen view. Record and close the graph after they have made sense to you.

- Why the output of the manually designed filter looks very different from those of random generated filter?
- What's the difference between the two volume filters `w` and –`w` in Part 1.2: Nonlinear gating (ReLU) ? Tip: observe the different edges captured by the two filters on each of the plots.
- Change the *stride*, *pad*, *pooling* and other variable values in the code to observe the change of the results and dimensions of corresponding variables.
- Try different images and record your results, write a report to describe your findings.

3. Classify an image dataset using pre-trained networks. Visit the following Matlab website: https://au.mathworks.com/help/vision/examples/image-category-classification-using-deep-learning.html. Download the image files from the following url: https://download.tensorflow.org/example_images/flower_photos.tgz, and unzip it into a folder. Next, copy the path to the downloaded image folder from your File Explorer address bar, e.g., C:\Documents\matlab\images\flower_photos and name the path as imageFolder in Matlab command line; e.g., at Matlab command line, type `imageFolder = ‘C:\Documents\matlab\images\flower_photos`’. Clear the Matlab workplace with a command ‘`clear`’ and use ‘`clc`’ command to clean the command window whenever necessary.
   - At command line, run: `imds = imageDatastore(imageFolder, 'LabelSource', 'foldernames', 'IncludeSubfolders',true)`

     .
   - Next, double click the ‘`imds`’ variable in Matlab Workspace, examine both the ‘`File`’ and ‘`Labels`’ arrays inside ‘`imds`’.
   - Next, at command line, run ‘`imshow(imds.Files{1})`’ to show the first image in the `imageDatastore`. Run ‘`imshow(imds.Files{n})`’ to show any image *n* in `imageDatastore`.
   - To show images under a particular label or class, use the following two command lines (k < = n): daisy = find(imds.Labels = = 'daisy' , n); %find n images into a vector daisy [ ] ; imshow(readimage(imds,daisy(k))). E.g., roses = find(imds.Labels = = 'roses' , 10); imshow(readimage(imds, roses(5))).
   - Now, follow the rest of the website, copy the code line by line and run each line at the command line. Observe and examine the output variables in the Workspace at each step of the running.

- Double click and examine the variable ‘`trainingFeature`’ in the Workspace, what’s the dimensions of each feature vector? Tip: double click the variable ‘`net`’ in Workspace and examine the layer 175: ‘`FullyConnectedLayer`’ in the ‘`net.Layers`’.
- Double click and examine the confusion matrix variable `confMat`, how to interpret the confusion matrix and do the figures in the matrix make sense to you? Tip: there are 70 images in each of the classes in the `testSet`.
- Try different learners such as *svm*, *kernel*, *knn*, *linear*, *naivebayes and tree*.
- Try a different network such as *vgg*16 using the same procedure as the *resnet*50, record your results and write a report to describe your findings.

4. Build a new CNN from scratch. Visit the following Matlab website: https://au.mathworks.com/help/deeplearning/examples/create-simple-deep-learning-network-for-classification.html. Clear the Matlab workplace with a command ‘`clear`’ and use ‘`clc`’ command to clean the command window whenever necessary. Now, follow the instructions of the website, copy the code block by block as shown in the gray areas on the web page and run each block of the code at the command line. Observe and examine the output variables in the Workspace at each step of the running. At the `trainNetwork` line, watch the progress of the training on the graph and wait until the four epochs of training finish. You can also copy all the code from the gray areas and combine them into a single Matlab program file, e.g., ‘`buildaCNN`’. Next, you can set a breakpoint at the first line of the program and run the program step by step.

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10. Image Annotation with Decision Tree

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We may be different, but we all share a common ancestor.

10.1 Introduction

The machine learning methods we discussed so far are typically black box type of classifiers, in the sense that the decisions they make are not transparent to users. In other words, these models are neither interpretable nor comprehensible to users. Another issue with these methods is that their decision-making process is a one path or non-conditional process, which means that there are no alternatives when the original decision was not appropriate.

Human beings, however, tend to make decisions in a step by step and hierarchical way. For example, when we look at an image with complex patterns, we tend to first organize the different patterns into groups using the most prominent attribute or feature, and then go further to identify the objects we are interested and analyze them in details using another types of attributes or features. This kind of hierarchical and step-by-step analysis is repeated until we are satisfied.

In machine learning, this kind of intuitive, hierarchical and step-by-step analysis can be modeled using a *decision tree* or DT. DT is a ‘divide-and-conquer’ approach to learn classification from a set of training samples. A DT is built from a training dataset by recursively dividing the dataset into several subsets based on the possible values of a selected attribute. The procedure starts at the root node and continues until all the instances of a subset have the same class label or there is no other attribute left to divide them.

A DT is typically built upside down with its root at the top, Fig. 10.1 shows an example of a DT on image classification [1, 2]. On the DT, an *internal node* (with outgoing branches) is labeled with an input feature or a selected attribute. The branches coming from a node are labeled with each of the possible values of the selected attribute. Each *leaf node* (without outgoing branch) of the tree is labeled with a class or a probability distribution over the classes.

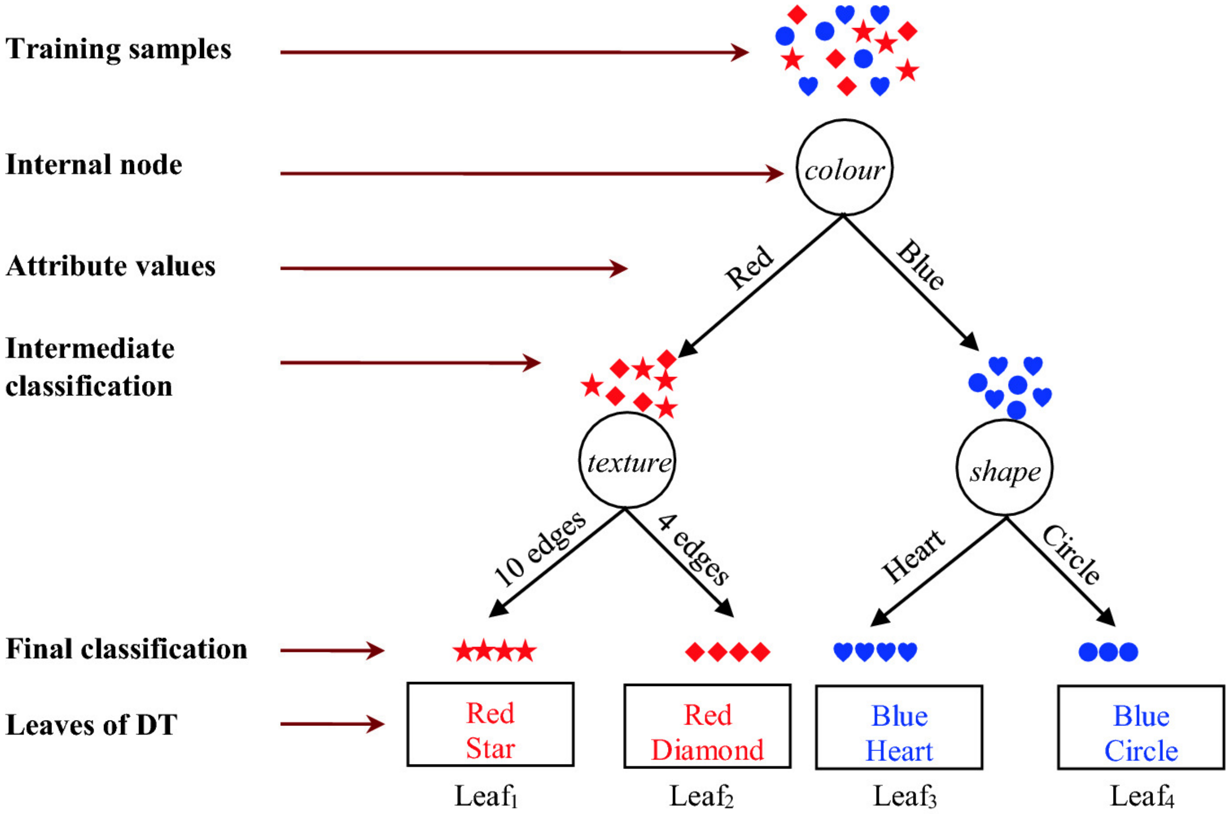

Training samples
Internal node
Attribute values
Intermediate classification
Final classification
Leaves of DT
colour
Red
Blue
texture
shape
10 edges
4 edges
Heart
Circle
Red Star
Red Diamond
Blue Heart
Blue Circle
Leaf1
Leaf2
Leaf3
Leaf4

Fig. 10.1 DT for image classification

The following is a list of terminologies associated with a DT:

1. *Root Node*. It represents the entire dataset, and it is to be divided into two or more homogeneous sets.

2. *Internal Node/Decision Node*. A node which can be split into two or more subnodes.

3. *Leaf Node/Terminal Node*. A node which cannot be split into subnodes.

4. *Branch/Subtree*. An edge coming out of a node is called a branch, and the section under a branch is called a subtree.

5. *Parent and Child Node*. A node which is divided into subnodes is called parent node, and a node under a parent node is called a child node.

6. *Splitting*. A process of dividing a node into two or more subnodes.

7. *Pruning*. A process of removing unwanted subnodes and branches. It is the opposite process of splitting.

Depending on the type of attribute values, a DT can be either a *classification tree* or a *regression tree*. A classification tree takes a *discrete* set of attribute values and the predicted outcomes are the class labels to which the data belong, while a regression tree takes *continuous* attribute values and the predicted outcomes are real numbers.

Quinlan [3] first formulated a DT algorithm called ID3 (Iterative Dichotomiser 3) which only accepts discrete features. ID3 is later extended to C4.5 [4] which accepts both discrete and continuous features. In the following, we describe the characteristics of different types of DTs.

10.2 ID3

The ID3 algorithm begins with a training dataset T and an attribute set A as the root node. It then checks every unused attribute of the attribute set A and calculates the entropy $info(T)$ (or information gain $IG(T)$) of that attribute. It then selects the attribute which has the smallest entropy (or largest IG) value. The set T is then split to subsets by the selected attribute. The above procedure is repeated on each subset until there is no unused attribute or the subset is homogeneous (all instances in the subset are from the same class). ID3 only accepts data with discrete or nominal values. The algorithm of the ID 3 can be summarized as the following.

```
ID3 ($T$, $A$) {
1. Create a root node Root.
2. If all instances in Root belong to the same class $C$ or $A$ is empty
    2.1. Stop and return Root with label = $C$
3. Else
    3.1. Select an attribute $A_i$ with possible values $A_i^1, A_i^2, \ldots, A_i^n$
    3.2. Partition $T$ into subsets $T_1$, $T_2$, ..., $T_n$ according to the values of $A_i$.
    3.3. For each $T_j$,
        3.3.1. Add a new branch under Root to connect $T_j$ with Root.
        3.3.2. If $T_j$ is homogeneous,
            3.3.2.1. Then, below this new branch add a leaf node with label = $A_i^j$.
        3.3.3. Else, below this new branch add the subtree ID3 ($T_j$, A – {$A_i$}).
}
```

This algorithm, in fact, is a *general DT algorithm*. Central to a DT algorithm is step 3.1, which requires an attribute selection criterion or a splitting criterion. This splitting criterion determines how the tree looks like and the performance of a DT as well.

10.2.1 ID3 Splitting Criterion

Because the split criterion is critical to the success of a DT, variety of criteria have been proposed. The rule is to select an attribute which reduce the maximum amount of uncertainty in data, because the higher the uncertainty in data is, the more difficult it is to predict the class of an instance. Intuitively, this is equivalent to selecting the most useful or most telling attribute to make a decision. Information gain is a statistical measurement of reducing the uncertainty in data. Therefore, in ID3, the attribute which gives the highest information gain, is selected as the test attribute.

Information gain of an attribute measures how much information we can save or gain if it is selected to split the training set. Mathematically, it is measured as the *difference* between information needed to classify an instance before and after the attribute splits the training dataset.

Information before the splitting:

- Given a training set $T = \{(\mathbf{x}_1, y_1), (\mathbf{x}_2, y_2), ..., (\mathbf{x}_N, y_N)\}$, where $\mathbf{x}_i$ is the data or sample, y_i is the class label for $\mathbf{x}_i$, and $y_i \in \{C_1, C_2, ..., C_m\}$.
- Instances in T are characterized with the set of attributes $A = \{A_1, A_2, ..., A_n\}$.
- Each attribute A_i has possible values $A_i^1, A_i^2, \ldots, A_i^{n_i}$.
- The probability that an instance of T belongs to class C_j is given as,

$$P_j = \frac{||C_j||}{||T||} \tag{10.1}$$

where $|| C_j ||$ is the number of instances in C_j.

To classify an instance in T, the information needed (or the *entropy*) is given as

$$info(T) = -\sum_{j=1}^{j=m} P_j \times \log P_j \tag{10.2}$$

The negative sign before the sum is to make the information a positive value, this is because $P_j \leq 1$ and $\log P_j \leq 0$. Generally, *entropy* refers to *disorder* or *uncertainty* in a dataset; a smaller *info*(T) means a more predictable class. This is consistent with our understanding of information. An event with higher chance of occurrence carries little to zero information such as sunrise/sunset, while an event with less chance of occurrence carries more information such as rain/sunshine. In English language, frequent words such as 'a', 'the', 'this' carry almost zero information, while rare words such as 'Delphi', 'nirvana', 'dialectics' carry a lot of information. In terms of a dataset, a data source (or a class) with higher probability value carries less information than a data source with lower probability value. Therefore, a DT learning algorithm attempts to split T into subsets so that the expected information needed is minimized after a split.

Information after the splitting:

Suppose, an attribute A_i has n_i nominal values such as $A_i^1, A_i^2, \ldots, A_i^{n_i}$. If attribute A_i is selected at the current node, it splits the training set T into $T_i^1, T_i^2, \ldots, T_i^{n_i}$. After the splitting, the *expected information* is calculated as,

$$E(A_i) = \sum_{j=1}^{j=n_i} \frac{\|T_i^j\|}{\|T\|} \times info(T_i^j) \tag{10.3}$$

The information gain is the difference between info(T) *and* $E(A_i)$:

$$IG\,(A_i) = info\,(T) - E\,(A_i) \tag{10.4}$$

The attribute which gives the highest *IG* is chosen for splitting the training set. Because *info*(T) in (10.2) is the same for all attributes, the attribute A_i which gives the highest gain has lowest expected information $E(A_i)$. Therefore, the attribute which leads to the least expected information is selected.

10.3 C4.5

C4.5 build a DT from a training dataset in the same way as ID3, except C4.5 has made a number of improvements to ID3:

- Using *gain ratio* (GR) instead of IG to build a better DT.
- Accept both *continuous* and *discrete* attributes. For continuous attributes, C4.5 creates a threshold and then splits the list into those whose attribute value is above the threshold and those that are less than or equal to it.
- Handling *incomplete data* points. C4.5 allows attribute values to be marked as '?' for missing data.
- Apply different *weights* to the attributes.
- Overcome *over-fitting* problem by a bottom-up *pruning*. C4.5 goes back through the tree once it's been created and remove branches that are deemed unnecessary by replacing them with leaf nodes.

10.3.1 C4.5 Splitting Criterion

In ID3, IG is used as splitting criterion. However, the disadvantage of using IG as splitting criterion in ID3 is that it favors the highly branching attributes, that is, the attributes which have a large number of possible values. Let us think about the extreme case where the instance ID is used an attribute. Say, it is denoted as A_{ID}, and it has a distinct value for each instance. If A_{ID} is used to split the dataset T, each subsequent subset will have only one instance. According to (10.3), $E(A_{ID})$ is zero because each subset has zero entropy (information). Therefore, $IG(A_{ID})$ will be the highest and A_{ID} will be selected. However, such a selection tells nothing about the nature of the decision and leads to no classification at all. To reduce the effect of high branching factor on information gain, a modified measure called *gain ratio* (GR) or *normalized IG* is proposed by Quinlan in C4.5. The gain ratio is defined as IG normalized by split information [4],

$$GR(A_i) = \frac{IG(A_i)}{splitInfo(A_i)} \tag{10.5}$$

where $splitInfo(A_i)$ is calculated based on the proportion of each subset resulted from the split by using attribute A_i, regardless the class information inside each subset. Specifically, it is defined as,

$$splitInfo(A_i) = -\sum_{j=1}^{j=n_i} \left(\frac{\left\|T_i^j\right\|}{\|T\|} \times \log\left(\frac{\left\|T_i^j\right\|}{\|T\|} \right) \right) \tag{10.6}$$

It can be observed that the higher the number of attribute values of A_i, the larger the magnitude of $splitInfo(A_i)$ and the lower its gain ratio. Therefore, by using gain ratio, the high branching behavior is penalized.

10.4 CART

In machine learning, a DT can be either *classification tree* or a *regression tree*. For a classification tree, the predicted outcome is a class such as tree, tiger and water, while for a regression tree, the predicted outcome is a real number, such as stock price and queueing time.

CART stands for classification and regression tree, and it is an umbrella term used to cover both classification DT and regression DT. It was first introduced by Breiman et al. in 1984 [5]. A CART tree is a *binary* DT that is constructed by splitting a node into two child nodes repeatedly, beginning with the root node that contains the entire training data. The splits are done using the twoing criteria, and the obtained tree is pruned by cost–complexity technique. CART can handle both numeric and nominal attributes, and it can also handle outliers.

10.4.1 Classification Tree Splitting Criterion

A CART uses a splitting criteria called the *twoing criteria* for a classification tree, which is defined as (10.7):

$$\Delta i\left(t\right)=\frac{P_LP_R}{4}\left(\sum_{j=1}^{m}\left|p\left(j|t_L\right)-p\left(j|t_R\right)\right|\right)^2 \tag{10.7}$$

where

- t is the node to be split.
- $\Delta i(t)$ indicates the *impurity* of node t.
- P_L is the proportion of data split into the left node t_L and similar for P_R.
- $P_L = ||t_L||/||t||$ and $P_R = ||t_R||/||t||$, where t is the parent node of t_L and t_R, $||t||$ is the total number of data in node t.
- $p(j|t_L)$ is the proportion of data belonging to class j at the left node t_L.
- m is the number of classes in the training set.

The twoing criteria measures the difference between the two split nodes, and a split is achieved by maximizing the difference or $\Delta i(t)$.

Gini impurity can also be used to define a splitting criterion for a classification tree. First, the Gini index (GI) or GIs are computed for both the left split node t_L and right split node t_R, which are given in (10.8) and (10.9), respectively.

$$GI\left(t_L\right)=1-\sum_{j=1}^{m}\left[p\left(j|t_L\right)\right]^2 \tag{10.8}$$

$$GI\left(t_R\right)=1-\sum_{j=1}^{m}\left[p\left(j|t_R\right)\right]^2 \tag{10.9}$$

It can be observed from (10.8) and (10.9) that:

- A GI is maximum or $GI = (1 - 1/m)$ when records in a node are equally distributed among all classes, indicating maximum uncertainty.
- A GI is minimum or $GI = 0$ when all records in a node belong to one class, indicating minimum uncertainty.

A split is achieved by minimizing the *Gini impurity* which is defined as (10.10):

$$iG(t) = [(\|t_L\| \cdot GI(t_L) + \|t_R\| \cdot GI(t_R)] \,/\, \|t\| \tag{10.10}$$

The Gini impurity splitting algorithm works faster than twoing splitting algorithm; however, the twoing splitting criterion builds a more balanced DT and offers a superior performance on complex classification such as multiclass and noisy data.

10.4.2 Regression Tree Splitting Criterion

A regression tree is also called a prediction tree. Instead of identifying the class label for a training or unknown data, a regression tree predicts the likely target value of the data. For regression tree, the splitting criterion is typically given by the mean squared error (*MSE*). Given a training set $T = \{(\mathbf{x}_1, y_1), (\mathbf{x}_2, y_2), \ldots, (\mathbf{x}_N, y_N)\}$, where $\mathbf{x}_i$ is the data or sample and y_i is the target value for data $\mathbf{x}_i$. The splitting is determined by the two nodes which give the smallest *MSE*:

$$MSE = \frac{1}{N_L}\sum_{i=1}^{N_L}(y_i - \hat{y}_L)^2 + \frac{1}{N_R}\sum_{j=1}^{N_R}\left(y_j - \hat{y}_R\right)^2 \tag{10.11}$$

where

- N_L and N_R are the total number of samples falling into the left split node and the right split node, respectively.
- $\hat{y}_L$ and $\hat{y}_R$ are the prediction values for the left and right split nodes, respectively.
- $\hat{y}_L$ is typically given as the result of a *regression* from the data falling into the left node: $\hat{y}_L = \hat{f}_L(\mathbf{x}_i) = \boldsymbol{\beta}^T \cdot \mathbf{x}_i + b$.

A *regression* tree is basically a *piecewise linear* approximation of a dataset in space. Figure 10.2 demonstrates a contrast between a global linear regression and a regression tree approximation on a one variable dataset. In the figure, the green line shows an approximation from a global linear regression while the red lines represent a regression tree approximation of the same data. It can be observed that the regression tree gives a much closer approximation than the global linear regression model.

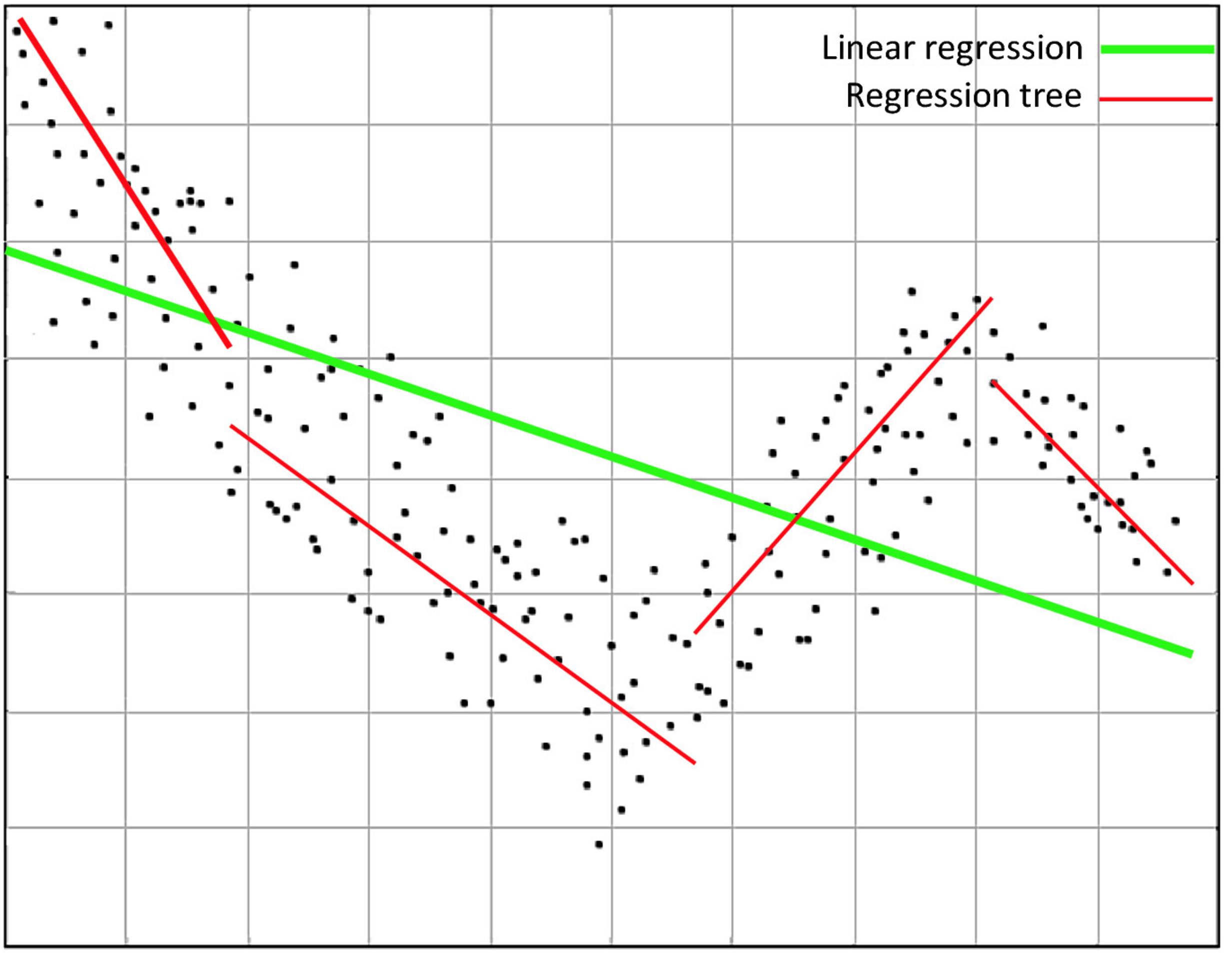


Fig. 10.2 Contrast between linear regression and regression tree

10.4.3 Application of Regression Tree

The prediction value $\hat{y}_L$ in (10.11) can also be estimated by the *mean* of the left node $\hat{y}_L = \frac{1}{N_L}\sum_{i=1}^{N_L} y_i$ (similar for $\hat{y}_R$). The tree built in this way provides a *piecewise constant* approximation of the data. The mean prediction model is a much faster method to build a regression tree.

Figure 10.3 shows a mean prediction tree for predicting median house price of California based on the two variables: latitude and longitude. The actual data map and the tree partitions are shown in

Fig. 10.4. It can be seen that the finer partitions are concentrated at the darker areas.

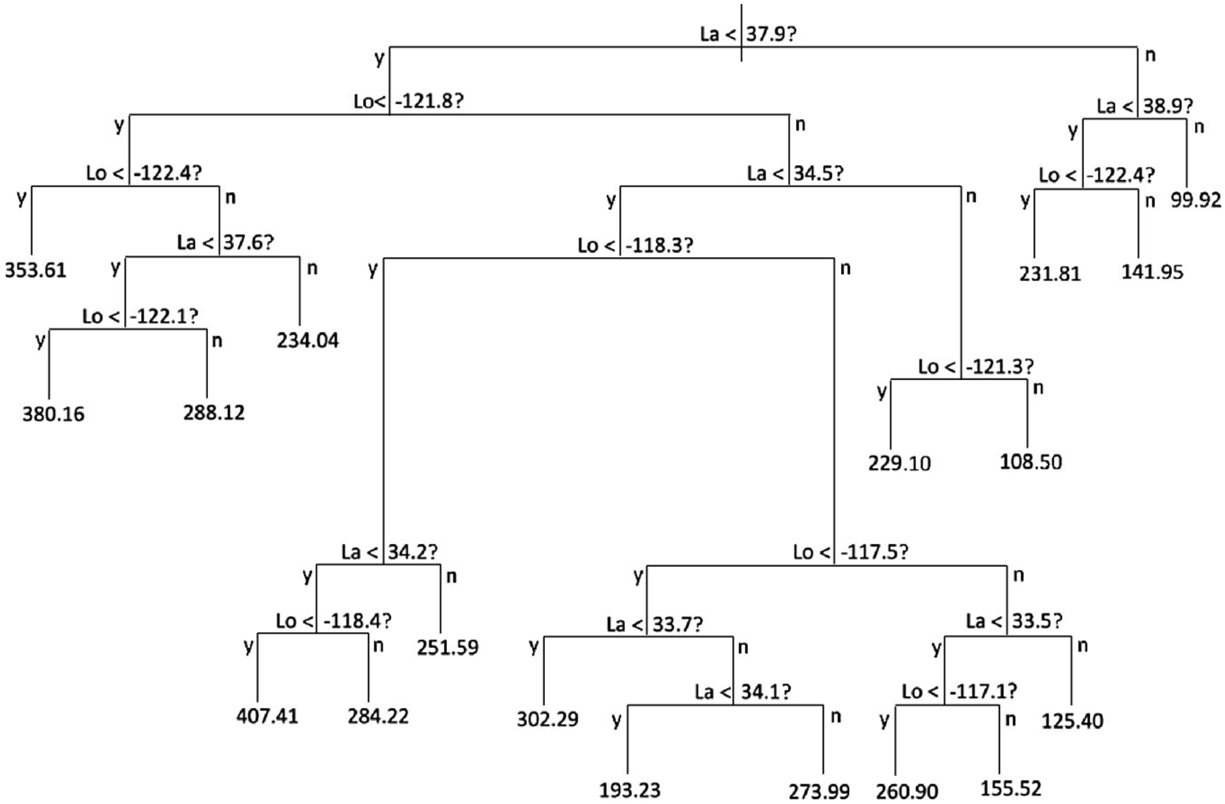

La < 37.9?
y
n
Lo< -121.8?
y
n
La < 38.9?
y
n
Lo < -122.4?
y
n
La < 34.5?
y
n
Lo < -122.4?
y
n
99.92
353.61
La < 37.6?
y
n
Lo < -118.3?
y
n
231.81
141.95
Lo < -122.1?
y
n
234.04
380.16
288.12
Lo < -121.3?
y
n
229.10
108.50
La < 34.2?
y
n
Lo < -117.5?
y
n
Lo < -118.4?
y
n
251.59
La < 33.7?
y
n
La < 33.5?
y
n
407.41
284.22
302.29
La < 34.1?
y
n
Lo < -117.1?
y
n
125.40
193.23
273.99
260.90
155.52

Fig. 10.3 Regression tree for predicting median house price ('000) in California from the geographic coordinates of Fig. 10.4. Legend: La = latitude, Lo = longitude, y = yes, n = no

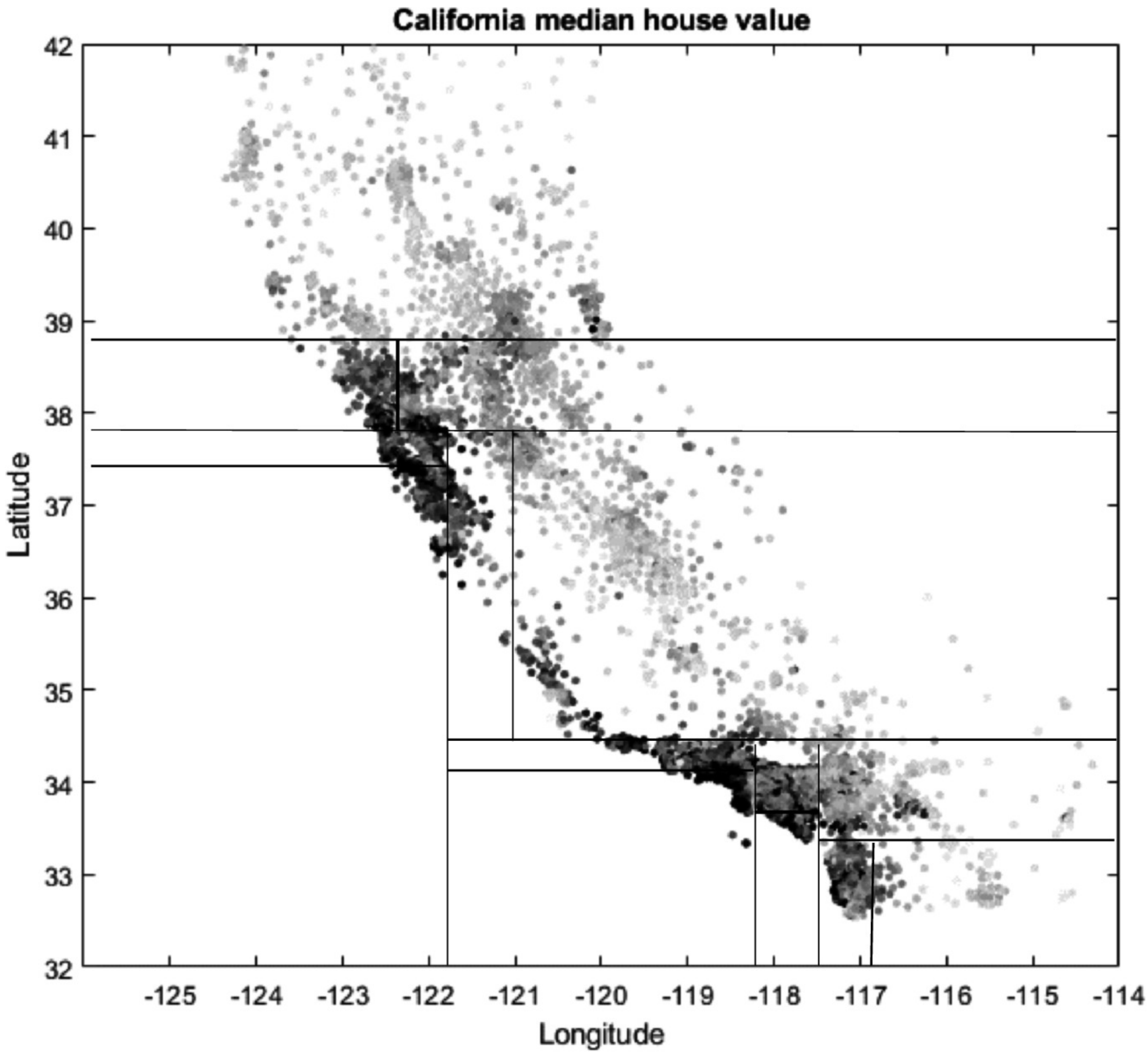


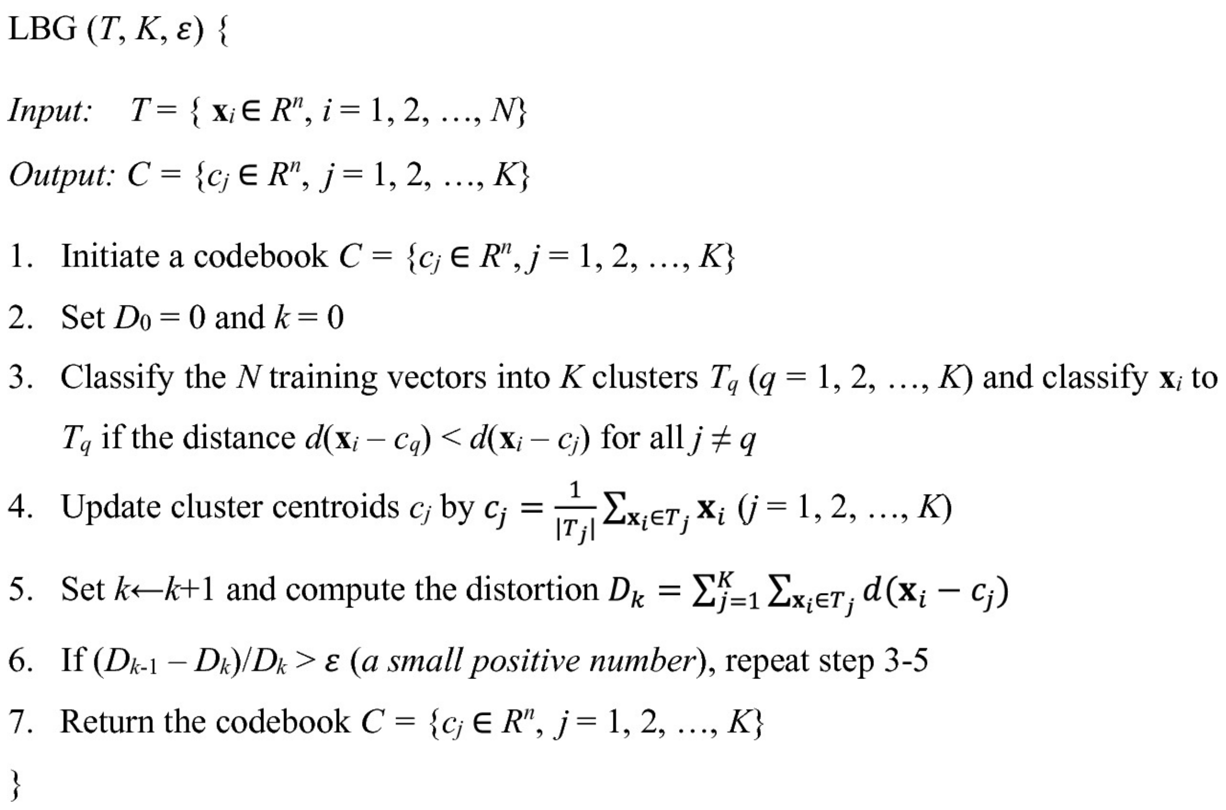
Fig. 10.4 Data map of actual median house prices in California and the tree partition of the data map, the darker the color, the higher the house value

10.5 DT for Image Classification

Images are complex data. A typical image usually has multiple regions/objects and has multiple interpretations. Therefore, the first step is to segment an image into individual regions and represent each region with a n-dimensional feature vector: $\mathbf{x} = (x_1, x_2, \ldots, x_n)$. For color images, each image region is represented with a color feature vector $\mathbf{x}_C$ and a texture feature vector $\mathbf{x}_T$. Because certain types of image regions can be best described by both color and texture, a third feature is also created by combining both color and texture into a single feature vector $\mathbf{x}_{CT}$.

10.5.1 Feature Discretization

The three types of features $\mathbf{x}_C$, $\mathbf{x}_T$ and $\mathbf{x}_{CT}$ are all continuous features, and in order to classify these regions using a classification DT, the features need to be quantized into discrete values using a vector quantization (VQ) technique. The idea of a VQ technique is to cluster similar image regions into clusters which are then assigned with nominal values such as 0, 1, 2, ..., K. These nominal values correspond to class labels such as sky, water, grass, firework and tiger which are used for DT classification. Common VQ algorithm is the LBG algorithm [6] which is given as following:



```
LBG ($T$, $K$, $\varepsilon$) {

Input:   $T = \{ \mathbf{x}_i \in R^n, i = 1, 2, \ldots, N\}$
Output: $C = \{c_j \in R^n, j = 1, 2, \ldots, K\}$

1. Initiate a codebook $C = \{c_j \in R^n, j = 1, 2, \ldots, K\}$
2. Set $D_0 = 0$ and $k = 0$
3. Classify the $N$ training vectors into $K$ clusters $T_q$ ($q = 1, 2, \ldots, K$) and classify $\mathbf{x}_i$ to
   $T_q$ if the distance $d(\mathbf{x}_i - c_q) < d(\mathbf{x}_i - c_j)$ for all $j \neq q$
4. Update cluster centroids $c_j$ by $c_j = \frac{1}{|T_j|}\sum_{\mathbf{x}_i \in T_j} \mathbf{x}_i$ ($j = 1, 2, \ldots, K$)
5. Set $k \leftarrow k+1$ and compute the distortion $D_k = \sum_{j=1}^{K} \sum_{\mathbf{x}_i \in T_j} d(\mathbf{x}_i - c_j)$
6. If $(D_{k-1} - D_k)/D_k > \varepsilon$ (a small positive number), repeat step 3-5
7. Return the codebook $C = \{c_j \in R^n, j = 1, 2, \ldots, K\}$
}
```

By applying the LBG VQ algorithm on $\mathbf{x}_C$, $\mathbf{x}_T$ and $\mathbf{x}_{CT}$, three codebooks or visual dictionaries V_i (i = 1, 2, 3) are created:

$$V_i = \left\{v_1^i, v_2^i, \ldots, v_{n_i}^i\right\}, \quad i = 1, 2, 3 \tag{10.12}$$

where v_j^i represents a code word of V_i and n_i is the total number of code words in V_i.

For each image region R in the training dataset, it is represented as three discrete attribute values as the following:

$$R = (ind_1, ind_2, ind_3) \tag{10.13}$$

and

$$ind_i = \arg\min_j (dist(v^i, v_j^i)) \tag{10.14}$$

where

- $dist(v^i, v^i_j)$ is the distance between feature v^i and code word v^i_j.
- v^i is one of the feature vectors ($\mathbf{x}_C$, $\mathbf{x}_T$ or $\mathbf{x}_{CT}$) of R.
- v^i_j is the jth value of attribute V_i.
- ind_i is an index value of attribute V_i, and it is an integer between 0 and n_i.

Therefore, each image region in the training set is now associated with three discrete attributes $A_i = V_i$ ($i = 1, 2, 3$) which are ready for building a DT.

10.5.2 Building the DT

With a training set of image regions T and a set of visual attributes A, an image classification DT can be built using the following algorithm [1].

1. If all training regions of T belong to the same class C,
   1.1. The tree is a leaf node with the outcome C.

   1.2. Stop.

2. If the regions of T belong to more than one class but there is no attribute to separate them,

2.1. The tree is a leaf node. The outcome is determined as follows.

    2.1.1. If there is a single majority class in *T*, the outcome is that class.

    2.1.2. Else, the outcome is the majority class of the parent node.

2.2. Stop.

3. If the regions of *T* belong to more than one class and there are one or more attributes to separate them,

    3.1. Create an internal node.

    3.2. Calculate the *IG* or *gain ratio* for each attribute.

    3.3. Select the attribute A_i with the highest gain ratio:
    $A_i = \{v_1^i,\ v_2^i,\ v_3^i,\ \ldots, v_{n_i}^i\}$

    3.4. Use A_i as the test attribute for the internal node.

    3.5. Split the training set *T* into subsets: $T_i^0,\ T_i^1,\ T_i^2,\ T_i^3, \ldots,\ T_i^{n_i}$,

    where image regions in T_i^j have attribute value v_i^j.

    3.6. Remove attribute A_i from the attribute list.

    3.7. Repeat from Step 1 for each T_i^j.

A DT generated from the above algorithm can have nodes with isolated or noisy samples. A common practice is to include a pre-pruning procedure after each splitting to remove those nodes with noisy samples. The following pre-pruning procedure can be included as step 3.7 in the above algorithm, and name the original steps 3.7 as 3.8.

3.7. Pre-pruning [7]:

3.7.1. Calculate the probability P'_i for every class in subset T_i^j ($j = 0, 1, 2, \ldots, n_i$) as:

$$P'_i = \frac{\|p_j\|}{\|p_i\|} \tag{10.15}$$

where p_i and p_j are the number of instances of class C_i in T and T_i^j, respectively.

3.7.2. Remove those samples from subset T_i^j whose class probability P'_i is less than a threshold k.

3.7.3. Remove T_i^j if it's an empty subset after sample removal.

Figure 10.5 shows a DT learnt from a dataset of 570 image regions which have been quantized into 19 classes (30 images/class), and the pre-pruning threshold is $k = 0.1$ [8]. The meaning of the leave labels are as following: A = *Grass*, B = *Forest*, C = *Sky*, D = *Sea*, E = *Flower*, F = *Sunset*, G = *Beach*, H = *Firework*, I = *Tiger*, J = *Fur*, K = *Eagle*, L = *Building*, M = *Snow*, N = *Rock*, O = *Bear*, P = *Night*, Q = *Crowd*, R = *Butterfly*, S = *Mountain* and U = *Unknown*.

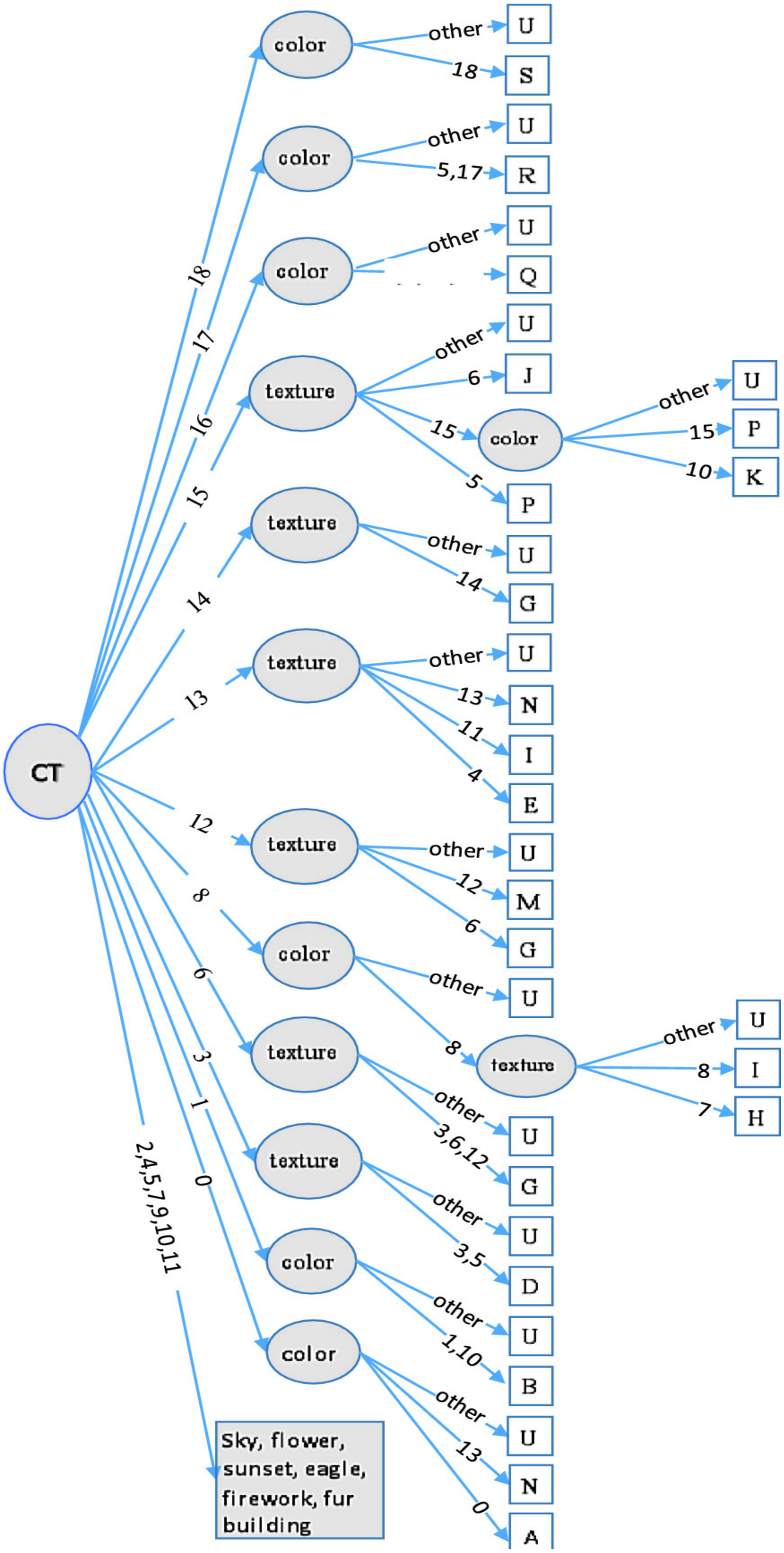

CT
18
17
16
15
14
13
12
8
6
3
1
0
2,4,5,7,9,10,11
color
other
U
18
S
color
other
U
5,17
R
color
other
U
Q
texture
other
U
6
J
15
color
other
U
15
P
10
K
5
P
texture
other
U
14
G
texture
other
U
13
N
11
I
4
E
texture
other
U
12
M
6
G
color
other
U
8
texture
other
U
8
I
7
H
texture
other
U
3,6,12
G
texture
other
U
3,5
D
color
other
U
1,10
B
color
other
U
13
N
0
A
Sky, flower, sunset, eagle, firework, fur building

Fig. 10.5 DT for image classification without post-pruning, CT = color and texture

A DT generated from the above algorithm can still be very complex and imbalanced. A post-pruning procedure is usually applied after the initial tree has been generated, and this can be added as step 4 in the above DT algorithm. The post-pruning is a procedure to *remove those isolated branches* and merge them with neighboring nodes.

1. Post-pruning [7]:
    a. If for more than one values of the attribute A_i, the outcome class labels are identical, i.e., C_i, then all the leaf nodes corresponding to these attribute values are merged as a single leaf node labeled with class C_i.
    b. If the outcomes for all the possible values of attribute A_i are identical, i.e., C_i, then the *subtree* rooted at A_i is replaced with a single leaf node with C_i as outcome.

Figure 10.6 shows the DT from Fig. 10.5 after post-pruning; it is a much simpler and more robust DT [7, 8].

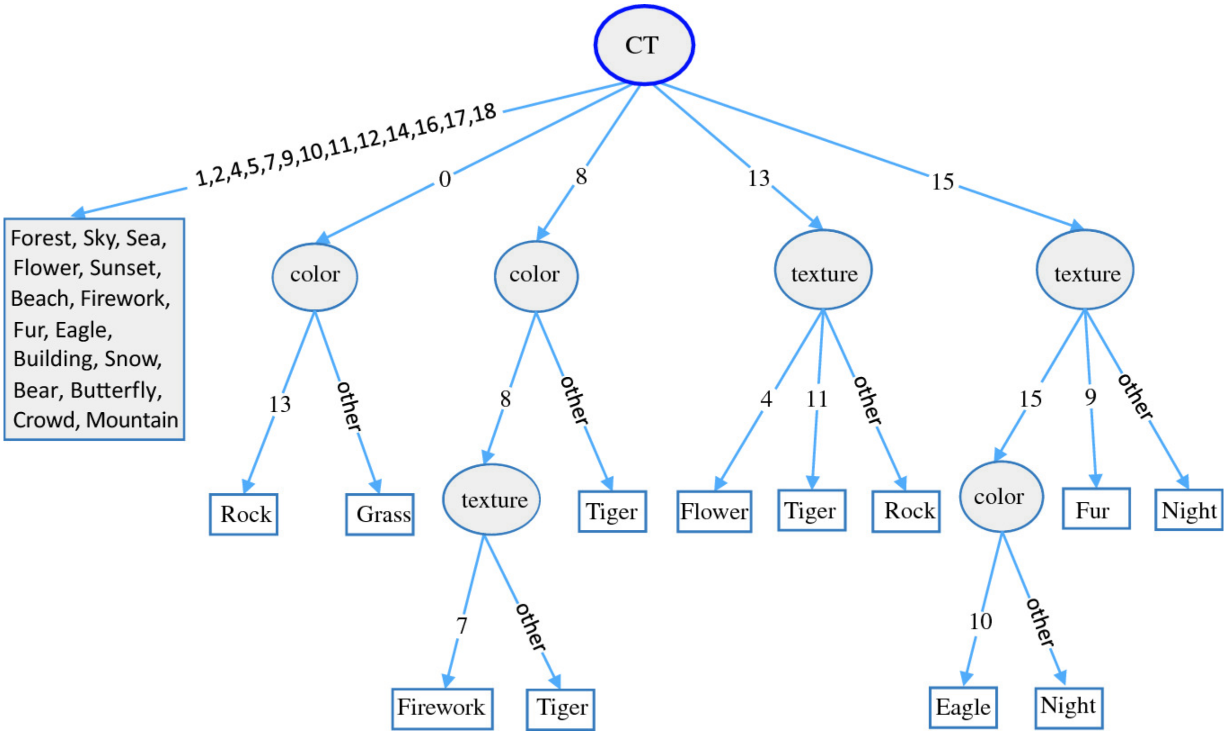
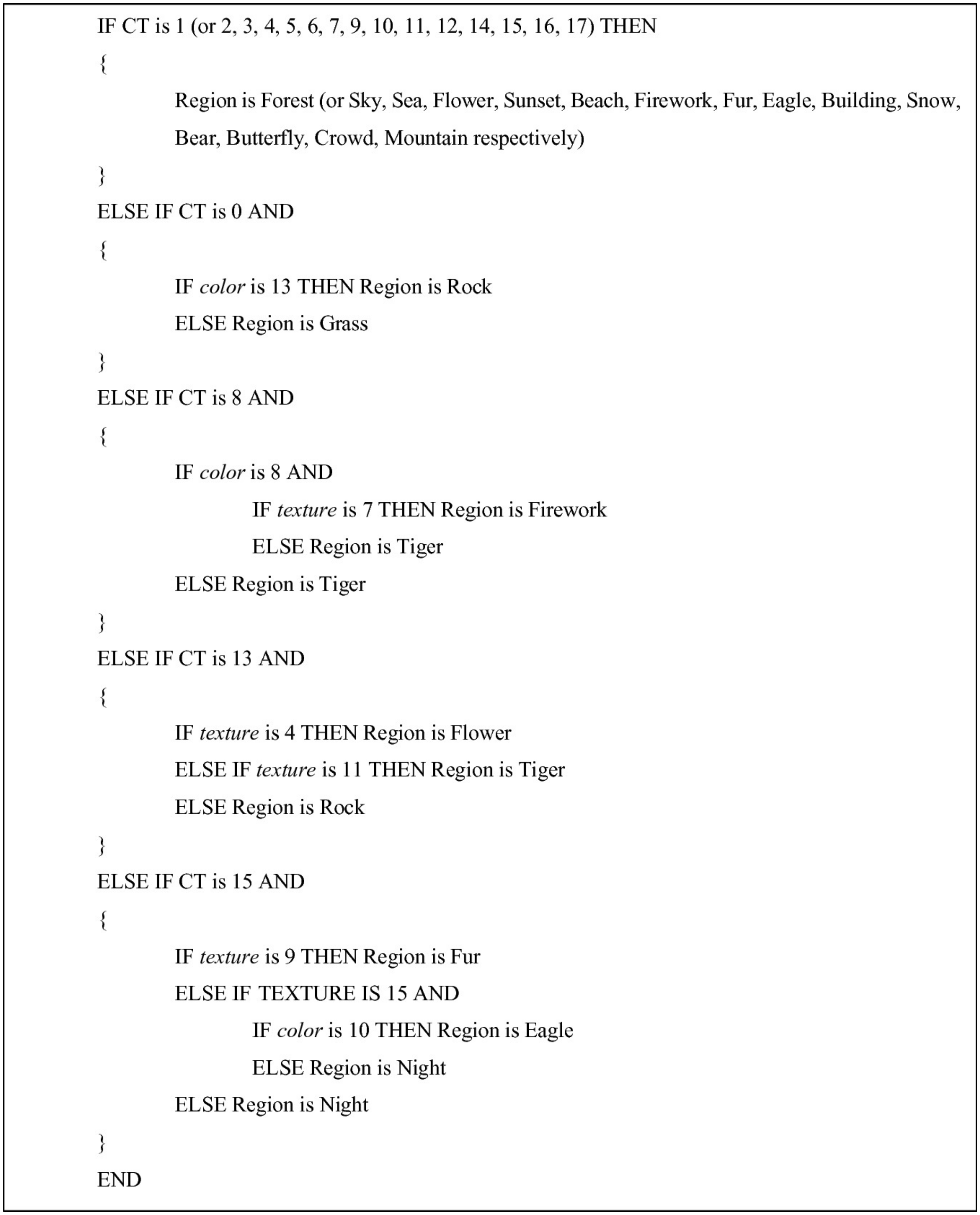

CT
1,2,4,5,7,9,10,11,12,14,16,17,18
0
8
13
15
Forest, Sky, Sea, Flower, Sunset, Beach, Firework, Fur, Eagle, Building, Snow, Bear, Butterfly, Crowd, Mountain
color
color
texture
texture
13
other
8
other
4
11
other
15
9
other
Rock
Grass
texture
Tiger
Flower
Tiger
Rock
color
Fur
Night
7
other
10
other
Firework
Tiger
Eagle
Night

Fig. 10.6 DT from Fig. 10.5 after pruning

10.5.3 Image Classification and Annotation with DT

Once the DT is generated from a training dataset, a set of rules or a *DT model* can be formulated from the DT by traversing the tree from the root to each of the leaf nodes. This DT model is to be used as an image classifier. The following is the DT model formulated from the DT shown in Fig. 10.6.



```
IF CT is 1 (or 2, 3, 4, 5, 6, 7, 9, 10, 11, 12, 14, 15, 16, 17) THEN
{
        Region is Forest (or Sky, Sea, Flower, Sunset, Beach, Firework, Fur, Eagle, Building, Snow,
        Bear, Butterfly, Crowd, Mountain respectively)
}
ELSE IF CT is 0 AND
{
        IF color is 13 THEN Region is Rock
        ELSE Region is Grass
}
ELSE IF CT is 8 AND
{
        IF color is 8 AND
                IF texture is 7 THEN Region is Firework
                ELSE Region is Tiger
        ELSE Region is Tiger
}
ELSE IF CT is 13 AND
{
        IF texture is 4 THEN Region is Flower
        ELSE IF texture is 11 THEN Region is Tiger
        ELSE Region is Rock
}
ELSE IF CT is 15 AND
{
        IF texture is 9 THEN Region is Fur
        ELSE IF TEXTURE IS 15 AND
                IF color is 10 THEN Region is Eagle
                ELSE Region is Night
        ELSE Region is Night
}
END
```

Fig. 10.7 DT annotation model

Given a new or unknown image, it is also segmented into regions using the same algorithm as that used by the training dataset. Each region is then represented as three discrete attribute values: $R = (ind_1,$

ind_2, ind_3), using the learnt visual dictionaries. Each of the regions R is then analyzed using the DT model of Fig. 10.7 and is classified into a class.

As can be observed that a DT model is completely transparent and comprehensible to a human user. A classifier working in this way can be easily modified and fine-tuned to adapt to the data. The other advantage of the DT model is that issues can be found and corrected at learning stage without much difficulty.

10.6 Summary

DT is a powerful image classification tool. Due to its hierarchical nature and piecewise approximation of data, it offers a middle ground between *generative* and *discriminative* approaches. Compared with other classification tools, DT has a number of advantages.

- DT is a tool known for its simplicity, transparency and comprehensibility.
- DT can handle both numeric and categorical attributes.
- DT can handle both noisy and missing data.
- DT offers an intuitive and step by step analysis based on selected attributes.
- DT does not require complex computation.
- DT generates rules which are easy to interpret.

A DT may grow too complex and imbalanced due to noise, fragmentation and missing data. Therefore, a pruning mechanism is essential to a DT algorithm. Common practice is to apply a post-pruning technique after the tree has been generated. However, many misplaced instances would have a better chance to be classified into more appropriate nodes if a pre-pruning is applied during the tree building. A well-designed pruning scheme can improve the DT performance significantly.

According to the Ockham's Razor principle, the simplest rule that is consistent with all observations is the best. In terms of DT, it means that the smallest decision tree that correctly classifies all the training examples is the best.

10.7 Exercises

1. DT classification. Open your Matlab editor and visit the following Matlab website: https://au.mathworks.com/help/stats/examples/classification.html. Run the block of code in the data section 'Fisher's Iris Data' (shaded areas) at Matlab command line. Make sure you understand the data `meas(:,1:2)` used in this exercise and how the groups of data have been plotted. Run the following code: '`[x,y] = meshgrid(4:.1:8,2:.1:4.5); x = x(:); y = y(:)`' at the command line. Skip the 'Linear and Quadratic Discriminant Analysis' and the 'Naive Bayes Classifiers' sections and move on to the 'Decision Tree' example. Run the first two blocks of code at Matlab command line. Analyze the DT classifier by referring to https://au.mathworks.com/help/stats/classificationtree-class.html:

   - Examine the `nodes`, `x`, `y` variables in the Workspace and check if the class labels or probabilities of the first 10 nodes match the class labels of the points `(x, y)` on the region graph (scatter plot).
   - Double click the `t` variable in Workspace and examine the following properties of `t`: `X`, `Y`, ClassNames, NumNodes, NumObservations and ResponseName.
   - Run the third block of code to visualize the tree and enlarge it to full screen size. Print the tree on to a paper. Next, click on each of the nodes on the screen to view the node number and mark the node number on each of thse nodes on the paper.
   - Examine the following properties of `t`: Children, Parent, IsBranchNode and ClassCount and check if each of those properties matches the nodes on the tree.
   - Examine the following properties of `t`: ClassCount, ClassProbability and NodeClass and check if they match each other.
   - Prune the tree using the following code: `[cost, secost, ntermnodes, bestlevel] = cvloss(t,'Subtrees','all'); pt = prune(t,'Level',bestlevel)`.
   - Compute and compare the cross-validation error of both `t` and `pt`.
   - Fit a tree for the four-dimensional data `meas(:,1:4)`, recalculate the cross-validation error of the tree and compare it with the

previous tree.

- Write a report to record all your findings from this exercise.

2. Regression tree. Open your Matlab editor and visit the following Matlab website: https://au.mathworks.com/help/stats/improving-classification-trees-and-regression-trees.html. Run the code in the "Cross Validate a Regression Tree" section. Analyze the rtree model by referring to https://au.mathworks.com/help/stats/classificationtree-class.html:

- Examine the properties of rtree as instructed in Exercise 1.
- Visualize the rtree using the view() function.
- Try the tree depth control technique on the page.
- Refer to https://au.mathworks.com/help/stats/examples/classification.html and run the following code:

```
load fisheriris;
for i=1:length(species)
    if(strcmp(species(i), 'setosa'))
        species_val(i)=1;
    elseif(strcmp(species(i), 'versicolor'))
        species_val(i)=2;
    else
        species_val(i)=3;
    end
end
```

- Fit a regression tree rtree to meas(:,1:2)and species_val.
- View the rtree and compare it with the classification tree.
- Create a grid using the following code: [x,y] = meshgrid(4:.1:8,2:.1:4.5); x = x(:); y = y(:).
- Use the rtree to do a prediction of the above grid and view the scatter plot of the prediction graph. Compare the scatter plot with that of the classification tree.
- Compute the re-substitution error and the cross-validation error for the rtree. Compare them with those of the classification tree.
- Write a report to record all your findings from this exercise.

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Part IV
Image Retrieval and Presentation

Quality over quantity

Image retrieval (IR) is a set of techniques to retrieve images from a very large image database to meet a user's expectation, e.g., find a group of 'computer' images on the web. The database is either classified or not. Even if an image database is classified, to retrieve similar images from the database is still a challenging task. This is due to two reasons. First, the database is typically very large, a commercial image database typically numbers from millions to billions of images. Second, the classification is not perfect given current classification technology. In fact, the classification accuracy is usually quite low especially for very large database with vast varieties of images.

IR is an intensive research area, research on IR mostly focuses on four major topics: feature extraction, image indexing, image ranking and image presentation. The first topic has been comprehensively covered in Part II, in this part of the book, we focus on the remaining three topics.

Image indexing is to organize the image database into data structure such as a list or a tree to facilitate fast search. Image ranking is a technique to assess the similarity between database images, so that given a query image, images which are similar to the query can be identified and retrieved. Image presentation is a method of presenting similar images to the user so that browsing the retrieved images is the most convenient and efficient.

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11. Image Indexing

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Order is our favourite, but the truth is beyond order.

11.1 Numerical Indexing

11.1.1 List Indexing

In numerical indexing, each image *I* in the database has been represented as a *k*-dimensional feature vector: $\mathbf{x} = (x_1, x_2, \ldots, x_k)$. The simplest way of a numerical indexing is to create a list of (image_id, **x**) as shown in the following:

$$\begin{gathered}(I_1, \mathbf{x}_1) = [I_1,\ (x_{11}, x_{12},\ \ldots, x_{1k})]\\ (I_2, \mathbf{x}_2) = [I_2,\ (x_{21}, x_{22},\ \ldots, x_{2k})]\\ \vdots\\ (I_N, \mathbf{x}_N) = [I_N,\ (x_{N1}, x_{N2},\ \ldots, x_{Nk})]\end{gathered}$$

where *N* is the total number of image in the database.

A list is simple and useful for a small image database; however, it's impossible to use it for a very large commercial image database because it would take long time to search the entire list of millions even billions of images. Therefore, a more efficient data structure is needed to index large image databases. One of the simplest yet efficient data structure is the *k*–*d tree* indexing.

11.1.2 Tree Indexing

The simplest *k*–*d* tree is a binary tree. A binary *k*–*d* tree is an algorithm of repeatedly splitting the database into two subsets by cyclically dividing the *k* dimensions of the data. Given *N* number of *k*-dimensional feature vectors: $\mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_N$, a *k*–*d* tree first divides the *N* data into two sets or branches of approximately equal size according to the values of the first dimension of the *N* feature vectors. Next, each of the left and right branches is further divided into two subbranches of approximately equal size according to the values of the second dimension of the feature vectors. This division process continues until the *k*th dimension when the next division returns to the first dimension. The cycle goes on until no node is divisible any more.

Figure 11.1 shows an example of a *k*–*d* tree for a 2D dataset. Given a 2D dataset of 10 data: (56, 2), (36, 91), (52, 76), (2, 19), (11, 31), (61, 81), (85, 72), (71, 71), (51, 52), (26, 41), the binary *k*–*d* tree for this dataset is shown in Fig. 11.1. The labels on the left-hand side of the tree are the splitting criteria or the dimensions to be split.

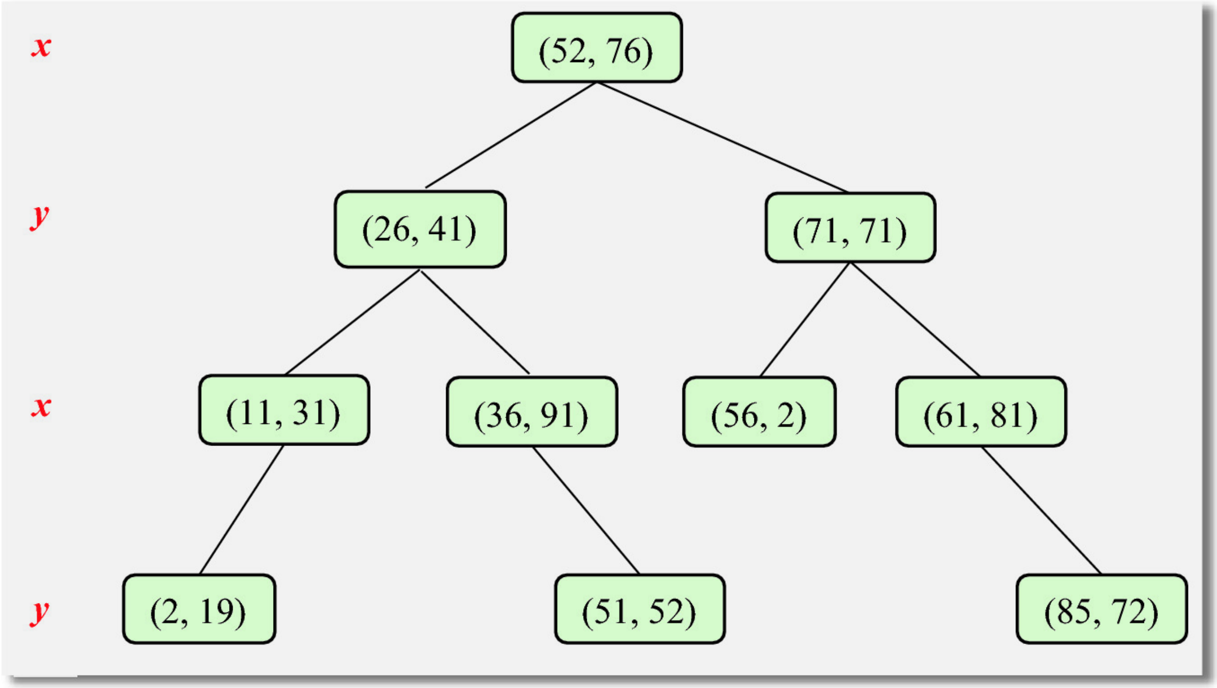

Fig. 11.1 A *k*–*d* tree for a 2D dataset of 10 data

A k–d tree reduces the search cost of a list of N data from an average O(N/2) to an average of O(ln N), e.g., for a database of 10,000 images, the average search cost of a k–d tree is *integer* [ln (10,000)] ≈ 14, which is way smaller than 5000 which would be needed for an exhaustive search of a data list. For very large image database, more efficient data structures can be used such as n-ary k–d tree, *quad-tree*, *octree*, *R-tree*, *cluster* tree, etc.

11.2 Inverted File Indexing

The data structures described above are for numerical data. If images in a very large database have been labeled with nominal or discrete values, they are equivalent to structured textual documents as shown in Fig. 11.2 [1]. Therefore, labeled images can be indexed using the same technique used for textual document indexing. In this section, we first review the inverted file for textual documents indexing and then introduce the inverted file for image indexing.

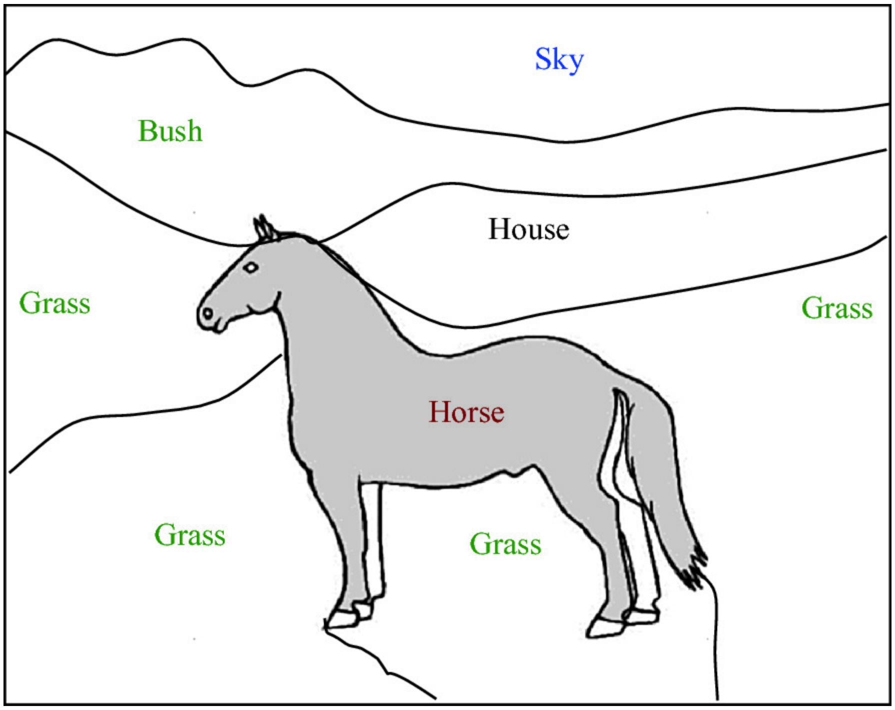

Fig. 11.2 Image with labeled regions

11.2.1 Inverted File for Textual Documents Indexing

In textual document indexing, a technique called *inverted file* is used. An inverted file is a (*terms, docs*) table instead of an ordinary (*docs, terms*) table. The reason for using an inverted file for document indexing is that a large amount of documents (millions/billions, e.g., webpages) can be indexed using a much shorter list of dictionary words (thousands). This makes the search for large amount of documents very efficient.

The ith entry in an inverted file is a vector: ($term_i$, doc_1, doc_2, ..., doc_n), where every document doc_j has $term_i$. Because a term carries a different amount of information in each of the documents, $term_i$ is given a different weight tw_j for each doc_j. Therefore, an inverted file can be shown as Table 11.1.

Table 11.1 Conceptual inverted file for textual document indexing

Term ID	Terms	Documents (weighted)
1	Apple	(doc_{11}, tw_{11}), (doc_{12}, tw_{12}), (doc_{13}, tw_{13}), ...
2	Computer	(doc_{21}, tw_{21}), (doc_{22}, tw_{22}), (doc_{23}, tw_{23}), ...
3	Tree	(doc_{31}, tw_{31}), (doc_{32}, tw_{32}), (doc_{33}, tw_{33}), ...
...		
n	Zebra	(doc_{n1}, tw_{n1}), (doc_{n2}, tw_{n2}), (doc_{n3}, tw_{n3}), ...

Since the documents are typically sorted in descending order of importance according to term weights (tw_j), the term weights can be omitted after sorting. Therefore, an actual inverted file is as simple as Table 11.2.

Table 11.2 Inverted file after sorting

Term ID	Terms	Documents (ranked)
1	Apple	doc_{11}, doc_{12}, doc_{13}, ..., doc_{1n}, ...
2	Computer	doc_{21}, doc_{22}, doc_{23}, ..., doc_{2n}, ...
3	Tree	doc_{31}, doc_{32}, doc_{33}, ..., doc_{3n}, ...
...	...	...
n	Zebra	doc_{n1}, doc_{n2}, doc_{n3}, ..., doc_{nn}, ...

The *term weight* (*tw*) of a term *t* in a document *d* is determined by two factors: the *term frequency* of *t* in document *d* and the *inverse document frequency* of *t* in the entire database *D*. Specifically, *tw* is defined as following:

$$tw\,(t,d) = tf\,(t,d) \times idf\,(t,D) \tag{11.1}$$

where *tf* stands for *term frequency* and *idf* stands for *inverse document frequency*. The *tf* and *idf* are given in (11.2) and (11.3), respectively.

$$tf\,(t,d) = \frac{f\,(t,d)}{\sum_{t_i \in d} f\,(t_i,d)} \tag{11.2}$$

$$idf\,(t,D) = log\left(\frac{\|D\|}{df\,(t)}\right) \tag{11.3}$$

where

- $f(t, d)$ is the number of occurrence of term *t* in document *d*;
- $df(t)$ stands for the *document frequency* of *t*, it is the number of documents in *D* which have term *t*;
- $||D||$ is the total number of documents in *D*.

Recent research shows that the location where a term appears in a document is also a factor in determining the term weight, e.g., a term *t* in the *title* or *head* section of a web document is given a much higher score because the information of a term in a title or a head is much more important than that in the *body* text.

11.2.2 Inverted File for Image Indexing

The inverted file indexing method can also be applied to image indexing. Once the regions in an image database have been labeled with semantic concepts, images in database are essentially translated into textual documents. Therefore, images can now be indexed and retrieved the same way as textual documents. Specifically, images in the database are indexed using an inverted file structure where each index is a vector of the form: (*term*, *image1*, *image2*, …).

Since each term of an image is associated with a number of image regions, the term weight of an image term is determined by three factors: *area*, *position* and spatial *relationship* [1, 2]. As a result, three corresponding weights have been defined respectively: *aw*, *pw* and *rw*.

11.2.2.1 Determine the Area Weight aw

Let

- $aw(t)$ be the *area weight* of term t in image I;
- $R(t)$ be the area of a region which is labeled with term t in image I.

Then, $aw(t)$ is defined as the sum of all $R(t)$ in image I normalized by the area of the image. $aw(t)$ is equivalent to the term frequency in the textual document indexing. Mathematically,

$$aw(t) = \frac{\sum_{R \in I} R(t)}{\|I\|} \tag{11.4}$$

For example, in Fig. 11.3 [2], the four pink and reddish regions in the center of the image are all labeled as a term of 'flower' by a classifier; therefore, the weight of the term 'flower' is determined by the total area of the four regions, which is the area of the single flower in the image.

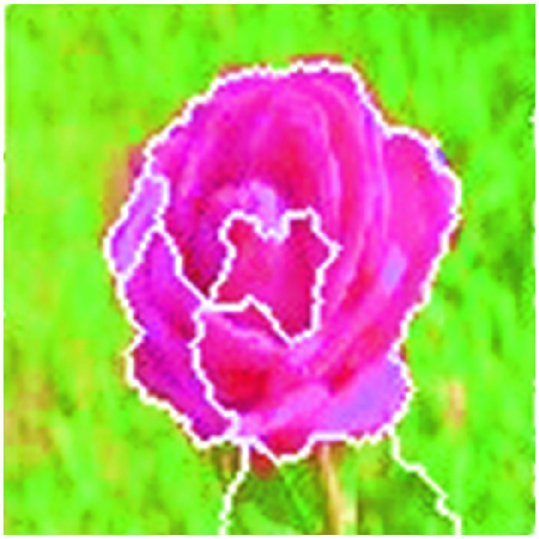

Fig. 11.3 Flower in the center with four segmented regions

11.2.2.2 Determine the Position Weight pw

It is known that each type of objects usually has its natural position in an image, e.g., sky is naturally located at the top, grass is naturally located at the bottom, animals are naturally located at the center, etc. Based on this observation, a position weight can be defined for each term of an image document.

Let

- $R(t)$ be one of the regions in image I associated with term t;
- d_R be the distance between the centroid of the region $R(t)$ and the center of $R(t)$'s natural position in image I;
- $d_{\max}$ be the maximum distance between the center of $R(t)$'s natural position and the boundary of image I.

Then, the *position weight* of term t is defined as:

$$pw(t) = \sum_{R(t)\in I} 2 \times \left(1 - \frac{d_R}{d_{\max}}\right) \tag{11.5}$$

Figure 11.4 shows three examples of computing d_R and $d_{\max}$ [1, 2].

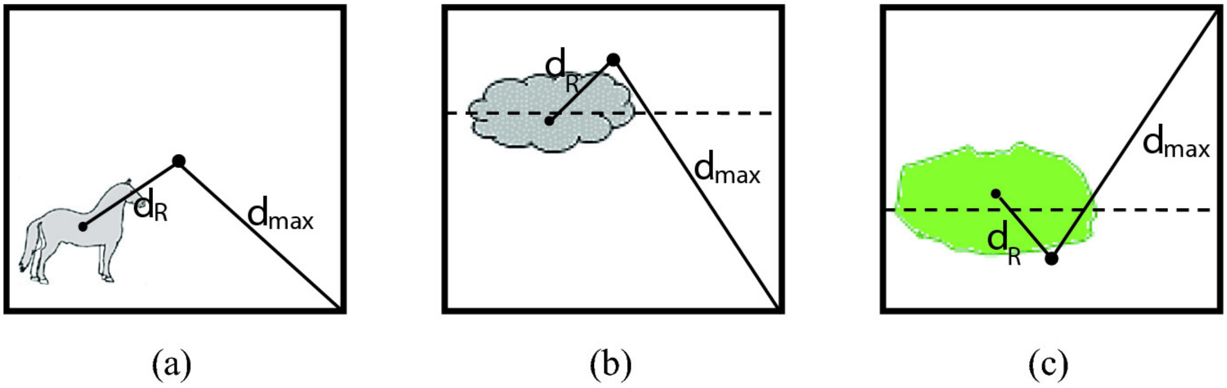

Fig. 11.4 Calculation of d and $d_{\max}$ for **a** animal, **b** sky and **c** grass regions

11.2.2.3 Determine the Relationship Weight rw

It is found that many types of objects usually go together in images such as, bird and sky, computer and desk, beach and water, mammals and grass, flowers and tree, car and road, clock and wall, window and building, etc. The *co-occurrence* relationship can be used to determine the weight on a term in an image. For example, if both a 'bird' term and a 'sky' term are detected in an image, the weight of the 'bird' term is doubled; if a 'kangaroo' term appears together with a 'tree' term and a 'grass' term, the weight of the 'kangaroo' term is tripled, so on so forth.

Let $r(t)$ be a term which co-occurs with term t in image I, then the relationship weight rw is given as

$$rw\,(t) = \sum_{r(t)\in I} r\,(t) \tag{11.6}$$

Now that we have defined the three-factor weights of a term t in image I, and the final term weight is defined as (11.7):

$$tw\,(t) = aw\,(t) \times pw\,(t) \times rw\,(t) \tag{11.7}$$

11.2.2.4 Inverted File for Image Indexing

Since each term in the dictionary has been given a weight in each of the images in the database, images in the database can be indexed using an inverted file the same way as in the textual document indexing. An example of an inverted file for image indexing is shown in Table 11.3.

Table 11.3 Conceptual inverted file for image document indexing

Term ID	Terms	Images (weighted)
1	Apple	$(im_{11}, tw_{11}), (im_{12}, tw_{12}), (im_{13}, tw_{13}), \ldots$
2	Computer	$(im_{21}, tw_{21}), (im_{22}, tw_{22}), (im_{23}, tw_{23}), \ldots$
3	Tree	$(im_{31}, tw_{31}), (im_{32}, tw_{32}), (im_{33}, tw_{33}), \ldots$
…		
n	Zebra	$(im_{n1}, tw_{n1}), (im_{n2}, tw_{n2}), (im_{n3}, tw_{n3}), \ldots$

After sorting the images at each row in descending order of importance according to the term weights, the above-inverted file is simplified as Table 11.4. The key difference between Tables 11.4 and 11.2 is that the terms in Table 11.4 are extracted from content features and by machine instead of interpretations by humans. Compared with textual documents, it’s more difficult to determine the weight of a term in an image. We will show how the inverted file is used in image retrieval in Sect. 13.5.

Table 11.4 Simplified inverted file from Table 11.3 after sorting

Term ID	Terms	Documents (ranked)
1	Apple	$im_{11}, im_{12}, im_{13}, ..., im_{1n}, ...$
2	Computer	$im_{21}, im_{22}, im_{23}, ..., im_{2n}, ...$
3	Tree	$im_{31}, im_{32}, im_{33}, ..., im_{3n}, ...$
...	...	...
n	Zebra	$im_{n1}, im_{n2}, im_{n3}, ..., im_{nn}, ...$

11.3 Summary

Image indexing is about to put images in an image database into a data structure or order so that images in the database can be retrieved similar to retrieving alphabetic data from a relational database management system (RDBMS). There are generally two types of approaches: numerical indexing and inverted file indexing.

If images are represented in numerical features, they can be indexed either using a list which is the simplest or using a tree structure. The list indexing is suitable for small image database, while for very large image database, the tree structure facilitates fast searching.

If images in a database have been semantically labeled using either machine learning or manual annotation, they can be indexed using an inverted file similar to textual documents indexing. The image database is then translated to a RDBMS. However, the difficulty lies in the determination of term weight. The chapter demonstrates a method of determining term weight using regional features of an image.

For large image databases, both numerical and inverted file indexing are necessary. As shown in Chap. 13, numerical indexing is typically used for query by example while inverted file indexing is used for query by keywords.

11.4 Exercises

1. Binary tree search. Visit the following website and download the `binarySearch( )` function: https://au.mathworks.com/matlabcentral/fileexchange/56271-binarysearch-a-n-num.
    - Study the code, inputs and usage of the function.

- Run `load fisheriris` at Matlab command line to load the fisheriris dataset into memory, it creates a data matrix `meas` and a class label vector `species` in the Workspace.
- Examine the first column of the `meas` variable: `meas(:, 1)` in Matlab Workspace.
- Find a value in `meas(:, 1)`, e.g., `num = 6.3` and note down the index `x` of the value `num`.
- Set a breakpoint (‘Breakpoints’ button is under the Editor menu) at the first line of `binarySearch( )` and run `binarySearch(A, n, num)` function line by line (by clicking the ‘Step’ button under the Editor menu) to find the index `y` of `num`.
- Compare `x` and `y`, check if they agree.
- Revise the code of `binarySearch( )` function for a 2D tree search shown in Fig. 11.1 and name it as `binarySearch2D( )`.Tips: the `num` must be a vector, e.g. `num = [6.3 2.5]` and two vectors can be compared using Matlab function `isequal( )`.
- Execute `binarySearch2D( )` on `meas(:, 1:2)` using the same steps described above.

2. Inverted file indexing. Randomly select 10 websites/webpages on the WWW to visit, such as CNN or BBC. For each of the 10 webpages you’ve visited, identify 5–10 keywords that best describe the page. Next, assign a weight (0–1 or 1–10) to each of the keywords according to its importance or position on the webpage. Once you’ve collected all the keywords and weights:

   - First created an inverted file as shown in Table 11.1.
   - Next, re-order the entries at each row of the table according to the weights (high to low)
   - Convert the above table to an inverted file as shown in Table 11.2.
   - Now, randomly choose a keyword from the list of keywords you’ve collected, go to the above table to find all the relevant webpages.

- Evaluate the results of your retrieval, e.g., how well do they agree with your expectation?
- Reflect on how a crawler and a search engine work by visiting the Google website: https://www.google.com/search/howsearchworks/.

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12. Image Ranking

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All that glitters is not gold.

12.1 Introduction

The image feature extracted is usually an N-dimensional feature vector which can be regarded as a point in R^N space. Once images are indexed into the database using the extracted feature vectors, the retrieval of images is essentially the determination of similarity between a query image and the target images in database, which in turn is the determination of distance between the feature vectors in R^N space. The desirable distance measure should reflect human perception. That is to say, perceptually similar images should have smaller distance between them while perceptually different images should have larger distance between them.

Therefore, given query, the higher the retrieval accuracy, the better the distance measure. For online retrieval, computation efficiency is also a factor to be considered when choosing a distance measure.

A variety of distance measures have been used in image retrieval; they include city block distance, Euclidean distance, cosine distance, histogram intersection distance, χ^2 statistics distance, quadratic distance and Mahalanobis distance [1]. In this chapter, commonly used similarity measures will be described and examined. A number of widely used performance measurements will also be discussed.

12.2 Similarity Measures

12.2.1 Distance Metric

A similarity measure $d(\mathbf{x}, \mathbf{y})$ between two feature vectors $\mathbf{x}$ and $\mathbf{y}$ is normally defined as a metric distance. $d(\mathbf{x}, \mathbf{y})$ is a metric distance if for any of two data points $\mathbf{x}$ and $\mathbf{y}$ in space, it satisfies the following properties:

(1) $d(\mathbf{x}, \mathbf{y}) \geq 0$ (non-negativity)

(2) $d(\mathbf{x}, \mathbf{y}) = 0$ if and only if $\mathbf{x} = \mathbf{y}$ (identity)

(3) $d(\mathbf{x}, \mathbf{y}) = d(\mathbf{y}, \mathbf{x})$ (symmetry)

(4) $d(\mathbf{x}, \mathbf{z}) \leq d(\mathbf{x}, \mathbf{y}) + d(\mathbf{y}, \mathbf{z})$ (triangle inequality).

12.2.2 Minkowski-Form Distance

The Minkowski-form distance is often called the L_p norm or L_p distance. Given a N-dimensional feature vector of a query image $\mathbf{x} = (x_1, x_2, \ldots x_n)$ and a target image in database $\mathbf{y} = (y_1, y_2, \ldots, y_n)$, the L_p distance is defined as:

$$L_p(\mathbf{x}, \mathbf{y}) = \left(\sum_{i=1}^{n} (x_i - y_i)^p \right)^{\frac{1}{p}} \tag{12.1}$$

When $p = 1$, L_1 is called the *city block distance* or *Manhattan distance*:

$$L_1(\mathbf{x},\mathbf{y}) = \sum_{i=1}^{n} |x_i - y_i| . \quad (12.2)$$

When $p = 2$, L_2 is called the *Euclidean distance*:

$$L_2(\mathbf{x},\mathbf{y}) = \sum_{i=1}^{n} (x_i - y_i)^2 \quad (12.3)$$

When $p \to \infty$, L_∞ is called *Chebyshev distance*:

$$L_\infty(\mathbf{x},\mathbf{y}) = \max_{1 \le i \le n} \{|x_i - y_i|\} \quad (12.4)$$

By varying the p values, various Minkowski distances can be created. However, among the many Minkowski-form distances, L_2 is the most widely used similarity measures. This is because L_2 is the most consistent with human perception on image similarity. The agreement between distance and perception is demonstrated in Fig. 12.1, where the unit circles of Minkowski distance with different p values are shown. Points on each of the unit circles all have the same distance under the corresponding p values. As can be seen, the L_2 unit circle agrees most with human perception among the three p values.

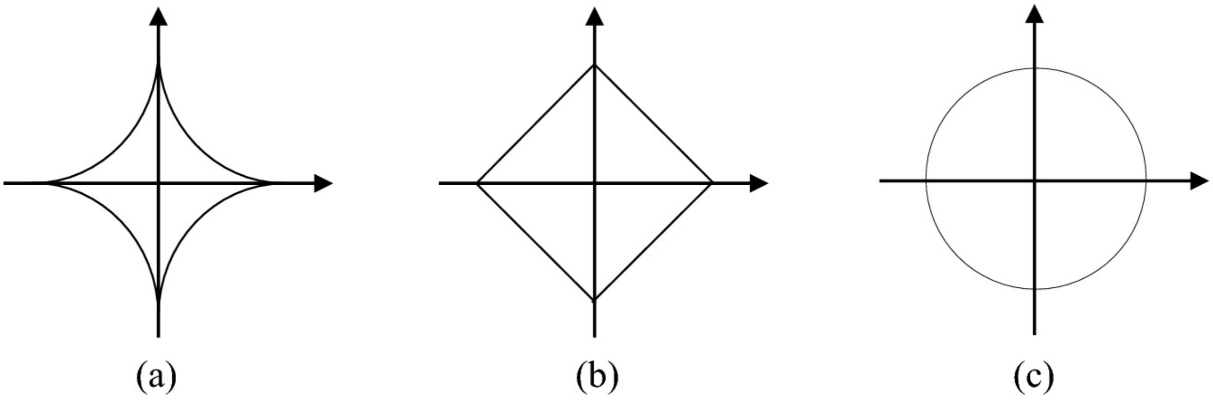


Fig. 12.1 Unit circles of Minlowski distance with different p values. **a** $p = \frac{1}{2}$; **b** $p = 1$; **c** $p = 2$

L_2 tends to emphasize or amplify the dimensions with high values due to the use of quadratic function. This can cause undesirable results because the distance value is often determined by a few dominant feature dimensions which are often due to local distortion or noise. This in turn can result in rejecting true positives which are perceptually similar images to the query but have local distortion or noise, e.g., a bite out apple would be rejected from the retrieval list using an intact apple as the query. Consequently, L_2 distance can expect lower recall compared with L_1 distance although it can return a top retrieval list with higher precision.

One solution to overcome the lower recall issues of L_2 distance is to apply a logarithm transform to the feature values to suppress the very high feature values and raise the lower feature values, so that all feature values have balanced contributions to the final distance value. Figure 12.2 (top) shows an example histogram from the flower image in Fig. 4.14, notice the histogram feature is dominated by the bins at the end of the histogram. The log transformed histogram feature vector is shown at the bottom of the figure, and it can be seen that while the difference between the feature dimensions has been reduced significantly, the top profile of the histogram has been kept.

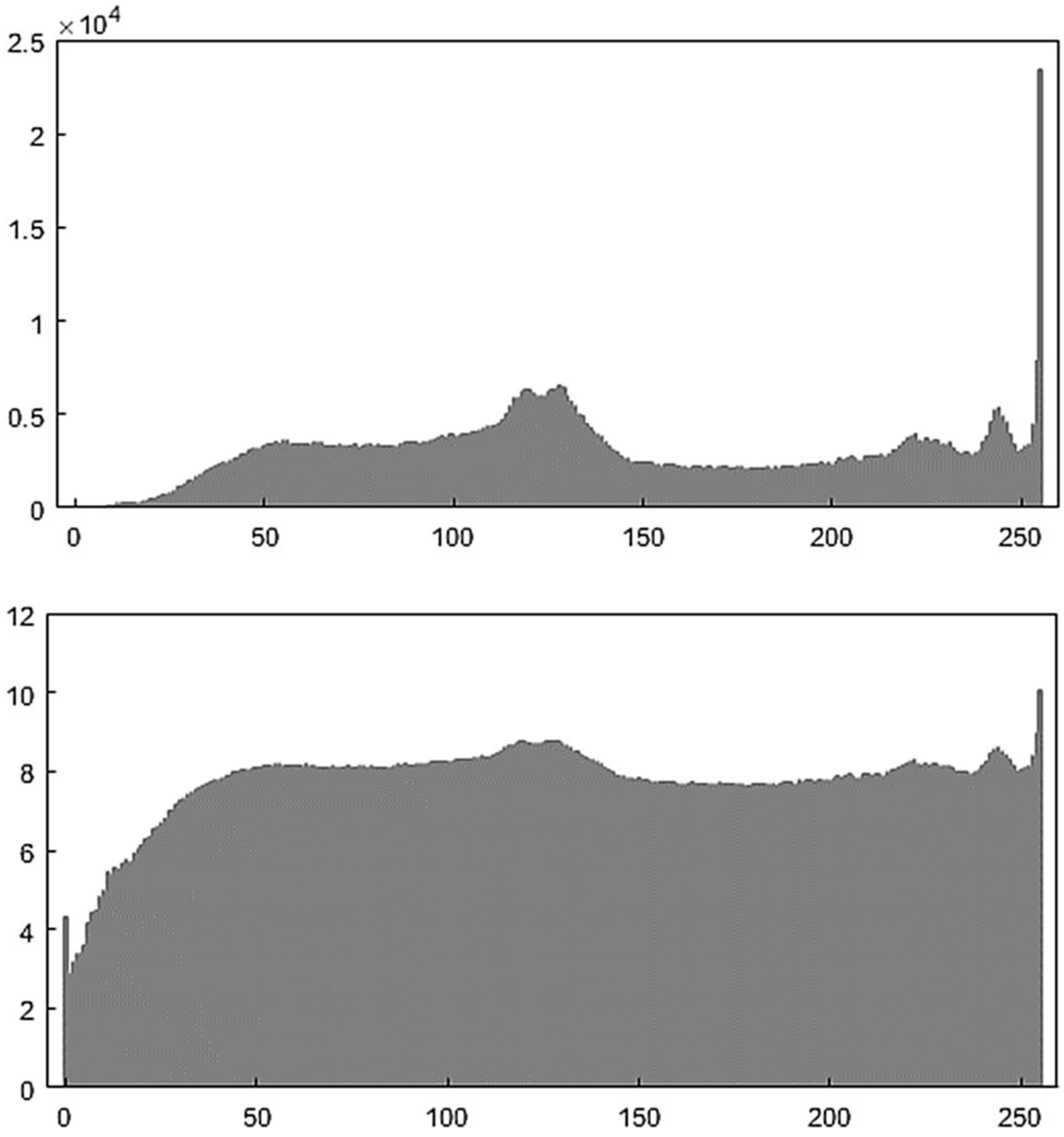


Fig. 12.2 Top: a histogram feature vector; Bottom: the log transformed histogram feature vector from the top histogram

12.2.3 Mass-Based Distance

Miknowski-form distance-based similarity measures are basically a matching of two images feature by feature. However, due to image features usually have very high dimensions and features are imperfect, this kind of detailed feature by feature matching can result in undesirable outcomes in many situations. For example, different images can have the same feature vector as shown in Fig. 12.3, and similar images can also have almost completely different feature vectors as shown in Fig. 12.4. In both cases, the L_p-based similarity measure would give a totally incorrect matching result.

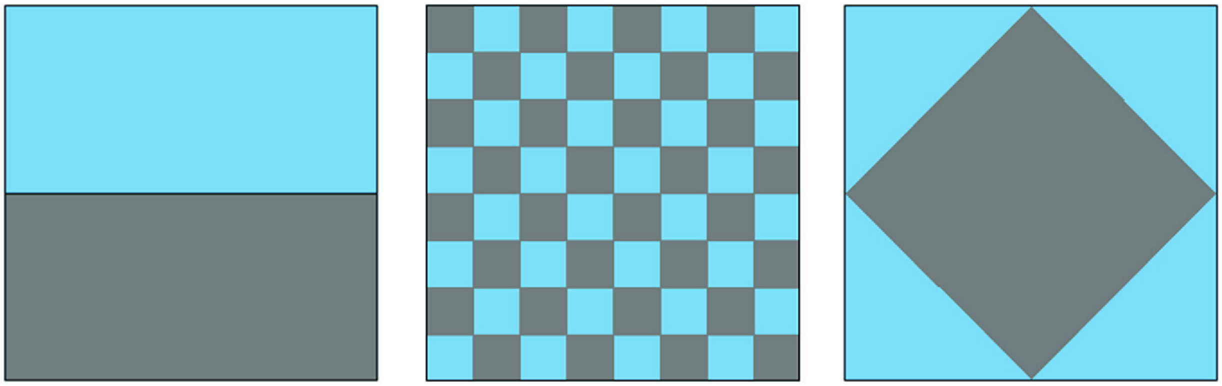


Fig. 12.3 Three images have the same histogram

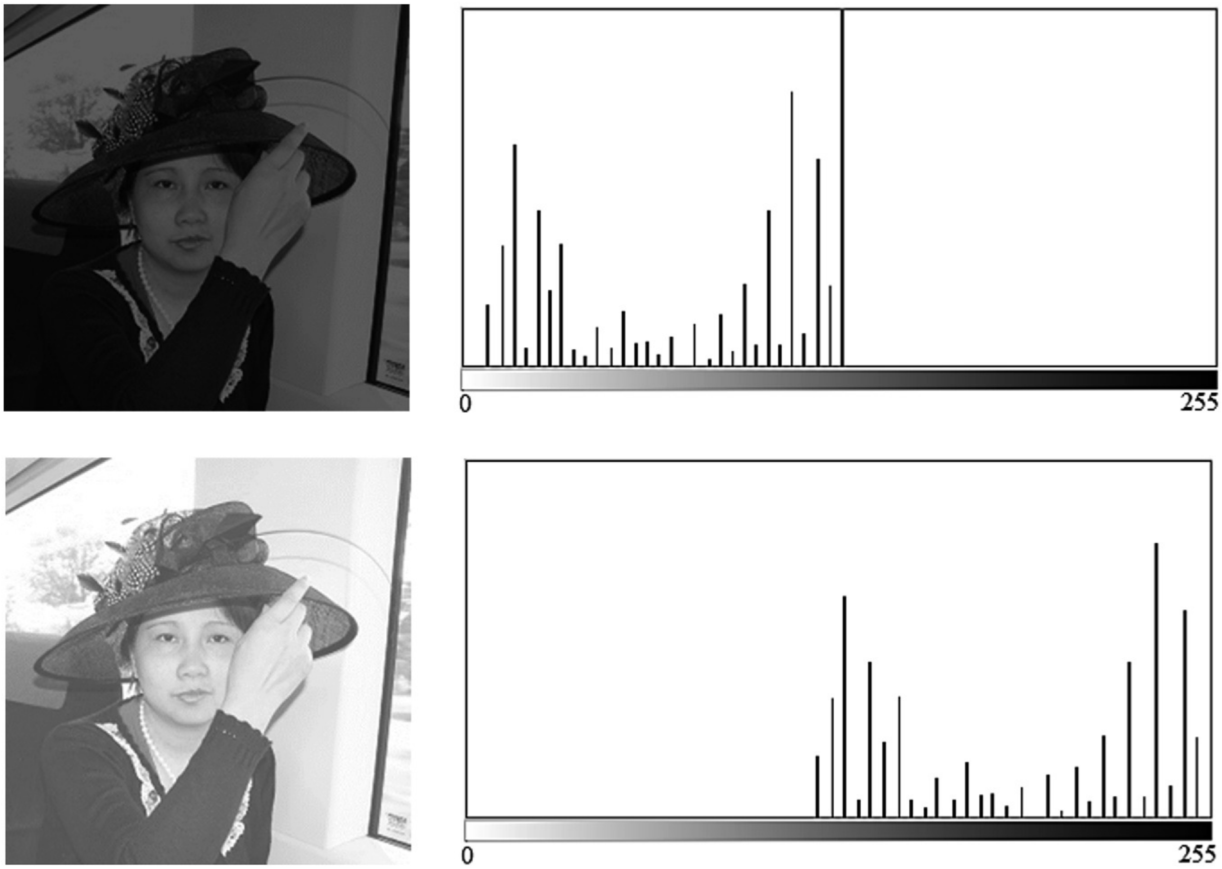


Fig. 12.4 Two images with different brightness have almost completely different histograms

The issue demonstrate L_p-based similarity measures are not robust. This drawback can be overcome by incorporating neighboring data in the decision making process.

To address the sensitivity issue of L_p, a mass-based similarity measure m_p has been proposed [2]. The idea of m_p is to use neighborhood data to make a similarity decision collectively instead of making a similarity decision just based on two instances alone. Specifically, m_p uses the neighborhood *data mass* at each subspace of R^d to replace the *difference* at each dimension in the Miknowski-form distance.

The idea of m_p is based on a distance-density model described by Krumhausl [3] and a psychological discovery that two instances in a sparse region are perceptually more similar than they are in a dense region.

Given two data points in R^n: $\mathbf{x}$ and $\mathbf{y}$, m_p works by defining a region $R(\mathbf{x}, \mathbf{y})$ between the two instances (including the two instances) and finding the data mass of the region. Data mass is the number of data instances from dataset that fall in this region. $R(\mathbf{x}, \mathbf{y})$ is a d-dimensional region, the ith dimension of $R(\mathbf{x}, \mathbf{y})$ is given as $R_i(\mathbf{x}, \mathbf{y})$, $i = 1, 2, \ldots, n$. The data mass of each $R_i(\mathbf{x}, \mathbf{y})$ depends on the distribution of the data in R^n space.

Specifically, the mass-based similarity measure m_p is defined as (12.5) [4]:

$$m_p(\mathbf{x}, \mathbf{y}) = \left(\frac{1}{n}\sum_{i=1}^{n}\left(\frac{|R_i(\mathbf{x}, \mathbf{y})|}{N}\right)^p\right)^{1/p} \qquad (12.5)$$

where

- $|R_i(\mathbf{x}, \mathbf{y})|$ is the data mass in region of $R_i(\mathbf{x}, \mathbf{y})$,
- N is the total number of instances in the dataset,
- $R_i(\mathbf{x}, \mathbf{y}) = [\min(x_i, y_i) - \sigma,\ \max(x_i, y_i) + \sigma]$,
- σ is a small number and $\sigma \geq 0$.

Figure 12.5 [4] illustrates a data distribution in 2D space and the calculation ota mass between two data points **x** and **y**. For convenience of calculation, σ is set as 0. With this data distribution, the data mass in $R_1(\mathbf{x}, \mathbf{y}) = [x_1, y_1]$ is $|R_1(\mathbf{x}, \mathbf{y})| = 63$ while the data mass in $R_2(\mathbf{x}, \mathbf{y}) = [x_2, y_2]$ is $|R_2(\mathbf{x}, \mathbf{y})| = 40$.

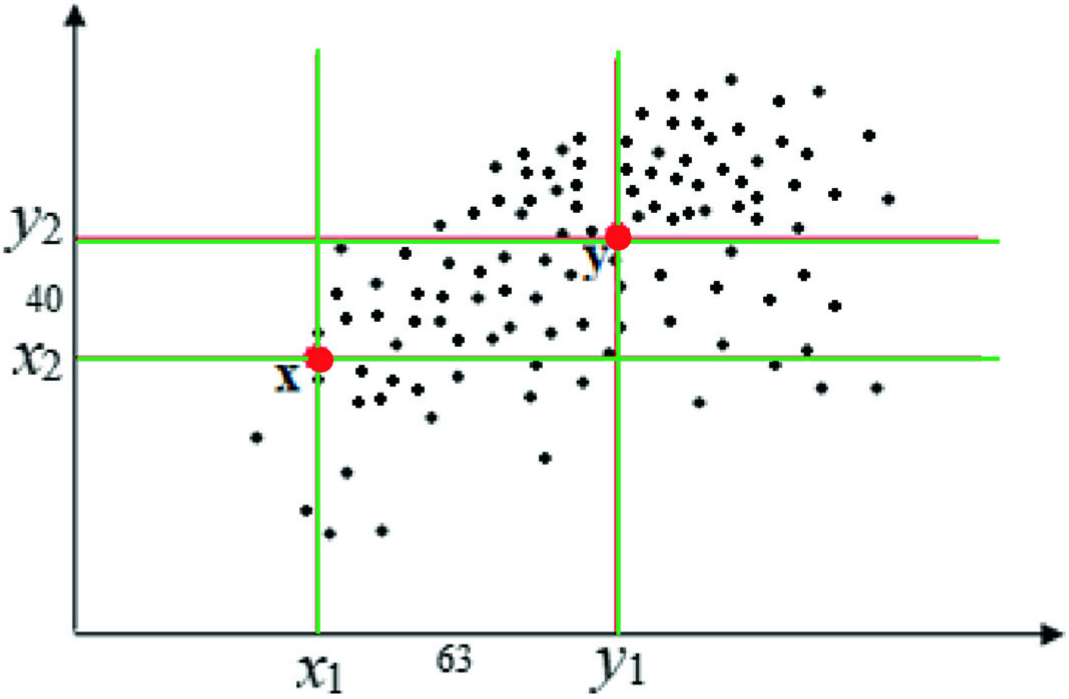


Fig. 12.5 Illustration of m_p dimension calculation between two data points **x** and **y**

L_p is essentially a *fine similarity measure* between two instances and is sensitive due to the use of feature by feature matching between two instances. It can result in completely incorrect match in cases shown in Figs. 12.2 and 12.3. On the other hand, m_p is essentially a *coarse similarity measure* between two instances, because it is computed using collective info from neighborhood data mass. Therefore, m_p can be *inaccurate* in situations when the features of the two instances are close.

To overcome the limitations of both the L_p and m_p, a hybrid similarity measure called h_p can be used, which is defined in (12.6):

$$h_p(\mathbf{x}, \mathbf{y}) = \left(\sum_{i=1}^{n} (|x_i - y_i| \times |R_i(x, y)|)^p \right)^{\frac{1}{p}}. \tag{12.6}$$

h_p is a compromise, and it overcomes the sensitivity drawback of L_p while preserves its accuracy. To prevent h_p from being disproportionally determined by a few dominant-dimensional features, a log transform on m_p is applied before computing h_p. The modified h_p is given as (12.7):

$$h'_p(\mathbf{x}, \mathbf{y}) = \left(\sum_{i=1}^{n} [|x_i - y_i| \times \log(|R_i(x, y)|)]^p \right)^{\frac{1}{p}} \tag{12.7}$$

12.2.4 Cosine Distance

The *cosine distance* computes the distance between two vectors in terms of direction, irrespective of vector lengths. The distance is computed based on the rule of dot product:

$$\mathbf{x} \cdot \mathbf{y} = |\mathbf{x}| \cdot |\mathbf{y}| \cdot \cos\theta \tag{12.8}$$

where θ is the angle between vector $\mathbf{x}$ and $\mathbf{y}$, $|\mathbf{x}|$ and $|\mathbf{y}|$ are the magnitudes of $\mathbf{x}$ and $\mathbf{y}$, respectively. The cosine distance is then defined as:

$$\cos(\mathbf{x}, \mathbf{y}) = 1 - \frac{\mathbf{x} \cdot \mathbf{y}}{|\mathbf{x}| \cdot |\mathbf{y}|} = \frac{\sum\limits_{i=1}^{n} x_i y_i}{\sqrt{\sum_{i=1}^{n} x_i^2}\sqrt{\sum_{i=1}^{n} y_i^2}} \tag{12.9}$$

If both x_i and y_i have been normalized to probability values between 0 and 1, cos($\mathbf{x}$, $\mathbf{y}$) becomes:

$$\cos(\mathbf{x}, \mathbf{y}) = 1 - \sum_{i=1}^{n} x_i y_i \tag{12.10}$$

The key feature of the cosine distance is that it is invariant to scale change in contrast to Minkowski distance. Figure 12.6 shows the comparison between the cosine distance and the two Minkowski-form distances in two-dimensional space. It can been observed that both L_2 and L_1 respond to scale changes while cosine distance does not, e.g., in Fig. 12.6b, $\cos(\mathbf{x}, \mathbf{y}) = \cos(\mathbf{x}_1, \mathbf{y})$, while $L_1(\mathbf{x}, \mathbf{y}) \neq L_1(\mathbf{x}_1, \mathbf{y})$ and $L_2(\mathbf{x}, \mathbf{y}) \neq L_2(\mathbf{x}_1, \mathbf{y})$. The scale invariance can be useful in situations where directional features are more important than magnitudes, e.g., if cosine distance is used, two similar colors will keep their similarity after scaling of the color components.

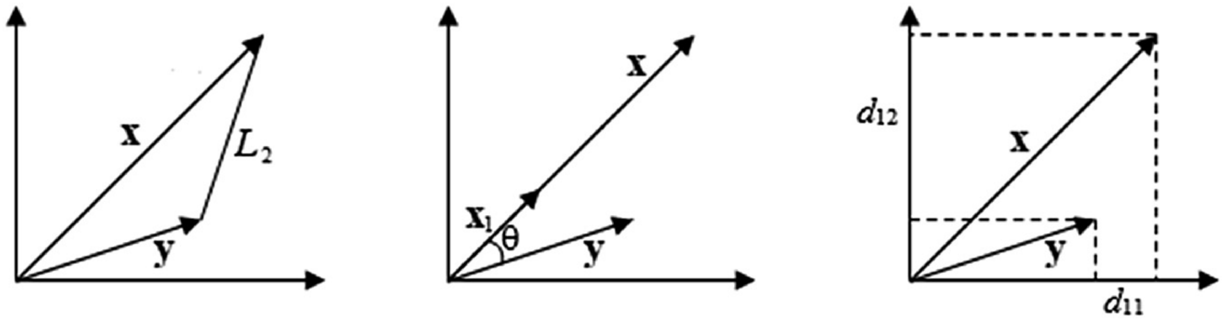


Fig. 12.6 Comparison between the cosine distance and L_p distance. **a** $L_2(\mathbf{x}, \mathbf{y}) = L_2$; **b** $\cos(\mathbf{x}, \mathbf{y}) = \cos\theta$; **c** $L_1(\mathbf{x}, \mathbf{y}) = d_{11} + d_{12}$

12.2.5 χ^2 Statistic

In χ^2 test, both **x** and **y** are treated as random variables, and the χ^2 statistic is then used to test if the two variables are correlated/independent each other, and how much they are correlated. Formally, χ^2 statistic is defined as (12.10).

$$\chi^2(\mathbf{x}, \mathbf{y}) = \sum_{i=1}^{n} \frac{(x_i - m_i)^2}{m_i} \tag{12.11}$$

where $m_i = (x_i + y_i)/2$, which is regarded as the *expected value* for dimension i. A low χ^2 value means that both **x** and **y** are from the same probability distribution and there is a high correlation between the two feature vectors, which indicates the images represented by the two feature vectors are similar. An advantage of using χ^2 statistic is that it can overcome the mismatch between two histograms from images with very different lighting conditions as shown in Fig. 12.4.

12.2.6 Histogram Intersection

A histogram is a distribution function with a particular shape of area. The histogram intersection is to test how much area two distributions **x** and **y** share; the more area they share, the more similar the two distributions are (Fig. 12.7). Mathematically, a histogram intersection is defined as:

$$HI(\mathbf{x},\mathbf{y}) = \frac{\sum_{i=1}^{n} \min(x_i, y_i)}{\min(|\mathbf{x}|, |\mathbf{y}|)} \tag{12.12}$$

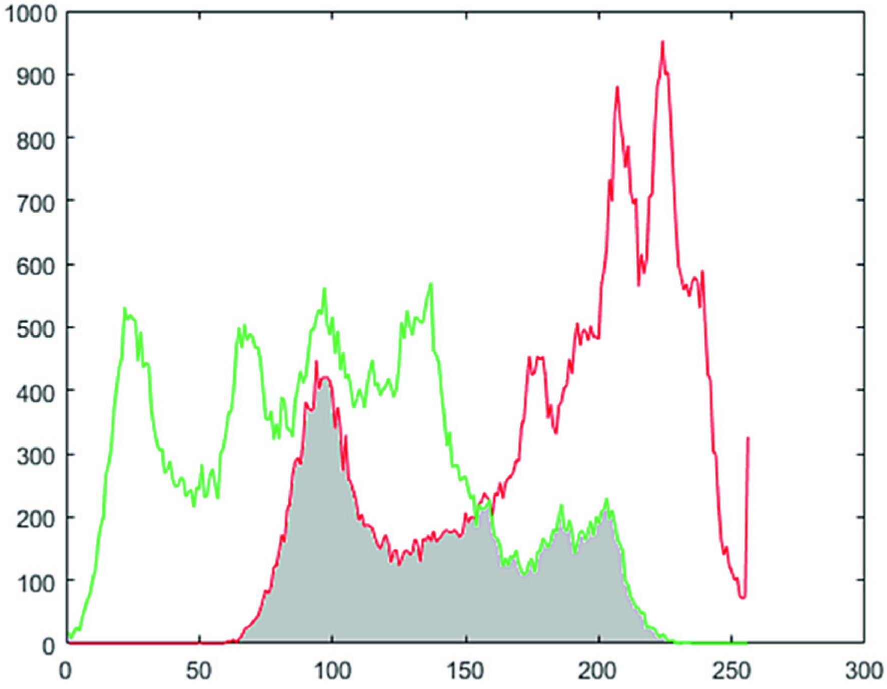


Fig. 12.7 Histogram intersection of two histograms shown as gray area

If both x_i and y_i have been normalized to probability values between 0 and 1, *HI* is simplified as (12.12):

$$HI(\mathbf{x},\mathbf{y}) = \sum_{i=1}^{n} \min(x_{i,}y_i) \tag{12.13}$$

For two identical histograms, their *HI* value is the maximum 1, and for two similar histograms, their *HI* value is a high. For two completely different histograms such as the two histograms shown in Fig. 12.4, their *HI* value is a zero. The *HI* distance is defined as:

$$d_{HI}(\mathbf{x},\mathbf{y}) = 1 - \sum_{i=1}^{n} \min(x_{i,}y_i) \tag{12.14}$$

d_{HI} also has the same histogram mismatching issue as the L_p distance.

12.2.7 Quadratic Distance

The distances or measures we have introduced so far all make two implicit assumptions: (a) The two feature vectors to be measured **x** and **y** have equal number of dimensions; (b) the dimensions of **x** and **y** are independent. However, there are applications and situations where these two conditions are not met. For example, the dominant color descriptors described in Chap. 4 typically have different number of dimensions, and colors of neighboring histogram bins are correlated each other. The quadratic distance measure is one of the methods to address the unequal number of dimensions between two feature vectors and capture the cross-dimension information in a feature vector.

The quadratic-form distance between two *n*-dimensional feature vectors **x** and **y** is given by:

$$d_q(\mathbf{x},\mathbf{y}) = \left[(\mathbf{x}-\mathbf{y})^T \mathbf{A}(\mathbf{x}-\mathbf{y})\right]^{\frac{1}{2}} \tag{12.15}$$

where

- T means transpose
- $\mathbf{A} = [a_{ij}]$ is an $n \times n$ matrix
- a_{ij} is the similarity coefficient between dimensions i and j

- $a_{ij} = 1 - d_{ij} / d_{\max}$
- $d_{ij} = |x_i - y_j|$
- $d_{\max} = \max_{1 \le i, j \le n} d_{ij}.$

For numerical calculations, (12.15) is expanded as (12.16):

$$d_q = \left(\sum_{i=1}^{n} \sum_{j=1}^{n} a_{ij} x_i x_j + \sum_{i=1}^{n} \sum_{j=1}^{n} a_{ij} y_i y_j - 2 \sum_{i=1}^{n} \sum_{j=1}^{n} a_{ij} x_i y_j \right)^{\frac{1}{2}} \qquad (12.16)$$

The a_{ij} is the similarity coefficient between x_i and y_j, it is a *weight* on a cross-dimension element of the two feature vectors and the higher the correlation between the two cross-dimensions, the more the weight is given on that element.

For two feature vectors **x** and **y** with different dimensions *n* and *m*, respectively, the quadratic distance between **x** and **y** is given as (12.17):

$$d_q = \left(\sum_{i=1}^{n} \sum_{j=1}^{n} a_{ij} x_i x_j + \sum_{i=1}^{m} \sum_{j=1}^{m} a_{ij} y_i y_j - 2 \sum_{i=1}^{n} \sum_{j=1}^{m} a_{ij} x_i y_j \right)^{\frac{1}{2}} \qquad (12.17)$$

If the dimensions of both the two feature vectors **x** and **y** are independent each other, e.g., after certain decorrelation operations, the quadratic distance between **x** and **y** is given as (12.18):

$$\begin{aligned} d_q &= \left(\sum_{i=1}^{n} x_i^2 + \sum_{j=1}^{m} y_j^2 - 2 \sum_{i=1}^{n} \sum_{j=1}^{m} a_{ij} x_i y_j \right)^{\frac{1}{2}} \\ &= \left(\sum_{i=1}^{n} \sum_{j=1}^{m} a_{ij} \left(x_i - y_j \right)^2 \right)^{\frac{1}{2}} \end{aligned} \qquad (12.18)$$

Equation (12.18) is a *weighted Euclidean distance*, one can expect that d_q is a more desirable similarity measure than both L_2 and d_{HI}; however, the determination of the weights is an issue.

12.2.8 Mahalanobis Distance

The *Mahalanobis distance* is a special case of the quadratic-form distance (12.15) in which the transform matrix is determined by the *covariance matrix* obtained from a training set of feature vectors, that is $\mathbf{A} = \Sigma^{-1}$. In order to apply the Mahalanobis distance, a feature vector $\mathbf{x}$ is regarded as a multivariate random variable $\mathbf{x} = (x_1, x_2, \ldots, x_n)$ from certain probability distribution. Then, the correlation matrix is given by $\mathbf{R}$ where:

- $\mathbf{R} = [r_{ij}]$
- $r_{ij} = E\{x_i x_j\}$ which is the mean of the random variable $x_i x_j$
- The covariance matrix Σ is given by $\Sigma = [\sigma_{ij}^2]$
- where $\sigma_{ij}^2 = r_{ij} - E\{x_i\}E\{x_j\}$.

The Mahalanobis distance between two feature vectors $\mathbf{x}$ and $\mathbf{y}$ is given as:

$$d_m(\mathbf{x}, \mathbf{y}) = [(\mathbf{x} - \mathbf{y})\Sigma^{-1}(\mathbf{x} - \mathbf{y})]^{\frac{1}{2}} \tag{12.19}$$

In the special case where x_i are statistically independent but have unequal variances, Σ is a diagonal matrix as following:

$$\sum = \begin{bmatrix} \sigma_1^2 & & & 0 \\ & \sigma_2^2 & & \\ & & \ddots & \\ 0 & & & \sigma_n^2 \end{bmatrix} \tag{12.20}$$

In this case, the Mahalanobis distance is reduced to a simpler form:

$$d_m(\mathbf{x}, \mathbf{y}) = \left(\sum_{i=1}^{n} \frac{(x_i - y_i)^2}{\sigma_i^2}\right)^{\frac{1}{2}} \tag{12.21}$$

Equation (12.21) is another *weighted Euclidean distance*. It gives more weight to dimensions with smaller variance and less weight to dimensions with larger variance. d_m can be regarded as a *standard*

Euclidean distance. The Euclidean distance is just a special case of Mahalanobis distance when the covariance matrix Σ is the identity matrix.

12.3 Performance Measures

After image ranking, we need a measure to tell how good is the ranking by a similarity measure we have discussed above. Specifically, we need to assess how many relevant images have been retrieved on the top list and how many relevant images have missed from the top list. The information from the top list of retrieval lets us to tell how well a similarity measure performs. A performance measure is usually based on statistics of a *subjective test* which is a test of identifying relevant images to the query and how relevant they are to the query. Different performance measures often use different subjective tests, resulting in different definitions of retrieval performance. In this section, several commonly used performance measures are described and discussed.

12.3.1 Recall and Precision Pair (RPP)

RPP is one of the most widely used retrieval performance measurement in literature. In RPP, for *each query image*, images in a dataset are divided into two categories: *relevant* images (1) and *irrelevant* images (0), based on their similarity to the query. The similarity is determined by a subjective test on a group of subjects. In the subjective test, each subject selects items relevant to the query from the dataset. An item selected by more than a number of subjects as a relevant image is given a label of ‘1’; otherwise, it is regarded as an irrelevant image and is given a label of ‘0.’

Now given a query image I and a retrieval list returned by a similarity measure, the *precision* (P) and *recall* (R) statistics are then computed based on the ‘0’ and ‘1’ images presented on the top retrieval list:

$$\begin{aligned} P &= \frac{r}{n_1} = \frac{number\ of\ relevant\ retrieved\ images}{number\ of\ retrieved\ images} \\ &= \frac{|\{relevant\ images\} \cap \{retrieved\ images\}|}{|\{retrieved\ images\}|} \end{aligned} \tag{12.22}$$

$$\begin{aligned} R &= \frac{r}{n_2} = \frac{number\ of\ relevant\ retrieved\ images}{number\ of\ relevant\ images\ in\ DB} \\ &= \frac{|\{relevant\ images\} \cap \{retrieved\ images\}|}{|\{relevant\ images\}|} \end{aligned} \tag{12.23}$$

P can be interpreted as the probability that a retrieved image is relevant, while R can be interpreted as the probability that a relevant image is returned by a retrieval.

The RPP is often given in the following form:

$$P = \frac{t}{t + f_\mathrm{p}} \tag{12.24}$$

$$R = \frac{t}{t + f_\mathrm{n}} \tag{12.25}$$

where t, f_p and f_n stand for ‘true positive’ (a hit), ‘false positive’ (a mismatch) and ‘false negative’ (a miss), respectively.

Precision measures the retrieval accuracy while recall measures the retrieval robustness, both are important for a similarity measure. Precision and recall are inversely related, i.e., precision normally degenerates as recall increases. Translating into actual image retrieval result, this inverse relationship means that the shorter the retrieval list (low recall), the higher the accuracy and vice versa.

The RPP based on a single query does not provide a complete picture of the performance of a similarity measure, usually a number of queries are tested and the P values at each of the R values are averaged. The average (R, P) values are then plot on a graph to get an approximate performance of a similarity measure.

Figure 12.8 shows a RPP curve from an averaged retrieval result. It can be observed from the figure, as the *recall* increases (longer retrieval list), the *precision* goes down rather sharply in this case.

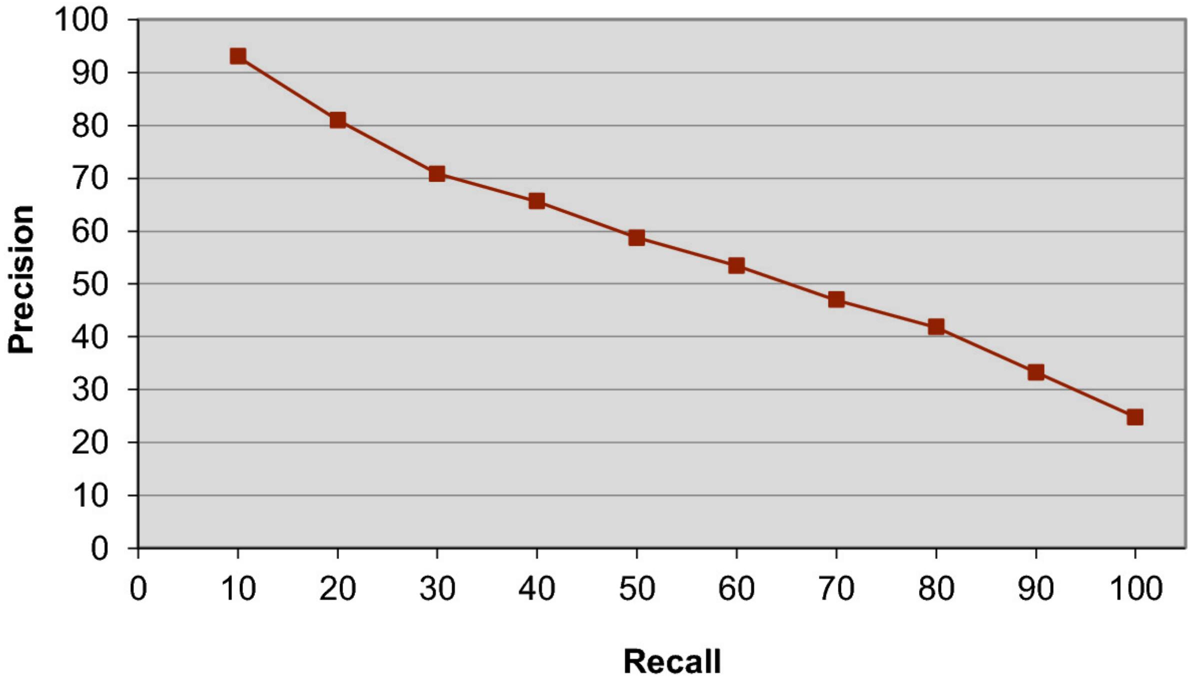


Fig. 12.8 RPP curve from an actual image retrieval

The RPP curve gives a good picture of a similarity measure's performance. A good similarity measure will have a RPP curve with two characteristics: (a) a high start (how high depends on applications), e.g., 70%+; (b) a gentle drop. However, it's often difficult to achieve both the two goals, a retrieval method usually either targets high precision on the top list of a retrieval result or targets higher recall depending on applications. Therefore, the *P* values at the lower recall values are much more important than those at higher recalls. For example, in Fig. 12.8, the *P* values before the 30% of recall are all above 70%, which indicates a good retrieval result although the full RPP curve does not look good.

Although RPP is intuitive, there are several drawbacks to this performance measure.

- **Need a ground truth**. In order to compute the *R* value, we need to know the total number of relevant images in a database which is essentially a ground truth. This limits the application of the RPP to databases with small scale.
- **Unrealistic relevance values**. The binary relevance value given to each of the images in the database is not realistic, because image similarity is probabilistic and between 0 and 1.

- **Missing ranking information**. All relevant images on the retrieval list are given the same relevance value, ranking information is not considered in defining the relevance values. However, a similar image at rank 1 is more relevant than a similar image at rank 10.
- **A pair of conflict values**. It is often awkward to tell the performance of a retrieval using *two* values which do not agree with each other. For example, if we have a retrieval which gives $P = 90\%$ and $R = 10\%$, it's difficult to tell how well is the retrieval result. Therefore, we need a measure to reconcile the P and R pair.

A number of other performance measures have been designed to address the above issues.

12.3.2 *F*-measure

A performance measure which reconciles the *precision* (P) and *recall* (R) into one is called the F-measure. It is defined as *harmonic mean* of P and R, which turns out to be the square of the *geometric mean* of P and R divided by the *arithmetic mean* of P and R.

$$F = \frac{P \cdot R}{\frac{P+R}{2}} = 2 \cdot \frac{P \cdot R}{P + R} \tag{12.26}$$

It can be shown that the following is true:

$$F = \alpha P + (1 - \alpha) R \tag{12.27}$$

where $= \frac{t+f_\mathrm{p}}{2t+f_\mathrm{p}+f_\mathrm{n}}$. Therefore, F turns out to be a weighted sum of P and R. The weight α can be adjusted to suit a specific data or application.

Figure 12.9 shows the F curve against the same P–R curve from Fig. 12.8. It can be observed that the F score has a low start and reaches the maximum value at the point where the P score is the closest to the R score. Before the peak point, precision is more important; after the peak point, recall is more important. Therefore, the peak point is the optimal trade-off between P and R. Overall, the higher the F score, the better trade-off between P and R. Therefore, for two similarity measures or retrieval results, the one gives a higher F score is usually better.

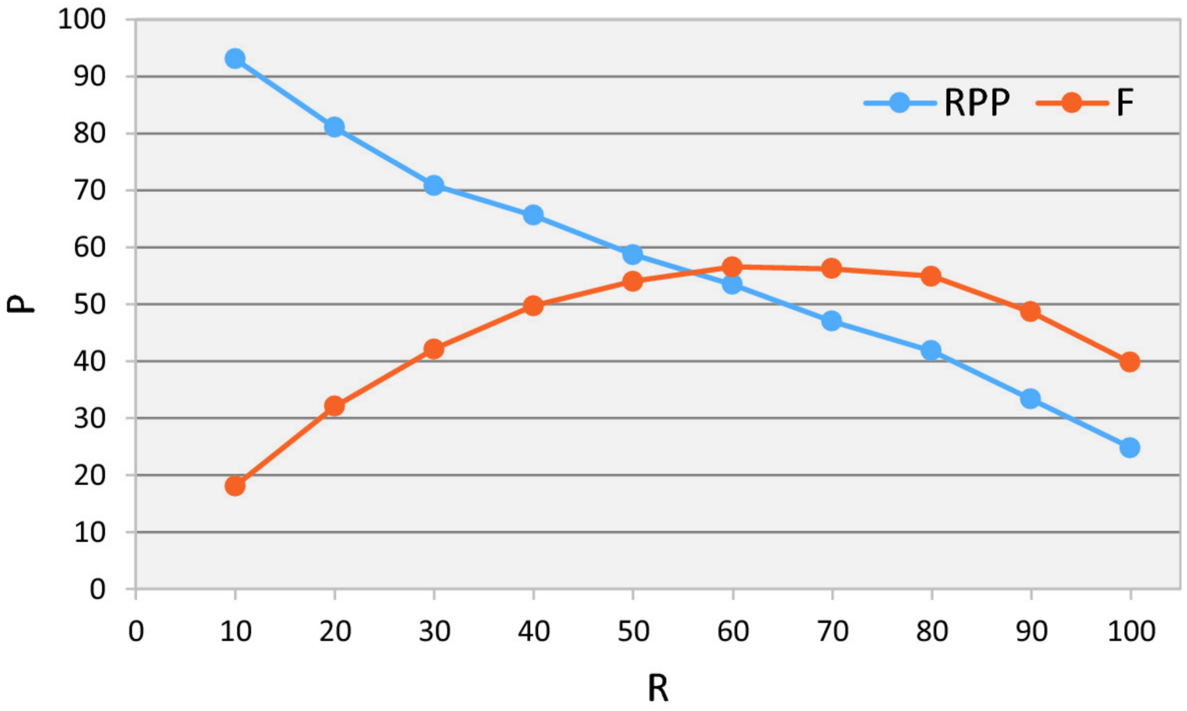


Fig. 12.9 *RPP* curve and *F* curve from an actual image retrieval

The advantage of using *F*-measure is that a single value can be used to tell the difference between two similarity measures or two retrieval results. However, it is not as intuitive as the RPP and it's not easy to interpret a *F* score. It appears we could have used an AUC or *area under* (the RPP) *curve*, as an alternative to *F*-measure. The AUC would be not only a single value but also as intuitive as the RPP. However, the AUC would not be able to differentiate a RPP with high start but sharp drop (a sliding RPP) and a RPP with low start but relatively flat (a steady RPP). The former RPP is usually more preferable than the later one, even though the former is not a good RPP either. Therefore, the AUC would not be as effective as the *F*-measure. For example, Fig. 12.10 shows a *sliding* RPP and a *steady* RPP with the same AUC. However, the maximum/optimal *F* score of the slide RPP is at middle of the RPP curve while the maximum/optimal *F* score of the steady RPP is at the very end of the RPP curve, which is undesirable, because it's unlikely that a user would wait until all the relevant images are shown up.

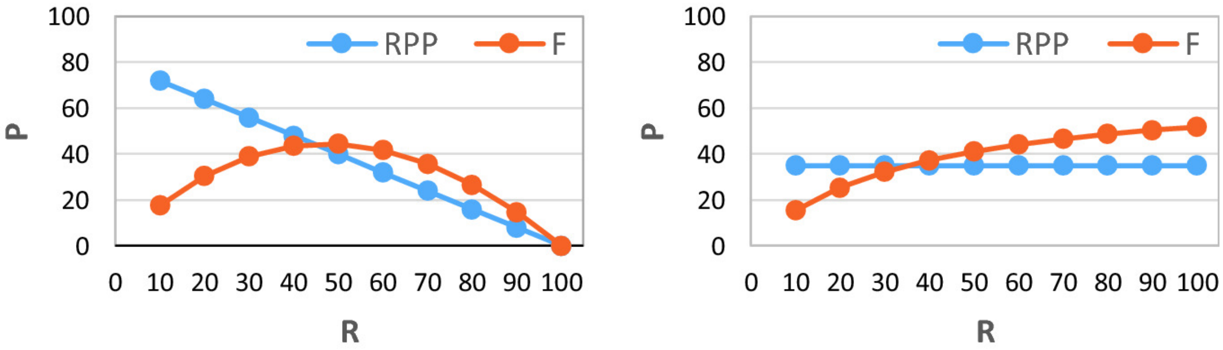


Fig. 12.10 *F* curves for two different RPP curves with the same area

12.3.3 Percentage of Weighted Hits (PWH)

The PWH can be regarded as a weighted recall. The subjective test is the same as in RPP, that is, each subject select items relevant to the query from the dataset. However, instead of measuring recall based on *binary relevance value* as in RPP, PWH assigns a *weighted relevance value* w_i to each item in the dataset. The sum of the weights w_i is equivalent to the number of subjects selecting item i as relevant or similar to the query. Therefore, PWH is defined as

$$\mathrm{PWH} = \frac{\sum_{i=1}^{n} w_i}{\sum_{i=1}^{N} w_i} \tag{12.28}$$

where n is the number of items retrieved and N is the total number of items in the database. It is easy to see that the R measure in RPP is a special case of PWH when w_i takes the value of 0 and 1. Similar to the R measure, PWH needs to identify every item in the database as relevant or not relevant to the query, this need for ground truth of the database limits its usage.

12.3.4 Percentage of Similarity Ranking (PSR)

PSR is a performance measure of detecting the agreement between an algorithm ranking and a human ranking [5]. In this method, each subject assigns a similarity rank to each item i in the dataset based on the item's similarity to the query j. For each query j, the final result of the subject test is a matrix $\{Q_j(i, k)\}$, where.

- $Q_j(i, k)$ is the number of subjects ranking item i at kth position.
- $\overline{p}_j(i)$ and $\overline{\sigma}_j(i)$ are the mean and variance of each row of $\{Q_j(i, k)\}$.
- $\overline{p}_j(i)$ represents the average ranking of the ith image to query j.
- $\overline{\sigma}_j(i)$ represents the degree of agreement among the subjects on ranking item i.

Given a query j, if a *retrieval algorithm* returns an item i at rank $P_j(i)$, the *percentage similarity ranking* $S_j(i)$ is defined as:

$$S_j(i) = \sum_{k=P_j(i)-\frac{\sigma_j(i)}{2}}^{P_j(i)+\frac{\sigma_j(i)}{2}} Q_j(i, k) \tag{12.29}$$

A plot of $S_j(i)$ as a function of item i show the retrieval performance of the retrieval algorithm. A high $S_j(i)$ curve indicates a high retrieval accuracy of the algorithm. An average PSR value can also be computed as the overall performance of the retrieval algorithm.

The PSR takes into account the number and agreement of human ranking. However, if for a query, the percentage of humans giving a particular item at particular ranking is high (high degree of agreement on ranking the item), then the variance for the ranking would be small. This would result in unusually low PSR if the retrieval algorithm's ranking differs from the subject mean ranking. On the other hand, if the variance of a ranking is large, the PSR would be unusually high even if the ranking by the retrieval algorithm differs substantially from the subject mean ranking.

12.3.5 Bullseye Accuracy

A simple Bullseye performance measure (BEP) is called *precision at K* or P@K, which is defined as the ratio of the 'number of relevant images on the top *K* retrieval' to *K*. This ratio is called a *Bullseye score*. The higher the Bullseye score, the better the retrieval. P@K is a very convenient and useful performance measure because it does not need the ground truth of the database. P@K measure is widely used in applications where the data is massive and the accuracy of the top retrievals is the most important. For example, in online web search, users only care about the relevance of the top pages returned by a search engine.

The K can be determined based on the actual data or application. If the total number of relevant images in the database is known to be N, K is typically determined as N or $2N$. In practice, Bullseye scores are obtained from a number of queries and an average Bullseye score is obtained as the overall performance value for a retrieval algorithm.

The *Bullseye score* can also be defined as the *average rank* (AR). In AR, instead of precisions, the ranks of relevant images on the top K retrieval list are averaged. The lower is the AR, the better is the retrieval result.

12.4 Hypothesis Testing

12.4.1 Introduction

Often there is a need to tell if a new feature or similarity measure has a significantly better performance than an existing one. In this situation, a *hypothesis test* or HT is conducted. In a hypothesis test, two hypothesises are designed: H_0 *and* H_1.

H_0: The new method has no significant difference from the existing one.

H_1: The new method is significantly different from or better than existing one.

H_0 is called the null hypothesis while H_1 is called the alternative hypothesis. In an actual HT, only H_0 needs to be tested. If the evidence supports H_0, it is accepted; otherwise, H_1 is accepted.

To conduct an HT, a sample of size n is collected from the new method, and a test statistic called z-score or t-statistic is calculated from the sample. The test statistic represents the *number of standard deviations from the mean*, which indicates if the sample mean under test is within a pre-determined *confidence interval* of a known population. If the test statistic falls outside the confidence interval of the known population, the null hypothesis H_0 is rejected and the alternative hypothesis H_1 is accepted. Therefore, a HT has the following components:

- A population or a sample from a population with known distribution to test against;
- A sample from an unknown population;
- A test statistic to measure the difference or distance between the two sample means;
- A significance level α to indicate the level of error we can accept for the difference. α determines our confidence interval.

12.4.2 Fundamental Theorems of Statistics

HT is based on two fundamental theorems of statistics: the law of large numbers (LLN) and the central limit theorem (CLT).

The Law of Large Numbers. *Given a population of unknown mean* μ*, if we take a sample of size n from the population and calculate the sample mean* $\bar{x}$*,* $\bar{x}$ *approximates to the population mean* μ *when n is sufficiently large. In other words,* $\bar{x} \rightarrow \mu \ for\ n \rightarrow \infty$.

The LLN states that we can use the sample mean to infer or predict a population mean as long as the sample size is large enough.

For example, suppose we want to know the proportion of men in a population. We take a sample of 1000 people from a region and find that the proportion is about 50%. If we want to be more certain, we can take a sample of 10,000 people across the country. The more people we sample, the closer is the proportion to 50%. The most accurate proportion is given by the country's census data from the entire population.

Other LLN examples are tossing a fair coin *n* times and count the average number of heads facing up; rotating a roulette wheel *n* times and count the average number of even numbers. The means of both experiments approximate to a stable figure 0.5 as *n* increases.

The Central Limit Theorem. *Given a population with mean* μ *and variance* σ^2*, if we repeatedly take a random sample of size n from the* *population to calculate the sample mean* $\bar{x}$ *and if n is sufficiently large* (*generally* ≥ *30*), *regardless of the population distribution*, *the following are true*:

- *The sample mean* $\bar{x}$ *is normally distributed around the population mean.*
- *The sample variance is given by the population variance divided by the sample size*: $s_n^2 = \frac{\sigma^2}{n}$ *and* $\frac{\sigma^2}{n} \to 0\, for\, n \to \infty$.

The CLT states that we can use the population statistics to infer or predict a sample's distribution. It also means that if we have a new sample, we can tell if the new sample is drawn from a given population. This is the key idea of HT. In the next, we will use examples to demonstrate how HT is done formally.

12.4.3 Properties of Normal Distribution

Before we do a HT, we need a good understanding of the normal distribution. Figure 12.11 shows some of the key figures of a normal distribution with 0 *mean* or $\mu = 0$ and *standard deviation* σ: $N(0, \sigma)$. When $\sigma = 1$, it's called the standard normal distribution or $N(0, 1)$.

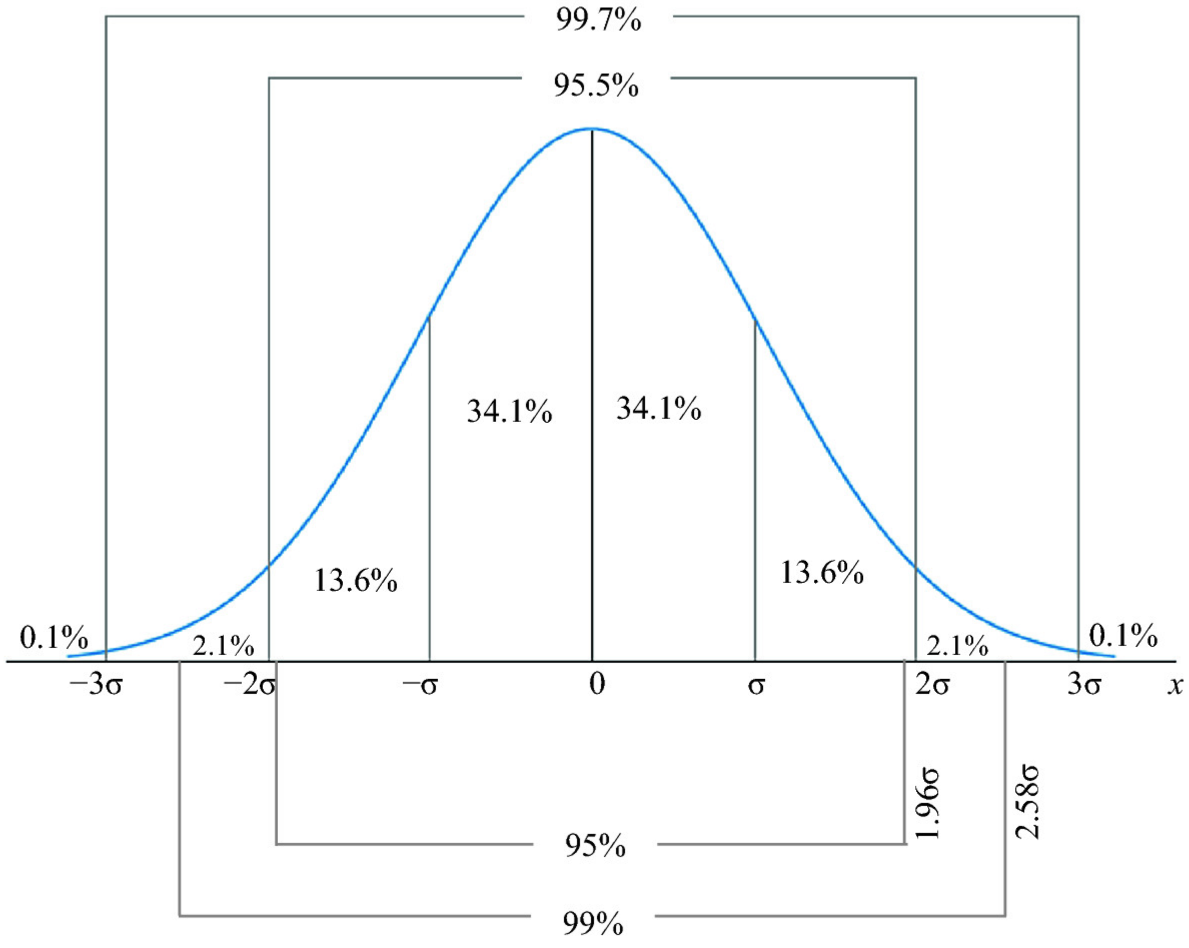


Fig. 12.11 Key figures of a normal distribution

The following important properties are obtained from a normal distribution shown in Fig. 12.11:

1. **μ and σ**. A normal distribution is completely determined by its mean μ and standard deviation σ (or variance σ^2).

2. **Symmetry**. A normal distribution function is symmetric around its mean, i.e., $P(x \leq -c) = P(x \geq c)$, for any $c > 0$, where P is the probability.

3. **Area under curve (AUC)**. Each AUC corresponds to the cumulative probability in a range of sample values. The total cumulative probability of a normal distribution is the total area under the normal curve, which is equal to 1.

4. **High density around the mean**. The closer a sample x to the mean, the more likely it belongs to the distribution; the further away a sample x from the mean, the less likely it belongs to the distribution. Almost all the samples of a normal distribution are within 3σ from the mean.

5. **95.5% samples in 2σ**. Around 95.5% of normal samples are within 2 *standard deviations from the mean*, which means:
   - $P(-2\sigma \le x \le 2\sigma) = P(|x| \le 2\sigma) = 95.5\%$.
   - The chance of a sample of a normal distribution falling beyond 2 standard deviations from the mean is just 4.5%.

6. **99.7% samples in 3σ**. Around 99.7% of normal samples are within 3 standard deviations from the mean, which means:
   - $P(-3\sigma \le x \le 3\sigma) = P(|x| \le 3\sigma) = 99.7\%$.
   - The chance of a sample of a normal distribution falling beyond 3 standard deviations from the mean is just 0.3%.

7. **95% confidence interval (CI)**. We have 95% confidence that samples of a normal distribution are within 1.96 standard deviations from the mean, which means:
   - $[-1.96\sigma, 1.96\sigma]$ is the 95% CI, or $P(-1.96\sigma \le x \le 1.96\sigma) = P(|x| \le 1.96\sigma) = 95\%$.
   - The total probability of the *two tails* given by $x < -1.96\sigma$ and $x > 1.96\sigma$ is just 5%.
   - The chance of a sample of a normal distribution falling beyond 1.96 standard deviations from the mean is just 5%.
   - $\pm 1.96\sigma$ are the *critical values* at 95% confidence level.
   - If the mean of a sample is either smaller than -1.96σ or greater than 1.96σ, the sample is significantly different from the test population at 95% *confidence level*.

8. **99% confidence interval**. We have 99% confidence that samples of a normal distribution are within 2.58 standard deviations from the mean, which means:

- $[-2.58\sigma, 2.58\sigma]$ is the 99% CI, or $P(-2.58\sigma \le x \le 2.58\sigma) = P(|x| \le 2.58\sigma) = 99\%$.
- The total probability of the *two tails* given by $x < -2.58\sigma$ and $x > 2.58\sigma$ is just 1%.
- The chance of a sample of a normal distribution falling beyond 2.58 standard deviations from the mean is just 1%.
- $\pm 2.58\sigma$ are the critical values at 99% confidence level.
- If the mean of a sample is either smaller than -2.58σ or greater than 2.58σ, the sample is significantly different from the test population at 99% confidence level.

9. **0.01 at one tail**. The left tail $x \le -2.33\sigma$ and right tail $x \ge 2.33\sigma$ both have the probability of 0.01, which means:
    - $P(x \le -2.33\sigma) = P(x \ge 2.33\sigma) = 0.01 = 1\%$.
    - $\pm 2.33\sigma$ are the critical values at 1% *significance level* for one-tail CI.

10. **0.05 at one tail**. The left tail $x \le -1.64\sigma$ and right tail $x \ge 1.64\sigma$ both have the probability of 0.01, which means:
    - $P(x \le -1.64\sigma) = P(x \ge 1.64\sigma) = 0.05 = 5\%$.
    - $\pm 1.64\sigma$ are the critical values at 5% significance level for one-tail CI.

11. **z-score**. A general normal distribution $x \sim N(\mu, \sigma)$ can be normalized to $N(0, 1)$ by a z-score variable: $z = \frac{x-\mu}{\sigma}$, which

    represents the number of standard deviations from the mean. This means:
    - $z \sim N(0, 1)$.
    - Probabilities of any normal distribution can be found from a $N(0, 1)$ lookup table or a z-table.
    - $P(x < c) = P\left(z < \frac{c-\mu}{\sigma}\right)$.

Therefore, to conduct a HT, it is important to remember the following quadriads (Table 12.1):

Table 12.1 Quadriads of a normal distribution

Confidence level	Significance level	Tails	Critical values
95	0.05	2	±1.96
95	0.05	1	±1.64
99	0.01	2	±2.58
99	0.01	1	±2.33

12.4.4 HT on a Single Population

An IT school suspects the results of students who are doing online study of a course are significantly poorer than students who are doing on-campus study. A random sample of 49 online students are selected, the average score of the sample is 62. The average score of the course from all students is 69 with standard deviation of 13. Suppose the significance level is $\alpha = 0.05$.

Summary of data:

- Population parameters of the course: $\mu = 69$, $\sigma = 13$;
- Sample data of online students: $\bar{x} = 62$, $n = 49$;
- Population mean of online students: μ_o;
- Significance level $\alpha = 0.05$.

Hypothesis test

1. H_0: $\mu_o = \mu$, the mean of the online students is the same as the mean of other cohorts or has no difference from that of other cohort

   H_1: $\mu_o < \mu$, the mean of the online students is significantly lower than that of other cohorts.

2. *z-score*. If H_0 is true, according to the CLT, $\bar{x} \sim N(\mu, \frac{\sigma}{\sqrt{n}})$. Now normalize $\bar{x}$ to $N(0, 1)$ using the z-score which indicates how significant is the difference between the means of the sample and the population:

$$z = \frac{\overline{x} - \mu}{\sigma / \sqrt{n}} = \frac{62 - 69}{13/7} = -3.769 \qquad (12.30)$$

3. *Critical value decision*. The z-score measures the number of standard deviations $\bar{x}$ is from the population mean, therefore, a quick decision can be made by comparing the z-score with the one-tail critical values of 95% CI. Details are as following.
   - Based on Fig. 12.11, if the z-score value is either positively too high or negatively too low, it indicates $\bar{x}$ is too far away from the population mean, which means the sample mean $\bar{x}$ is unlikely from the course population.
   - Z-score indicates our confidence of rejecting H_0, the larger the $| z |$ value, the higher the confidence of rejecting H_0, and vice versa, e.g., if $| z |=2$, we have at least 95% confidence to reject H_0; if $| z | = 3$, we have at least 99% confidence to reject H_0.
   - Intuitively, $z = -3.769$ is more than 3.7 standard deviations lower than the mean, which is very far away from the mean compared with the 3σ boundary.
   - The threshold of the z-score value to reject H_0 is given by the *critical value* z_α which is determined by the significance level α.
   - Because it is a one-tail test ($\mu_o < \mu$), the critical value is $z_\alpha = -1.64$ at the left tail based on the property 10 of Sect. 12.4.3.
   - Since $z = -3.769 < -1.64$, meaning z is far lower than the critical value or too far away from the population mean 69, we reject H_0.
   - This is because if the sample of online results was taken from the same population as that of other cohorts, the z value would be greater than -1.64 at 0.05 significance level.

4. *p-value decision*. To find how much evidence to reject H_0, we need to calculate the p-value (tailed-value) of the z-score. From the standard normal distribution table:
   - $p = P(z \leq -3.769) = 0.00008$.

- p is the chance of making an error if H_0 is rejected.
- However, our significance level is $\alpha = 0.05$, which is the maximum error (type I error) we would be willing to accept if we were to make a wrong decision.
- Now that $p = 0.00008 << 0.05 = \alpha$, our evidence of rejecting H_0 is very strong.
- p-value represents our evidence of rejecting the hypothesis H_0, the smaller the p-value, the stronger the evidence.
- p-value has an *inverse* relationship with the magnitude of z-score, the larger the $|z|$ value, the smaller the p-value, and vice versa.

The above test is a *one-tailed* HT, meaning we wish to know specifically if the sample mean is significantly *lower* than the population mean. However, if we simply wish to know if the sample mean is significantly *different* from the population mean, we can use a *two-tailed* HT.

- In this case, we would compare the z-score value −3.769 with the critical value −1.96 based on the property 7 of Sect. 12.4.3.
- Because $z = -3.769 < -1.96$, we conclude that the online results are significantly different from other cohorts and again we reject H_0.
- Because $z = -3.769 < -2.58$, we actually have 99% confidence to reject H_0 based on property 8.
- The confidence of a HT can also be shown from another perspective, i.e., the confidence of accepting H_1, or the *power of test*.

To summarize the above test process:

- We are trying to test if the following two distributions are from the same population: $N(\mu, \sigma)$ *versus* $N(\bar{x}, \frac{\sigma}{\sqrt{n}})$.
- The idea is to test if the means of the two distributions are close enough, or if the distance $d = |\mu - \bar{x}|$ is small enough.
- If the σ of the population under test is known, we measure d in terms of the number of standard errors ($\frac{\sigma}{\sqrt{n}}$) the population mean μ is from the sample mean $\bar{x}$, or z-score: $z = \frac{\bar{x}-\mu}{\sigma/\sqrt{n}}$.

- If the σ of the population under test is unknown, the number of standard errors ($\frac{\sigma}{\sqrt{n}}$) the population mean μ is from the sample mean $\bar{x}$ is given by this z-score: $z = \frac{\bar{x}-\mu}{s/\sqrt{n}}$, where s^2 is the variance of the sample.
- To make a quick or rough decision on whether to reject H_0, the z-score is used to compare with a corresponding critical value z_α.
- However, to make a more sensible and accurate decision, p-value is used to tell how much evidence to reject or not reject H_0.

12.4.5 Power of Test

We have just made a decision that the online student sample is drawn from a different population (H_1) than the course population (H_0), and the chance of error on this decision is about 0.008%. This is called the *type I error* which is made by rejecting a true H_0 or accepting H_1 when in fact the sample is drawn from H_0, i.e., $P(H_1|H_0)$. Type I error is like an error made by a jury which has convicted an innocent man (accept $H_1|H_0$) due to he is on the remote border of innocence.

But what is the chance of accepting a false H_0? This is called the *type II error* which is made by accepting H_0 when in fact the sample is from H_1, or $P(H_0|H_1)$. Type II error is like an error made by a jury which has acquitted a criminal (accept $H_0|H_1$) due to the man is on the cusp of innocence. Intuitively, the closer the means of the two distributions H_0 and H_1, the more the overlap between the two distributions, and the higher the chance of accepting H_0.

Type I error is named as α and often interpreted as the chance of 'rejecting/convicting a good guy,' 'false positive,' 'false hit,' 'false alarm,' etc. in different applications. Type II error is named as β and often interpreted as the chance of 'accepting/acquitting a bad guy,' 'a miss,' 'false negative,' 'failing to alarm,' etc.

Type I error and type II error have a reverse relationship as shown in Fig. 12.12, reducing α will increase β and vice versa and they cannot be minimized at the same time, e.g., minimizing conviction errors leads to increased acquittal errors in the court. Different applications choose to minimize a different type of error, e.g., the court system and search engines typically minimize type I errors (false positive), while security and medical applications typically minimize type II errors (false negative).

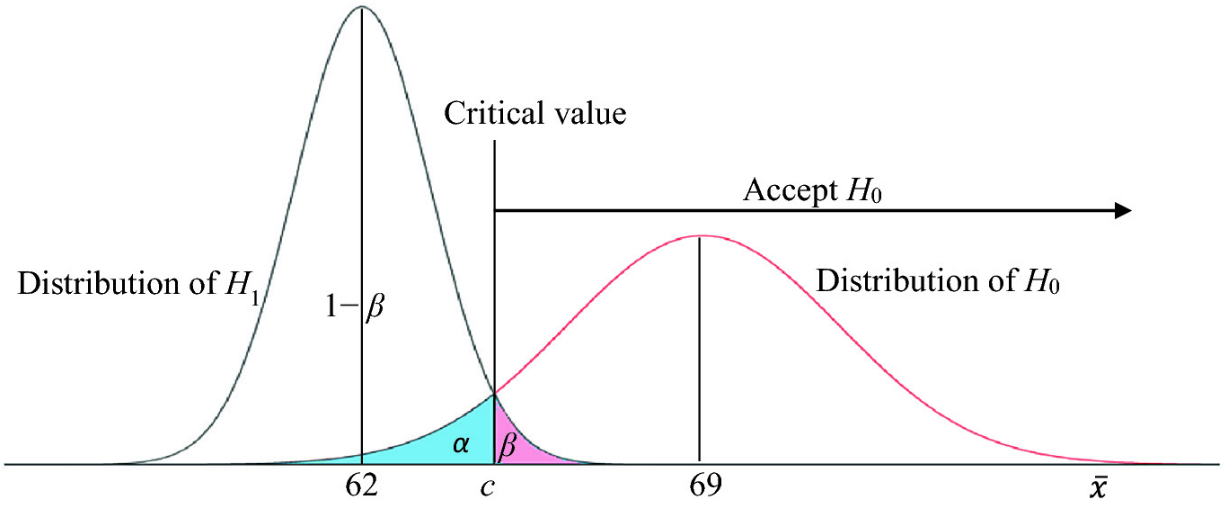


Fig. 12.12 Power of test (α and β are not in actual proportion)

To find out the chance of accepting H_0 given H_1 is true in the HT of Sect. 12.4.4, we need to calculate the overlap between H_1 and the acceptable region of H_0. Figure 12.12 shows this overlap as the pink region β. β is the type II error that samples from H_1 are incorrectly accepted into H_0 given H_1 is true.

$$\begin{aligned}\beta = P(H_0|H_1) = P(\bar{x} > c) = P\left(\bar{x} > \left(69 - 1.64\left(\frac{13}{7}\right)\right)\right) = P(\bar{x} > 65.95)\\ = P\left(z > \frac{65.95 - 62}{13/7}\right) = P(z > 2.13) = 0.0066\end{aligned} \tag{12.31}$$

Because the error β is very small, the population mean of the online students is highly likely to be 62 instead of 69. The *power of test* (PoT) in this case is $1 - \beta = 0.9934$ or 99.34%, which is very high. This is not surprising because there is about 3.77 standard deviations between H_0 and H_1. With this big distance, there is very little overlap between the two distributions, which means there is little chance of accepting H_1 as H_0. The PoT represents our confidence of accepting the hypothesis H_1; the higher the PoT, the higher the confidence.

Other hypothetical means such as 60, 61, …, can also be checked for the power of test in the similar way, and a PoT curve against different means can be plotted. For example, for hypothesis H_1: $\mu_o = 61$, the type II error is given by:

$$\beta = P\left(z > \frac{65.95 - 61}{13/7}\right) = P(z > 2.66) = 0.0039 \tag{12.32}$$

The PoT is $1 - \beta = 0.9961$ or 99.61%.

12.4.6 HT on Difference of Means

A researcher wants to compare a new classification method (A) he has developed with an existing method (B). He runs both methods A and B on a number of randomly selected subsets from a standard image database. The following are the average classification accuracy (%) from each run of the two methods:

- 10 classification results from method A: 23, 45, 21, 22, 17, 39, 45, 41, 51, 19.
- 6 classification results from method B: 33, 23, 19, 45, 32, 20.

Can he claim at the 5% significance level that method A outperforms method B? Suppose the sample of method A is from a population with mean μ_1 and the sample of method B is from a population with mean μ_2. The question can be answered by testing if the two samples are from same population or different population, that is, whether $\mu_1 = \mu_2$ or $\mu_1 > \mu_2$.

Summary of data:

- Method A: $\overline{x}_1 = 32.3$, $s_1^2 = 169.3$, $n_1 = 10$;
- Method B: $\overline{x}_2 = 28.7$, $s_2^2 = 99.4$, $n_2 = 6$;
- The pooled standard deviation:

$$s = \sqrt{\frac{(n_1 - 1)\, s_1^2 + (n_2 - 1)\, s_2^2}{n_1 + n_2 - 2}} = \sqrt{\frac{9 \times 169.3 + 5 \times 99.4}{14}} = 12 \tag{12.33}$$

- Because the sample sizes are smaller than 30, the t-statistic is used instead of z-score:

$$t = \frac{(\overline{x}_1 - \overline{x}_2) - (\mu_1 - \mu_2)}{s\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}} \tag{12.34}$$

- t follows the *student distribution* and the degree of freedom of the t-statistic is $n_1 + n_2 - 2 = 14$.

Hypothesis test

1. H_0: $\mu_1 = \mu_2$ (the two methods have no significant difference)
   H_1: $\mu_1 > \mu_2$ (method A is significantly better than method B).

2. t-statistic. If H_0 is true, the following t-statistic follows a student distribution with 14 degrees of freedom:

$$t = \frac{(\overline{x}_1 - \overline{x}_2) - 0}{s\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}} = \frac{32.3 - 28.7}{12 \times \sqrt{0.267}} = \frac{3.6}{6.2} = 0.58 \tag{12.35}$$

3. *Critical value decision*. The t-statistic is similar to the number of standard deviations from the mean, if the t value is positively too high or negatively too low we would reject H_0.
   - Intuitively, $t = 0.58$ is less than one standard deviation from the mean, which is close to the mean 0.
   - The threshold of t to reject H_0 is given by the *critical value* which is determined by the significance level α.
   - Use a t-table or an online t-table calculator such as the following website to work out the *critical value*: https://stattrek.com/online-calculator/t-distribution.aspx (Tip: at each calculation, only one of the *t-score* and the *probability* fields can be filled, but not both).
   - The critical value c for a t-distribution with 14 degrees of freedom and $\alpha = 0.05$ is $c = 1.76$.

- Since $t = 0.58 < 1.76$, we do not reject H_0, meaning H_1 is unlikely true.

4. *p-value decision*. To find out how much evidence to reject H_0, we need to calculate the p-value of the t-statistic. From the t-distribution table:
    - $p = P(t \geq 0.58) = 0.2855 = 28.55\%$.
    - p is the chance of making an error if H_0 is rejected.
    - However, our significance level is $\alpha = 0.05$, which is the maximum error we would be willing to accept if we were to make a wrong decision.
    - Now that $p = 0.2855 >> 0.05 = \alpha$, our evidence or confidence of rejecting H_0 is very weak. Therefore, we do not reject H_0.

12.4.7 Summary of HT

A hypothesis test can be summarized as the following seven steps:

1. Formulate a null hypothesis H_0;
2. Formulate an alternative hypothesis H_1;
3. Choose a significance level α;
4. Calculate the appropriate test statistic z (or t);
5. Find the corresponding tabulated statistic $\underline{\widehat{z}}$ or critical value c from a probability table;
6. Compare the calculated statistic z with c;
7. Decide whether to accept or reject the null hypothesis H_0.

12.4.8 Margin of Error

One of the key issues in a hypothesis test is the control of accuracy which is determined by sample size. If the sample size is too small, the test would not be accurate. On the other hand, it is too costly to do a large sampling. The question is what is the appropriate sample size to satisfy the expected accuracy while economic? Fortunately, the right sample size can be determined by using the CLT.

According to the CLT, given a population with mean μ and variance σ^2, if we repeatedly take random samples of size n from the population (with replacement), the sample means $\bar{x}$ follows the following normal distribution when n is sufficiently large:

$$\overline{x} \sim N\left(\mu, \frac{\sigma}{\sqrt{n}}\right) \tag{12.36}$$

Notice that the distribution of $\overline{x}$ has approximately the same mean as the population mean μ while the standard deviation of $\bar{x}$ is $\frac{\sigma}{\sqrt{n}}$ which is much smaller than the standard deviation σ of the population distribution.

The *confidence interval* of $\overline{x}$ at a confidence level γ (or significance level $\alpha = 1 - \gamma$) is given by $\left(\mu - z_\alpha \frac{\sigma}{\sqrt{n}}, \mu + z_\alpha \frac{\sigma}{\sqrt{n}}\right)$, where z_α is the z-score and $\frac{\sigma}{\sqrt{n}}$ is called the *standard error*. Therefore, the maximal distance between the mean of $\overline{x}$ and the mean of the population at a confidence level γ is given by E:

$$E = z_\alpha \frac{\sigma}{\sqrt{n}} \tag{12.37}$$

E is called the *margin of error*, which determines the accuracy of a sampling. The larger the sample size n, the smaller the E, and vice versa.

Therefore, the sample size n can be determined by:

$$n = \left(\frac{\sigma z_\alpha}{E}\right)^2 \tag{12.38}$$

For a data with '*yes*' or '*no*' outcome, which is typical in a classification experiment, the probabilities are given by proportion *p* for *yes* = 1 and *q* = 1 − *p* for *no* = 0. The mean of this distribution is *p* and the variance is $\sigma^2 = p(1-p)$. Therefore, the sample size can be determined by:

$$n = p(1-p)\left(\frac{z_\alpha}{E}\right)^2 \tag{12.39}$$

In the absence of population variance, the maximal variance is assumed, that is, max $\sigma^2 = \max p(1-p)$ = 0.25 at *p* = 0.5. Therefore, a conservative sample size can be determined by:

$$n = 0.25\left(\frac{z_\alpha}{E}\right)^2 \tag{12.40}$$

For example, at 95% confidence level, the *z*-score is 1.96, with a margin of error of 5%, the sample size is given by:

$$n = 0.25\left(\frac{1.96}{0.05}\right)^2 = 384 \tag{12.41}$$

If we want the margin of error to be smaller, e.g., *E* = 2%, the sample size *n* has to be larger:

$$n = 0.25\left(\frac{1.96}{0.02}\right)^2 = 2401 \tag{12.42}$$

12.5 Summary

Once images are stored and indexed, similarity measure and performance measure work together to rank images similar to a query.

To draw an analogy, image retrieval is like gold mining. A similarity measure is analogous to a refinery procedure in gold mining and the performance measure is equivalent to a laboratory test which determines if a refinery procedure produces sufficient yield of pure gold.

Design of similarity measures can be divided into three categories: (a) Geometric-based methods such as L_p, cosine distance. (b) Statistical methods such as $\chi 2$ statistic, histogram intersection d_{HI}, Mahalanobis distance d_m. (c) Hybrid methods such as h_p, m_p, quadratic distance d_q. Zhang and Lu [1] have made an evaluation of the commonly used similarity measures using the MPEG-7 shape image databases; it has been found that the *city block distance*, *Euclidean distance* and $\chi 2$ *statistic* are among the top performance similarity measures. The possible reason to explain this finding is that the three distances are all simple. The more complex a similarity measure is, the more unpredictable the result.

The design of a performance measures is based on three types of criteria: (a) Accuracy, such as P, P@K. (b) Robustness, such as R, PWH. (c) Both accuracy and robustness, such as RPP, F, PSR and AR. Each of these performance measures can be varied by how the relevance value is determined and how the ranking information is used. Overall, the RPP and P@K are the most intuitive and have the least complexity.

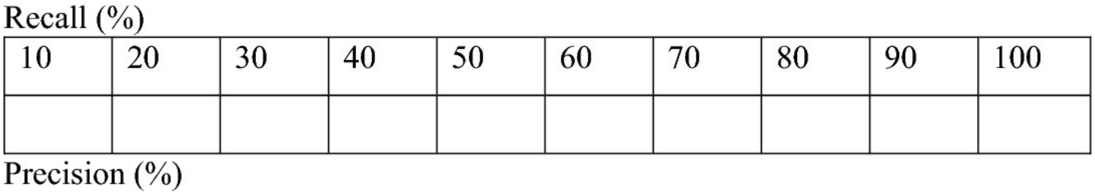
Hypothesis testing is another powerful tool of measuring performance. The difference between an HT and other conventional performance measures is that it not only tells the difference between different methods but also tells how significant is the difference. The result from an HT is usually more convincing. This chapter summarizes key statistical theories of HT with intuitive explanations and uses two examples as a toolkit to demonstrate the typical procedures of doing an HT.

Although we have only demonstrated how to use these performance measures to evaluate the performance of the similarity measures introduced in this chapter, they can also be used to evaluate the performance of different image features described in Part II in the same way.

12.6 Exercises

1. Similarity measures. Find two similar images, import them to Matlab Workspace using `I1` = `imread(image1)` and `I2` = `imread(image2)`. Next, compute the histogram of each image using `[h1, loc1]` = `imhist(I1)` and `[h2, loc2]` = `imhist(I2)`. Normalize each of the vectors `h1` and `h2` to [0, 1]. Compute the χ^2 statistic and histogram intersection distance between `h1 and h2`. Find two different images and recalculate the two distances, write a short report on your findings of the two similarity measures.

2. RPP. Search Google Images using each of these keywords: ‘cotton,’ ‘peanut,’ ‘sweet potato.’ Examine the retrieved images on screen, use ‘ctrl –’ to view more images per screen. Suppose there are 200 relevant images in total associated with each of the keywords. Use the following table to work out the precision value at each level of recall, e.g., the precision of the first 20 retrieved images (R = 10%), the first 40 retrieved images (R = 20%), so on so forth:



Recall (%)

10	20	30	40	50	60	70	80	90	100

Precision (%)

   - Next, copy the filled table to MS Excel and make a RPP graph shown in Fig. 12.8 using **Insert → Scatter → Scatter with Smoothed Lines and Markers**.
   - Compute the P@K values for the three retrieval results with different K values.
   - Contrast the pros and cons of RPP and P@K.

3. Statistical test. Marry is testing a new CNN she has developed against a pre-trained CNN which has a 78% classification accuracy on a subset of images from ImageNet. She tests her CNN using the same subset of images which consist of 100,000 images from 1000

categories. She randomly selects 100 categories of images and uses one vs all method to test the classification performance. The following are the classification results from her 100 trials. Marry wants to know if the performance of her CNN is significantly higher than the pre-trained CNN. Design a hypothesis test for Marry using a significance level of 0.01 and tell Marry the test result.

78	**84**	**75**	**86**	**84**	**81**	**84**	**89**	**78**	**98**
67	95	81	81	80	68	67	64	99	78
56	69	91	77	91	84	79	72	57	93
75	74	90	77	65	96	85	87	99	83
93	85	86	86	70	100	73	78	64	87
83	70	90	75	70	87	84	69	96	96
74	72	71	86	65	97	87	87	100	69
77	71	86	92	99	77	79	73	94	65
81	90	76	68	81	71	78	68	82	100
92	87	69	79	65	82	94	53	82	89

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13. Image Presentation

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The best usually is also the simplest.

13.1 Introduction

Image presentation is about how present the database images or retrieved images to the user in the most effective and efficient way. Given a query from a user, the list of images retrieved from the database can number from thousands to millions. Due to the limitation of both image features and image ranking, the retrieval list is usually full of irrelevant images. How to organize the retrieved images and present as many relevant images as possible in a very limit space is a great challenge in IR. Image presentation is part of the research on user interface and data visualization. It's a mixture of tech and arts. Many interesting image presentation methods have been developed, they include simple browsing, category browsing, content browsing, hierarchical organization, and sophisticated approaches involving user interaction, etc. In this chapter, we discuss a number of the most common approaches on image presentation.

13.2 Caption Browsing

If images in the database have been labeled with captions, the simplest way to find relevant images is through caption browsing. This is typically used in personal/family photo albums stored in PCs and photo galleries on webpages, which are usually labeled, dated and grouped by photo takers.

Caption browsing can also be used in image retrieval. If a retrieval list is not long, this method can be used to scan through the images on the list in order to find the most relevant images. Figure 13.1 shows a caption browsing given by MS Windows File Explorer.

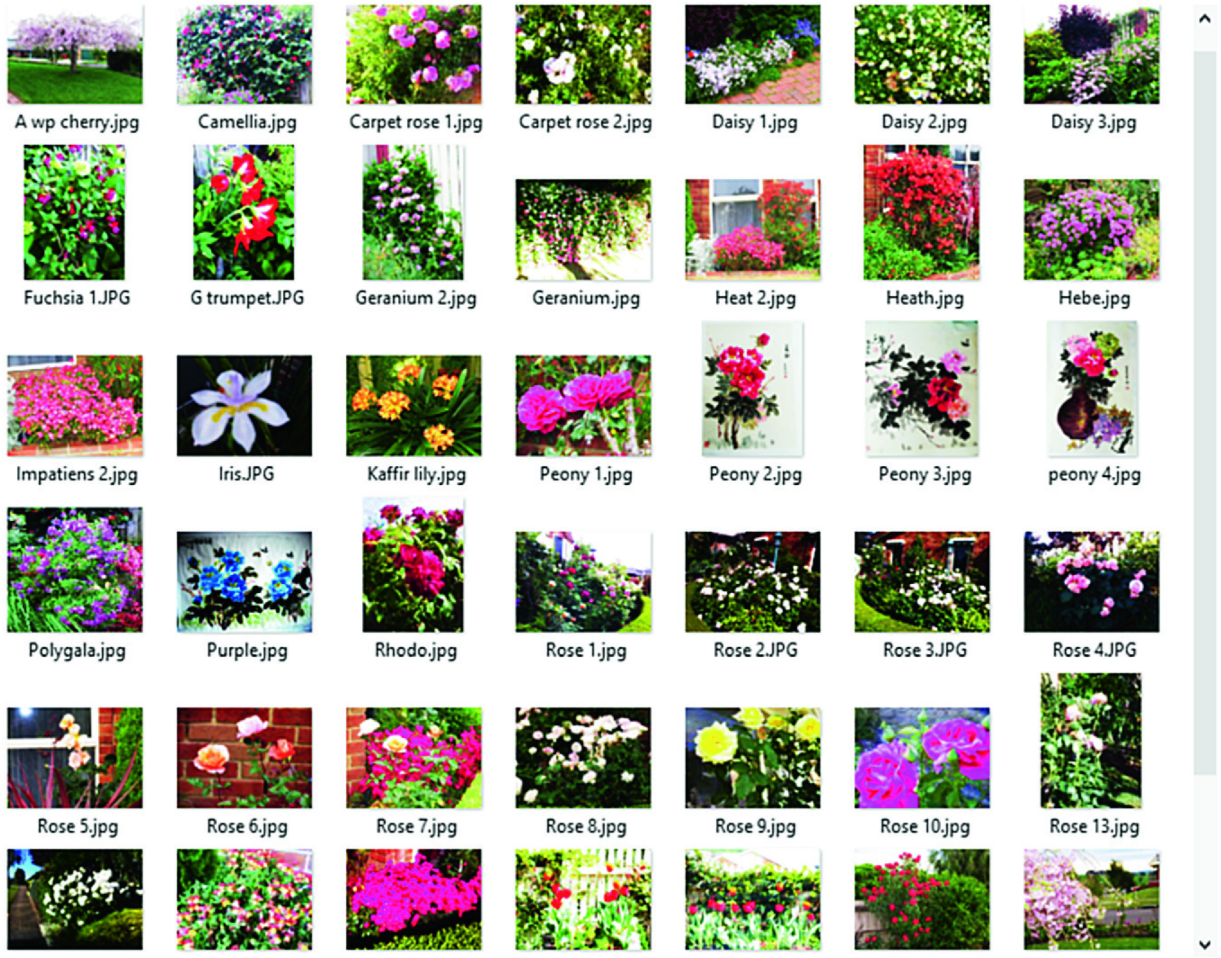

A wp cherry.jpg
Camellia.jpg
Carpet rose 1.jpg
Carpet rose 2.jpg
Daisy 1.jpg
Daisy 2.jpg
Daisy 3.jpg
Fuchsia 1.JPG
G trumpet.JPG
Geranium 2.jpg
Geranium.jpg
Heat 2.jpg
Heath.jpg
Hebe.jpg
Impatiens 2.jpg
Iris.JPG
Kaffir lily.jpg
Peony 1.jpg
Peony 2.jpg
Peony 3.jpg
peony 4.jpg
Polygala.jpg
Purple.jpg
Rhodo.jpg
Rose 1.jpg
Rose 2.JPG
Rose 3.JPG
Rose 4.JPG
Rose 5.jpg
Rose 6.jpg
Rose 7.jpg
Rose 8.jpg
Rose 9.jpg
Rose 10.jpg
Rose 13.jpg

Fig. 13.1 Browsing images using image captions by Windows File Explorer

The advantage of using caption browsing is that it is effortless and it suits for universal users. Furthermore, users can search images based on image captions or date information. For small image databases or a short image retrieval list, caption browsing is the best option. A major issue with caption browsing is that the caption labels are subjective, they are often confusing and even misleading.

13.3 Category Browsing

Category browsing is a typical approach for organizing image databases which are much larger than personal or family photo albums. Suppose images have been classified or annotated using the methods described in Part III, images can be organized into categories just like books are organized in library. Indeed, this is exactly how images are traditionally indexed in library and archives. Under each category, users can further filter the images by using a simple browsing. Figure 13.2 shows an example of category browsing used by MS Windows File Explorer.

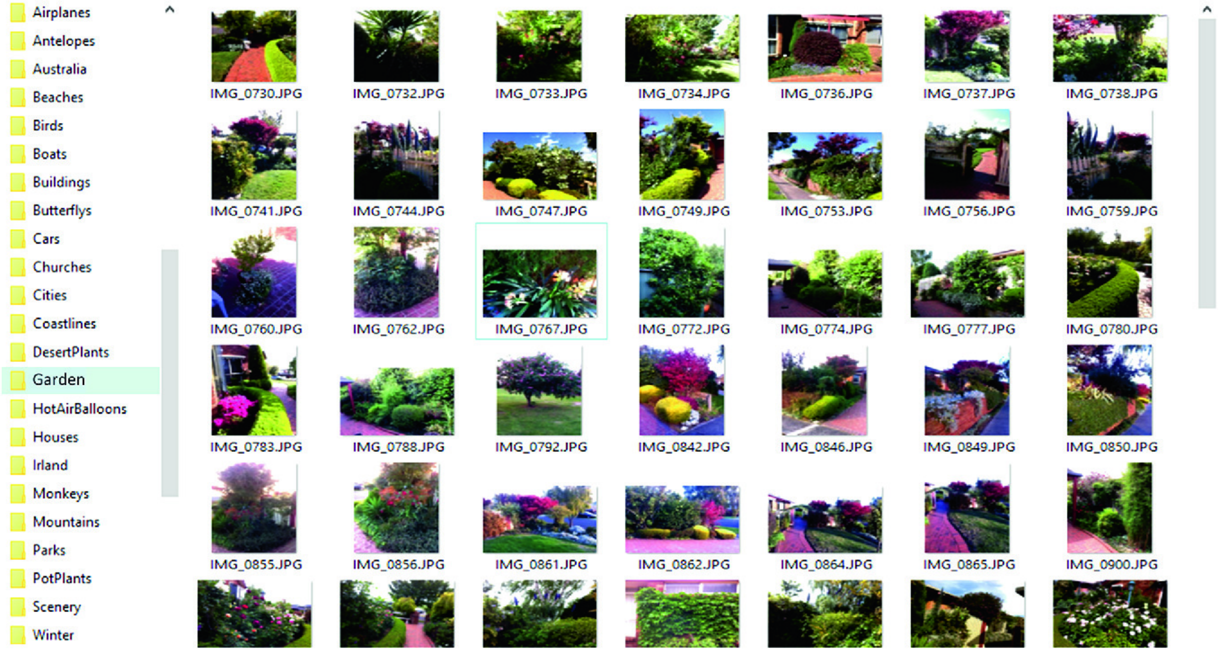
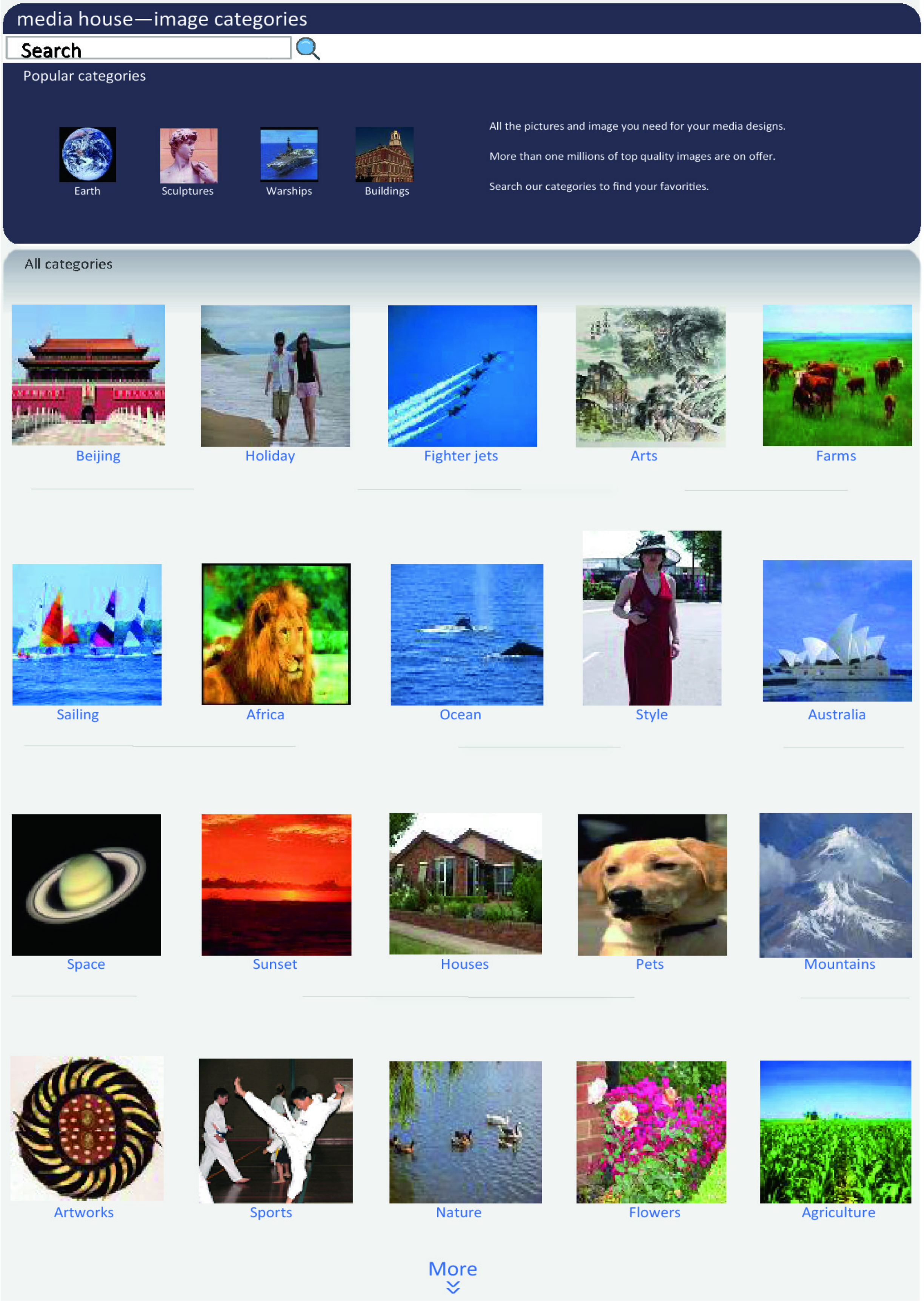

Airplanes
Antelopes
Australia
Beaches
Birds
Boats
Buildings
Butterflys
Cars
Churches
Cities
Coastlines
DesertPlants
Garden
HotAirBalloons
Houses
Irland
Monkeys
Mountains
Parks
PotPlants
Scenery
Winter
IMG_0730.JPG
IMG_0732.JPG
IMG_0733.JPG
IMG_0734.JPG
IMG_0736.JPG
IMG_0737.JPG
IMG_0738.JPG
IMG_0741.JPG
IMG_0744.JPG
IMG_0747.JPG
IMG_0749.JPG
IMG_0753.JPG
IMG_0756.JPG
IMG_0759.JPG
IMG_0760.JPG
IMG_0762.JPG
IMG_0767.JPG
IMG_0772.JPG
IMG_0774.JPG
IMG_0777.JPG
IMG_0780.JPG
IMG_0783.JPG
IMG_0788.JPG
IMG_0792.JPG
IMG_0842.JPG
IMG_0846.JPG
IMG_0849.JPG
IMG_0850.JPG
IMG_0855.JPG
IMG_0856.JPG
IMG_0861.JPG
IMG_0862.JPG
IMG_0864.JPG
IMG_0865.JPG
IMG_0900.JPG

Fig. 13.2 Category browsing using MS Windows File Explorer

The advantage of category browsing is that very large collections of images can be broadly organized into categories every efficiently, and there is no need to label individual images. This is particularly useful given there is massive amount of digital images on the Internet and most of the images are either unlabeled or mislabeled. However, images in categories of very large image collections are usually too diverse both perceptually and semantically. A common approach is to subdivide each of the categories into subcategories and a more efficient hierarchical category browsing is designed.

13.3.1 Category Browsing on the Web

More effective and efficient category browsing methods have been designed for the web where each category is initiated with one or more representative images. Figure 13.3 shows an example website using category browsing. It can be seen that the web category browsing is more effective and efficient than a desktop file explorer, because it not only visualizes each category with one or multiple iconic images but also provides a convenient searching mechanism. Furthermore, a web browsing system also provides a user with key information about the image collection and categories, such as the number of categories, number of images, types of images, source of images, instructions on retrieving the images, how to use the images, etc. More examples of category browsing on the web can be found online by googling for ‘image categories.’


media house—image categories
Search
Popular categories
Earth
Sculptures
Warships
Buildings

All the pictures and image you need for your media designs.

More than one millions of top quality images are on offer.

Search our categories to find your favorities.

All categories
Beijing
Holiday
Fighter jets
Arts
Farms
Sailing
Africa
Ocean
Style
Australia
Space
Sunset
Houses
Pets
Mountains
Artworks
Sports
Nature
Flowers
Agriculture
More

Fig. 13.3 Website of category browsing

13.3.2 Hierarchical Category Browsing

Categories of the same concept can be merged to organize the image database into a *hierarchical* or *tree* structure. On the other hand, if there are too many images in a category, it can be subdivided into subcategories. The subjective labeling issue in image categorization can be overcome by using a thesaurus such as the WordNet [1].

The design of a hierarchical category browsing system can be done either before the collection of images or during the collection of images. Due to the lack of standard image taxonomy, image categories are typically defined during the collection of images or defined ‘on the run.’ In this case, images should be put into as many categories as possible, so that higher level of categories can be created by merging similar subcategories using a thesaurus. Images can be most efficiently retrieved by using a standard hierarchy like the one used to classify animals or plants.

Figure 13.4 shows an example of hierarchical organization of image categories; each top-level category is demonstrated with a number of iconic images to give an idea on what’s inside the category. It can be seen that it’s a more effective and efficient presentation of image categories than that in Fig. 13.3, because more image categories can be shown to users in one web page.

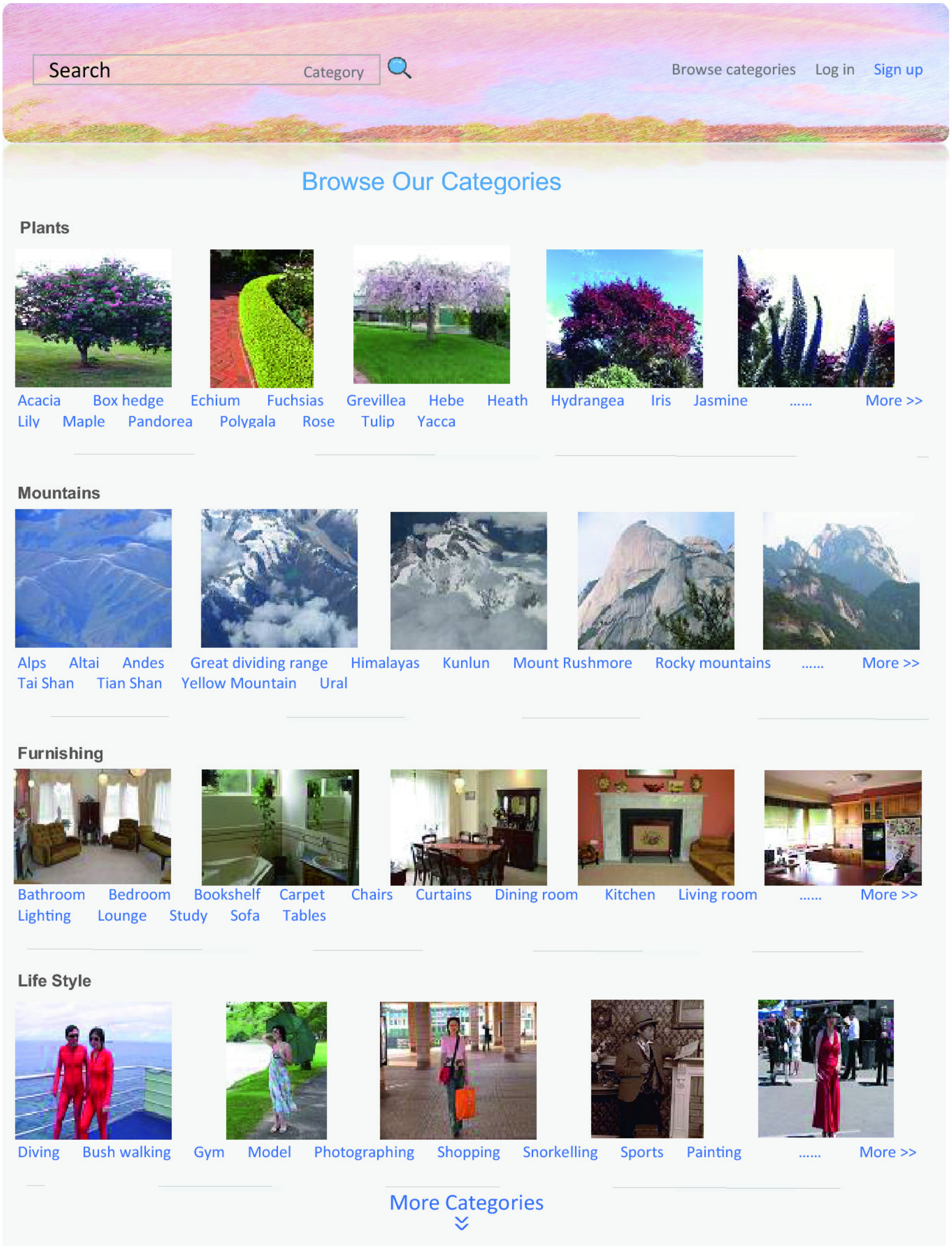

Search
Category
Browse categories
Log in
Sign up
Browse Our Categories
Plants
Acacia Box hedge Echium Fuchsias Grevillea Hebe Heath Hydrangea Iris Jasmine ...... More >>
Lily Maple Pandorea Polygala Rose Tulip Yacca
Mountains
Alps Altai Andes Great dividing range Himalayas Kunlun Mount Rushmore Rocky mountains ...... More >>
Tai Shan Tian Shan Yellow Mountain Ural
Furnishing
Bathroom Bedroom Bookshelf Carpet Chairs Curtains Dining room Kitchen Living room ...... More >>
Lighting Lounge Study Sofa Tables
Life Style
Diving Bush walking Gym Model Photographing Shopping Snorkelling Sports Painting ...... More >>
More Categories

Fig. 13.4 Hierarchical organization of image categories on a website

13.4 Content Browsing

Images in the database or on a retrieval list can also be organized based on *numerical image features* instead of semantic labels as shown in the above sections. Numerical image features are also called low level image features, perceptual features or *content features*. Therefore, image retrieval based on numerical image features is called *content-based image retrieval* or CBIR for short. The idea of *content browsing* is to convert and group retrieved images as thumbnails based on their perceptual similarity such as color, texture or shape. The organization of the thumbnails is then presented as an *image map* to guide a user to navigate to the most relevant images. This is very useful because people usually judge image similarity based on perception, and perceptual features are usually less subjective than semantic labeling which can vary widely from person to person. Figure 13.5 shows an example of content browsing.

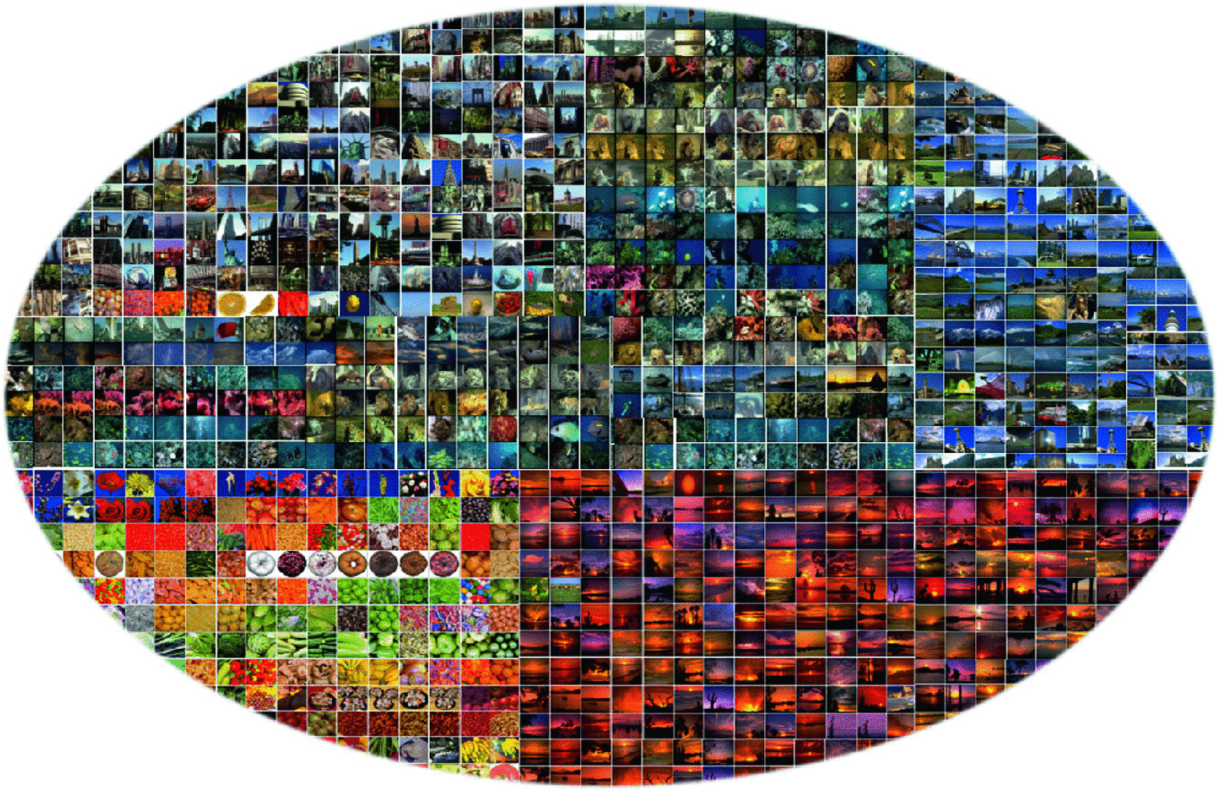


Fig. 13.5 Image presentation based on content browsing

Content browsing is a study of image *data visualization*. Key issues in content browsing include:

- **Features** of images. What image feature(s) to use? Typically images to be presented are grouped-based color, texture, shape or combination of them, it depends on the nature of the image data and application.
- **Similarity** measure. What similarity measure to use? Different similarity measure can lead to different perceptual experience on the content browsing.
- **Size** of thumbnails. Should they be equal size or different size depending on relevance?
- **Overlap** of thumbnails. Should thumbnails be overlapped and how much?
- **Structure and layout** of thumbnails. Should they be organized in row and column, spiral or graph?
- **Space** of presentation. Whether images are presented in 2D space or 3D space such as a cylinder or a sphere.
- **Interaction**. What type of interaction to use and how a user can interact with the thumbnails?

These factors are determined by research on how the physical world can be most effectively presented to human vision system.

13.4.1 Content Browsing in 3D Space

The limited space of a 2D screen can be extended by using a 3D cylinder (Fig. 13.6) [2], or a sphere (Fig. 13.7) to present more thumbnails in an image map [3]. Images can also be presented on a curved wall as shown in Fig. 13.8 to extend the visual space.

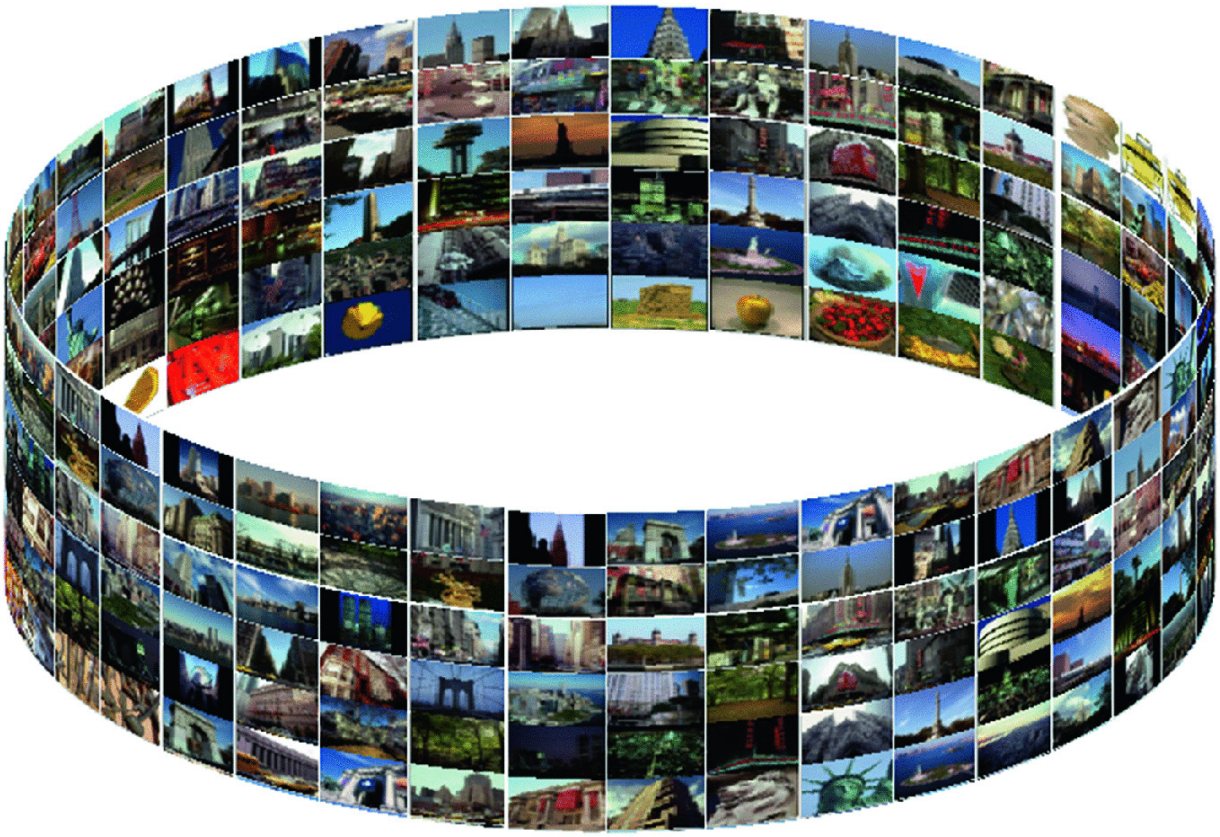


Fig. 13.6 Content browsing using a cylindrical image map

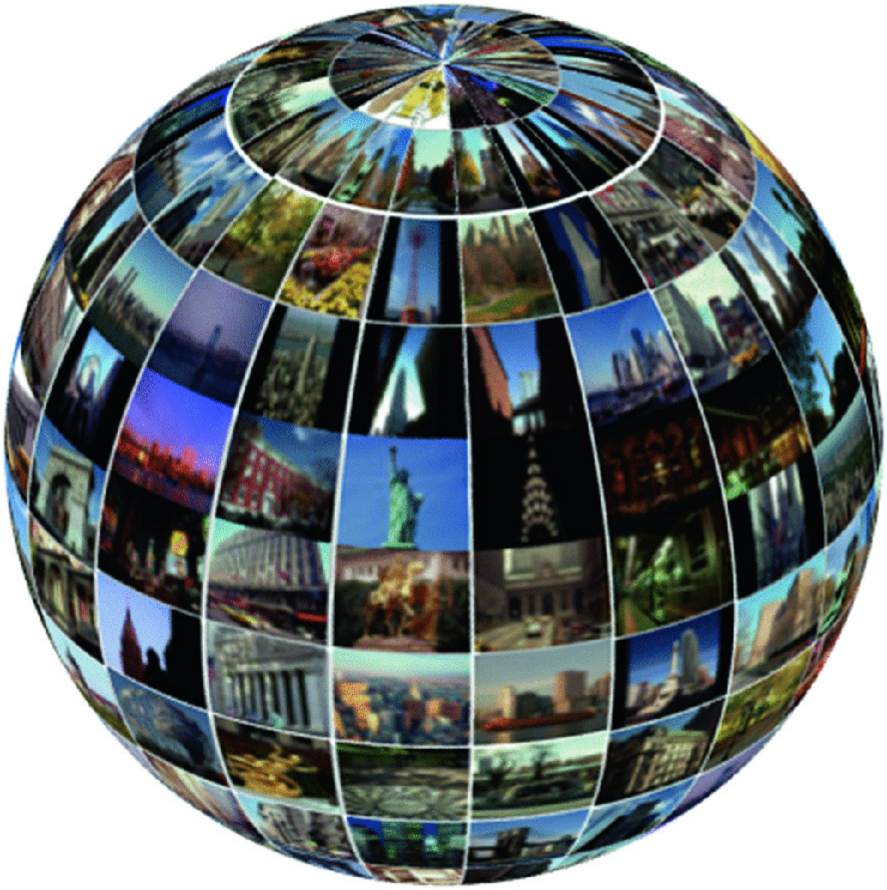


Fig. 13.7 Content browsing using a spherical image map

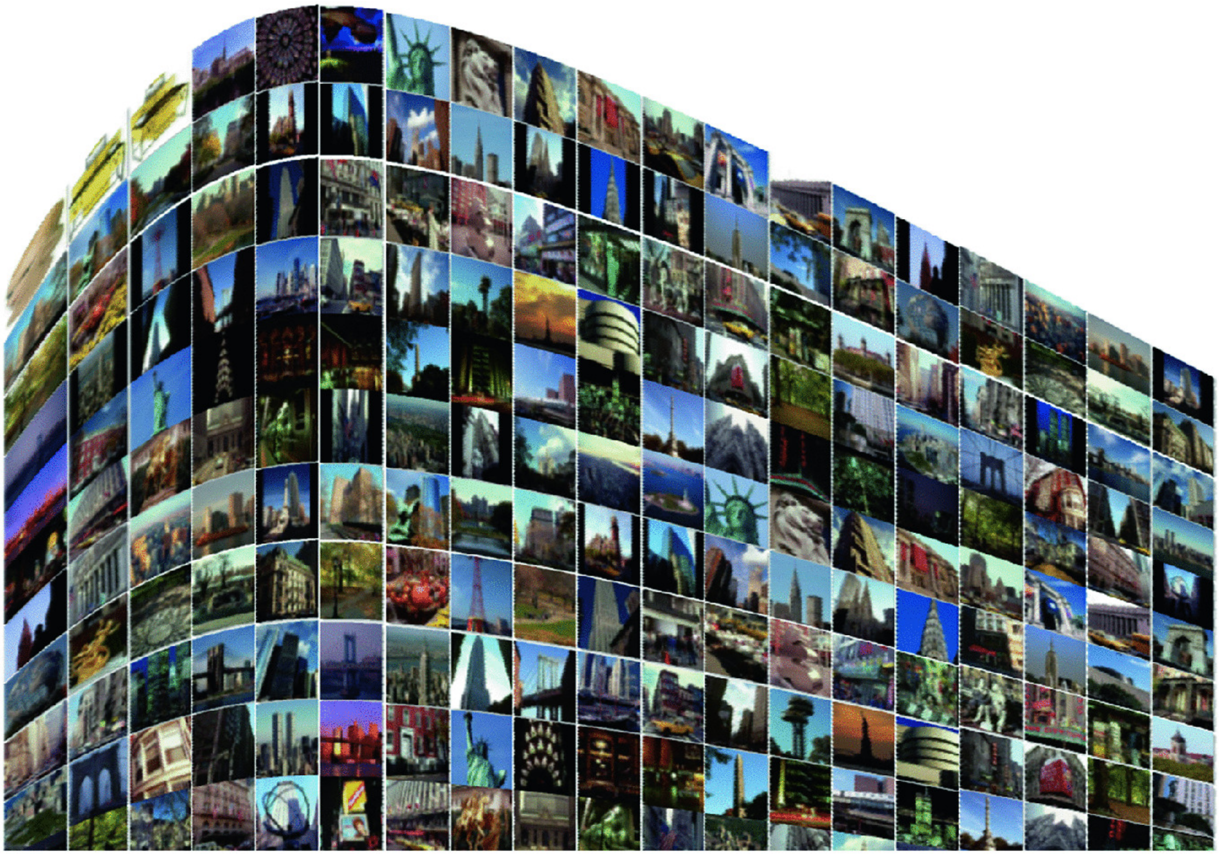


Fig. 13.8 Content browsing using a curved wall image map

13.4.2 Content Browsing with Fish Eye View

Content browsing with equal size thumbnails provides a global view of the visualized image data. Alternatively, a fish eye view of the image map provides a content browsing with *focus*. For example, in Fig. 13.9, images on the top of the retrieval list are given focus and presented in the center of the screen with larger size according to their similarity to the query image, and they are then arranged in a clockwise spiral order [4].

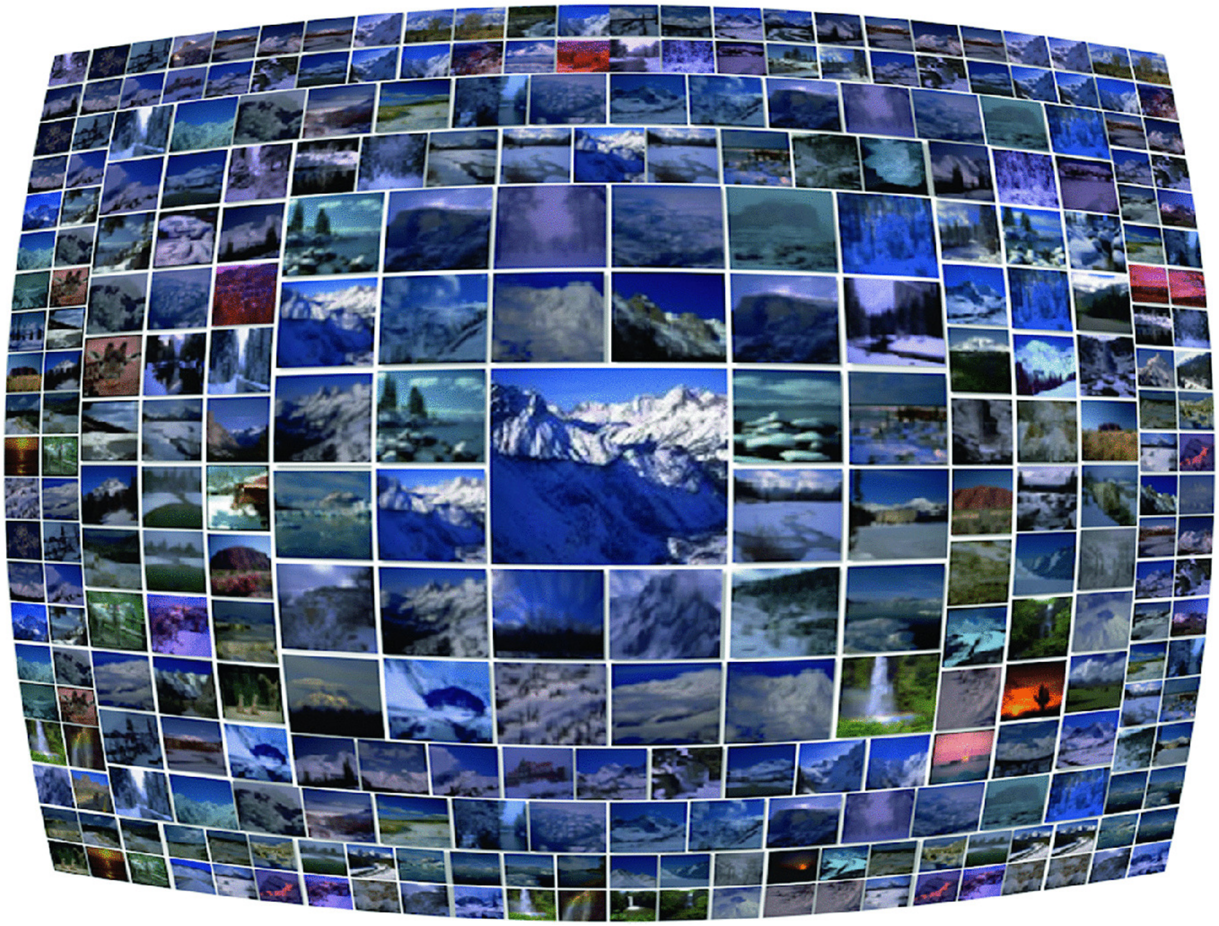
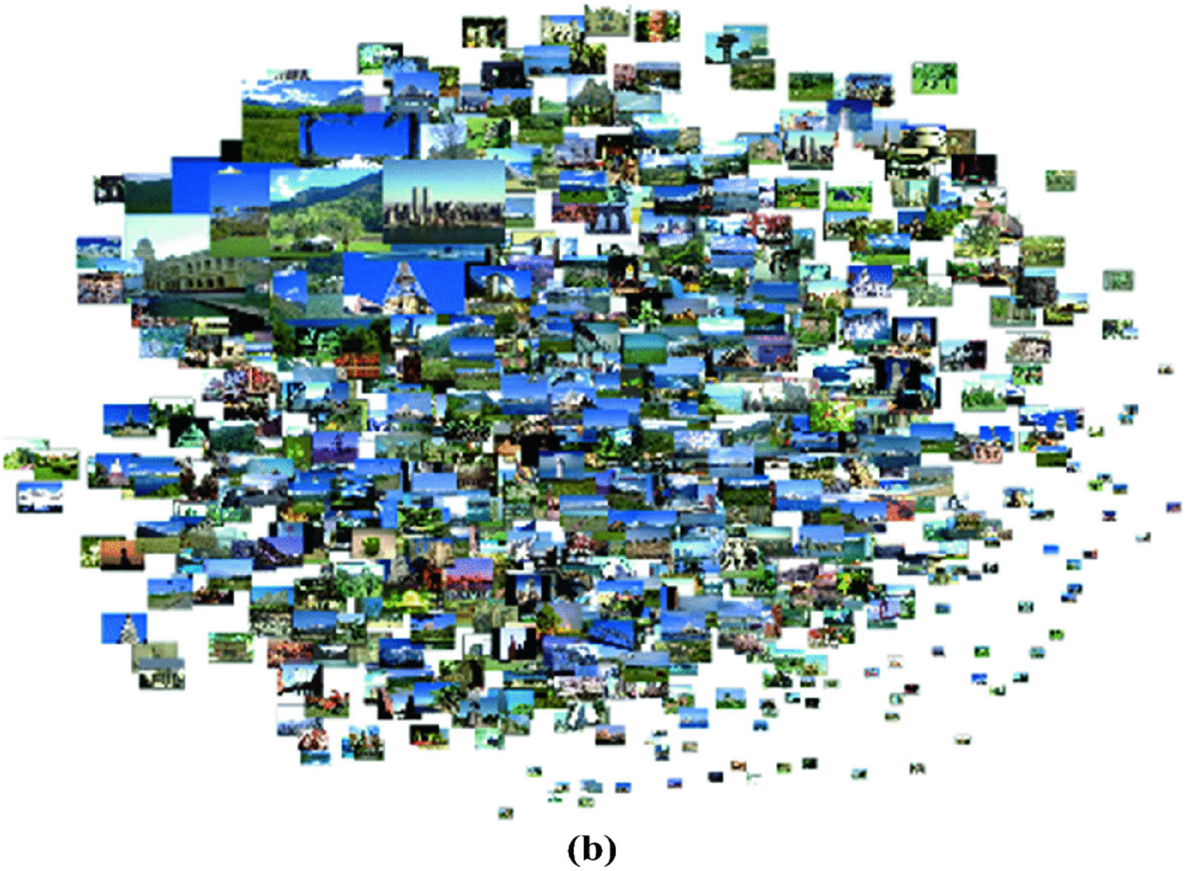


Fig. 13.9 Content browsing with fish eye view

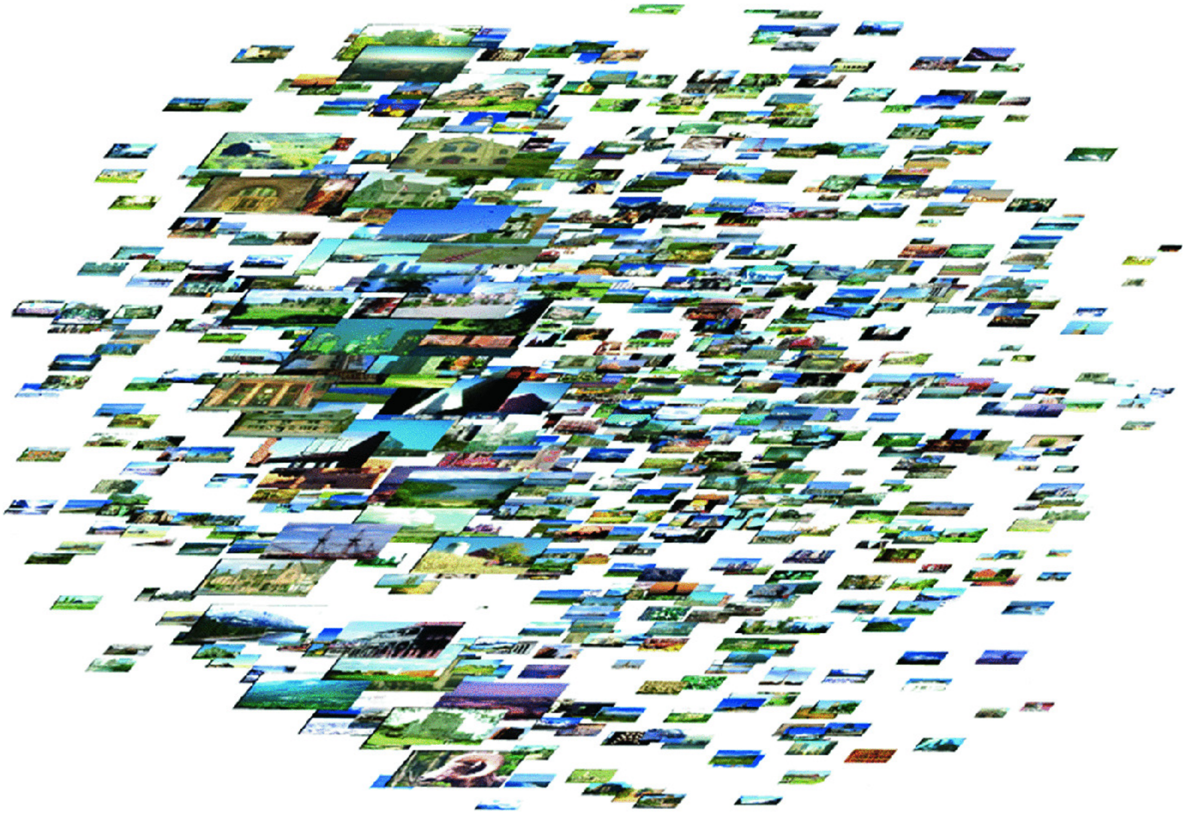
13.4.3 Force-Directed Content Browsing

Conventional content browsing does not have overlap between images and the distance between neighboring images is uniform. In a force-directed content browsing, images in a category or a retrieval list are regarded as planets in space and the distance between images is regarded as a force between them. If two images are similar enough, the force is strong enough to attract them together. The result of a force-directed visualization is an overlapped image map as shown in Fig. 13.10a. Figure 13.10b shows the force-directed image map in diminishing perspective. A bi-force-directed content browsing can be visualized using a 3D image map as shown in Fig. 13.10c. In the 3D image map, there are two types of forces representing two types of similarity between images, e.g., the horizontal force represents the color similarity and the vertical force represents the texture similarity. A close-up section of the 3D image map is shown in Fig. 13.10d.

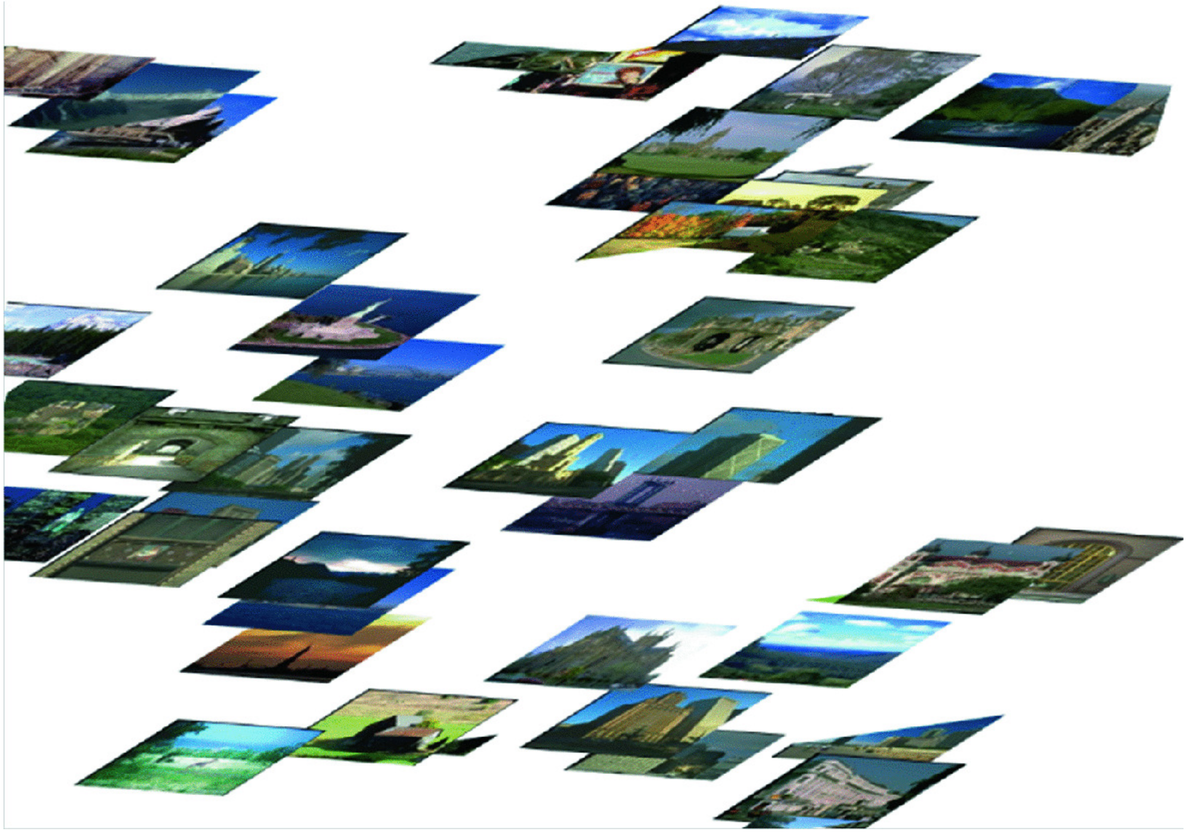
(a)



(b)



(c)



(d)

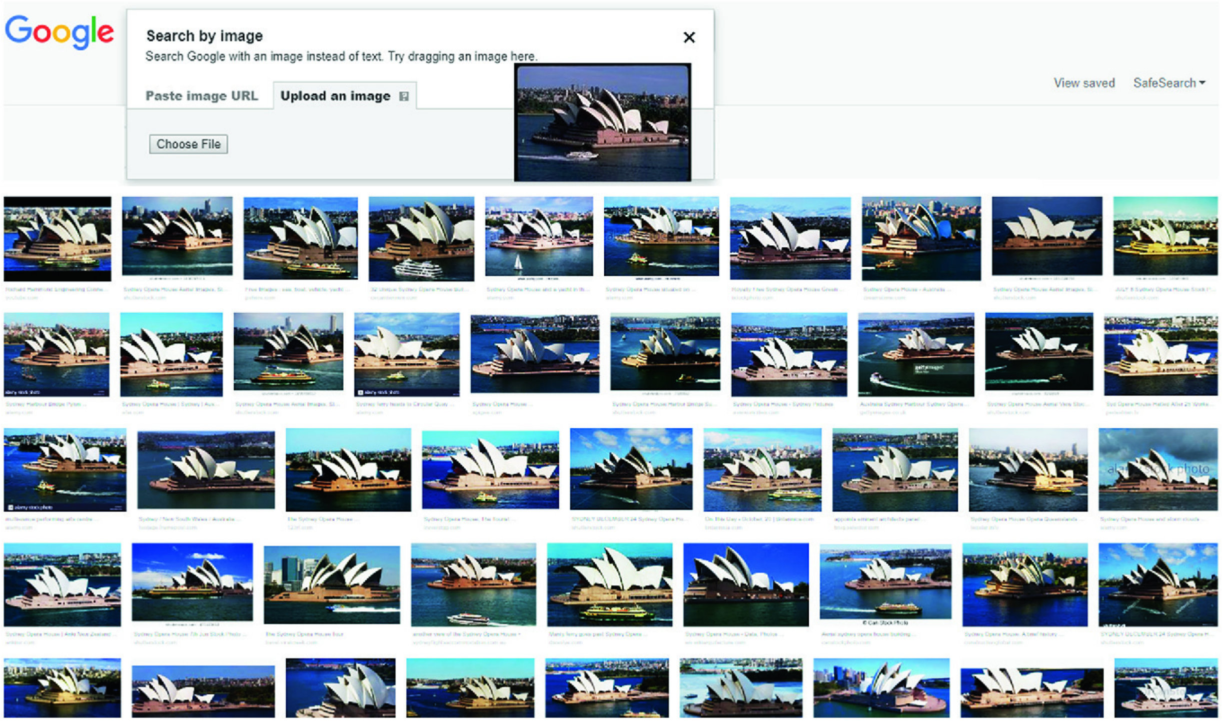
Fig. 13.10 Force-directed content browsing

Interactivity over an image map can also include keywords. For example, keywords can be used as a mouse-over feature of the image map. A *keyword map* and an *image map* can be created separately and put side by side, and the two maps are linked to provide a user with a joint content browsing [4].

13.5 Query by Example

When come to find a required image, one of the most challenging issues for a user is how to initiate the search, which includes how to start, where to start and how to formulate a search. One of the simplest ways to start a search is a *query by example* (QBE), or search based on an example image from the user. In QBE, similar images in the database are retrieved based on the *content features* of the query image. The justification for QBE is that often the requirement for an image cannot be described by words and a user has a sample image which is similar to what they actually want to find. The sample image can be used as equivalent keywords for a query. QBE is a useful functionality, because most of the images in the world are unlabeled, and these images can be retrieved based on content features. Therefore, QBE is an essential part of an IR system.

An example of QBE is Google's 'Search by image' as shown in Fig. 13.11 [5]. In the figure, the sample image was first *translated* to the keywords 'Sydney opera house' which are then used as the query for the actual image retrieval. Due to the translation, Google's search by an example image can be regarded as a semi-QBE, because labels of images in the database may not be obtained from image content. This works well when a query image is properly translated, however, when a query image is incorrectly translated, it results in completely wrong retrievals. For example, Fig. 13.12 shows three example queries which are translated to 'darkness,' 'comics' and 'computer,' respectively. As a result, the retrievals of the three queries are completely incorrect. Furthermore, when the hand image query is presented using two different copies, they are translated as 'Naya Rivera' and 'point cabrillo light,' respectively, which would not occur if content features are used for direct matching. This demonstrates that a CBIR-based QBE is a necessary component for an image retrieval system.


Google
Search by image
Paste image URL
Upload an image
Choose File
View saved
SafeSearch

Search Google with an image instead of text. Try dragging an image here.

Fig. 13.11 QBE example from Google

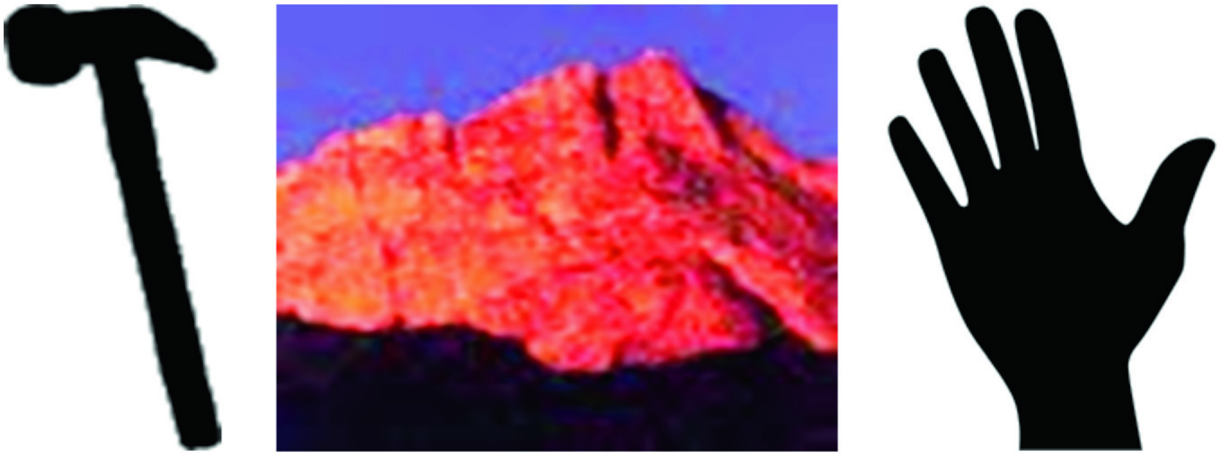


Fig. 13.12 Query images for Google's 'Search by image'

Although QBE is useful and convenient in many situations, it can be challenging to find an example image for a user. One of the ways to find example images is to use *query by keywords* or QBK which will be introduced in the following section.

13.6 Query by Keywords

People describe the visual world using textual language such as a blue sky, green trees, red flowers, a cheerful street, violent protests etc. One of the natural ways to search images is to use *query by keywords* or QBK. In a QBK system, images in database are all labeled with keywords and indexed using inverted files, and the search for images is just the same as search for textural documents. Unfortunately, most of the images in the world are either unlabeled or mislabeled. In a typical QBK system, image labels are obtained from image content through automatic image classification/annotation. A typical QBK system is shown in Fig. 13.13 [6, 7]. Image labels can also be obtained by analyzing textual description of images in web pages on the Internet.

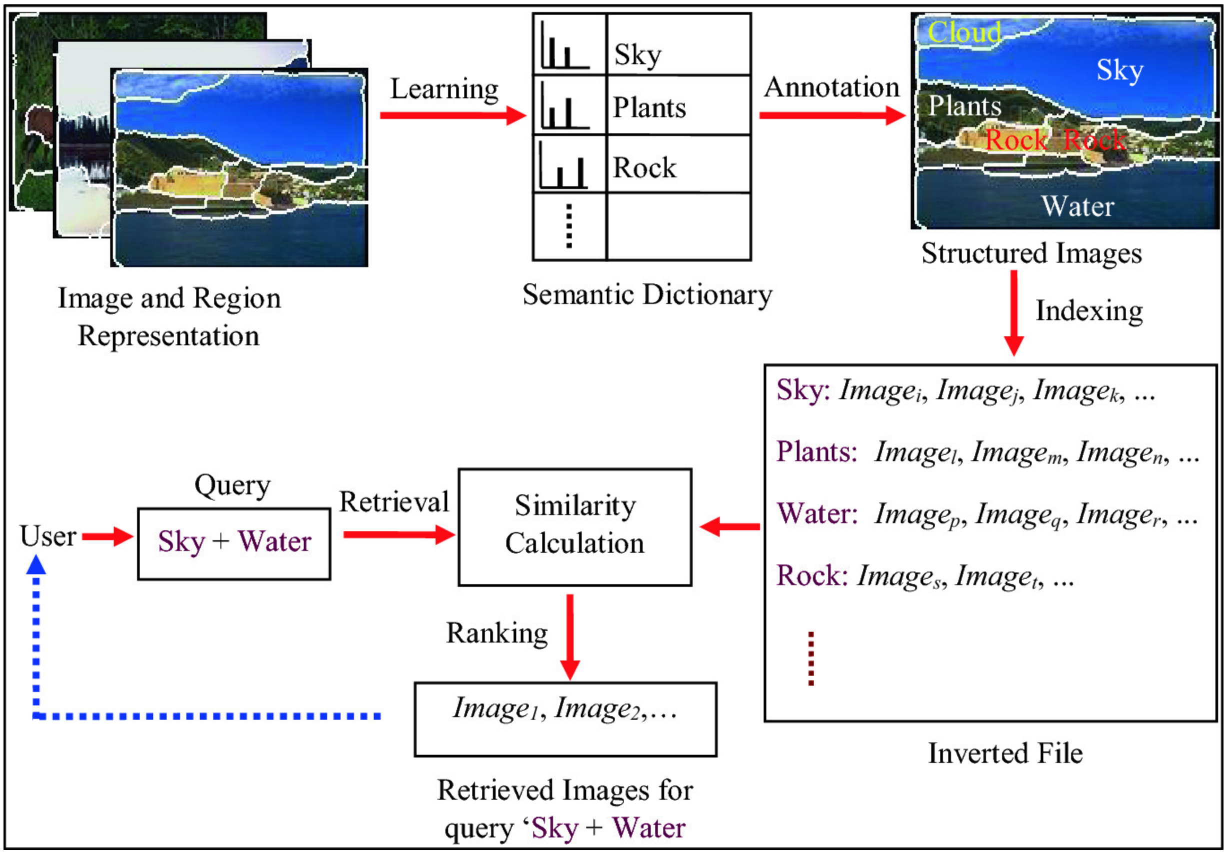
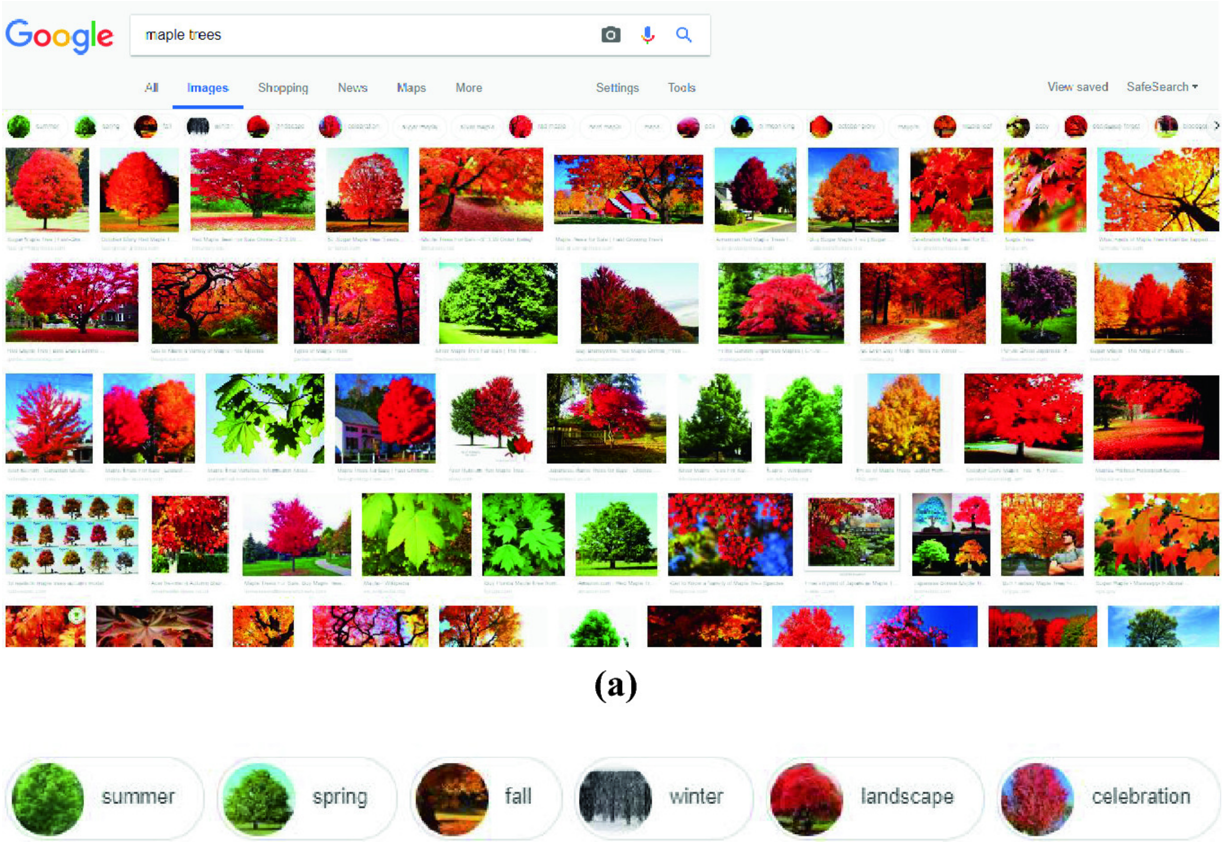

Learning
Sky
Plants
Rock
Annotation
Cloud
Sky
Plants
Rock
Rock
Water
Image and Region Representation
Semantic Dictionary
Structured Images
Indexing
Sky: $Image_i$, $Image_j$, $Image_k$, ...
Plants: $Image_l$, $Image_m$, $Image_n$, ...
Water: $Image_p$, $Image_q$, $Image_r$, ...
Rock: $Image_s$, $Image_t$, ...
Inverted File
Query
User
Sky + Water
Retrieval
Similarity Calculation
Ranking
$Image_1$, $Image_2$,…
Retrieved Images for query ‘Sky + Water

Fig. 13.13 Content-based QBK system

One of the most widely used QBK systems is Google’s Image search as shown in Fig. 13.14a [5]. The key features of Google’s Image search are summarized as following:


Google
maple trees
All
Images
Shopping
News
Maps
More
Settings
Tools
View saved
SafeSearch
summer
spring
fall
winter
landscape
celebration

(a)

(b)

Fig. 13.14 QBK example from Google. **a** Example from Google's Image search; **b** category browsing from Google's Image search

- **Simplicity**. The textual input is the simplest and most intuitive query interface. It is a universal user interface.
- **Caption browsing**. Retrieved images are presented as caption browsing which is simple and intuitive.
- **Category browsing**. The categories at the top of the browsing area provide users with category browsing (Fig. 13.14b).
- **Content browsing**. QBE is included as an option for the QBK interface, shown as a camera icon at the query field (Fig. 13.14a). Some of the category browsing are also based on content features such as colors.
- **Interactivity**. An enlarged version of an image is shown as focus when a user clicks any of the images in the browsing area, the enlarged image is also linked to the image source (Fig. 13.15).

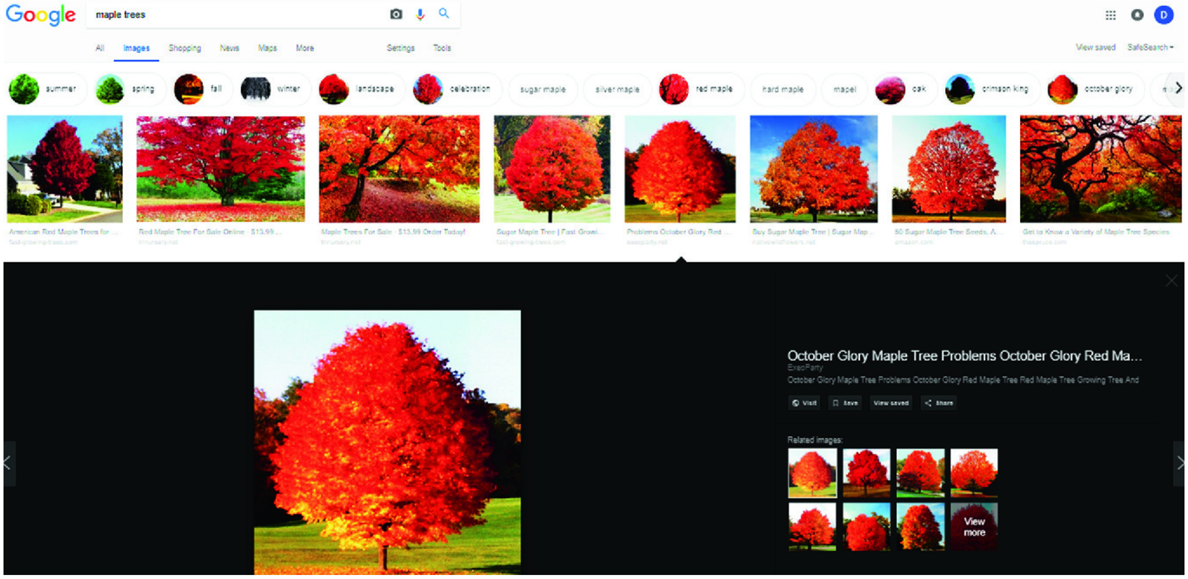

Google
maple trees
All
Images
Shopping
News
Maps
More
Settings
Tools
View saved
SafeSearch
summer
spring
fall
winter
landscape
celebration
sugar maple
silver maple
red maple
hard maple
mapel
oak
crimson king
october glory
American Red Maple Trees for ...
Red Maple Tree For Sale Online · $13.99 ...
Maple Trees For Sale · $13.99 Order Today!
Sugar Maple Tree | Fast Growi...
Problems October Glory Red ...
Buy Sugar Maple Tree | Sugar Map ...
50 Sugar Maple Tree Seeds, A...
Get to Know a Variety of Maple Tree Species
October Glory Maple Tree Problems October Glory Red Ma...
ExeoParty
October Glory Maple Tree Problems October Glory Red Maple Tree Red Maple Tree Growing Tree And
Visit
Save
View saved
Share
Related images:
View more

Fig. 13.15 Hierarchical QBK in Google. An enlarged image at the black strip and its relevant category at the right-hand side of the enlarged image

- **Hierarchical structure**. When a user clicks an image in the browsing area, it also shows the category of images similar to the clicked image at the right-hand side (Fig. 13.15). This kind of interaction can also be regarded as a QBK supported QBE.

At this moment, Google's Image search is predominantly done by QBK due to the limited capability of CBIR techniques. However, it's often a challenge for a user to formulate an image query using keywords only. In many cases, a query for an image can only be described by a visual form or QBE. As CBIR techniques become more mature, it is expected that both QBE and QBK will play equal roles in image search.

An effective *relevance feedback* or RF mechanism is an essential feature to an image retrieval system. This is because an initial retrieval result is likely inaccurate; the RF provides a user a chance to interfere and refine the retrieval result. RF works by letting a user to select a number of relevant images from a retrieval list, the IR system then uses these relevant images as a collective query (instead of a single query) to refine or update the retrieval list so that it meets the user's expectation. RF is particularly useful for mass scale image search such as Google, because the chance of identifying relevant images from the top of a retrieval list is high.

13.7 Summary

In this chapter, different image presentation techniques have been discussed. Once images in an image database have been classified, indexed and ranked, the next step is how to present the images to users. We have introduced a number of common methods of image presentation including caption browsing, category browsing, content browsing, QBE and QBK, etc. Each of them has its applications and limitation. As image databases become larger and larger, an image retrieval system needs to integrate all of these individual image presentation techniques so that images can be found both effectively and efficiently.

An example of such kind of integrated image retrieval system has been shown using Google Image search application. It is shown that Google Image search has integrated caption browsing, category browsing, hierarchical category browsing, QBE and QBK into a single IR system. The success of Google's search engine shows that in terms of design a retrieval system, the simplest is the best. The chapter also demonstrates that powerful image visualization techniques such as a Google earth like image map can be utilized to enhance user experience on an IR system.

13.8 Exercises

1. Image retrieval. Describe how CBIR and Google Image search work respectively. Next, contrast the pros and cons of CBIR and Google Image search in terms of query methods, feature representation, indexing methods, and convenience of use.

2. Image DB visualization. Download the image scatter plot functions from the following website: https://au.mathworks.com/matlabcentral/fileexchange/63123-image-scatter-plots.
    - Create an image DB of 100 images in a folder: 'yourImageDir.' Tip: yourImageDir can be copied over directly from the address bar of Windows File Explorer.

- Use the following code to load the image DB into memory and save the code as ‘image_dir.m’:

```
% Read m jpg color images.
jpgfiles = dir('yourImageDir\*.jpg');
m = length(jpgfiles);
for k = 1:m
    fullFileName = fullfile('yourImageDir\',
                   jpgfiles(k).name);
    imageData = imread(fullFileName);
    im = imresize(imageData, [100, 100]);
    I(:,:,:,k)=im;
end
```

- Use the following code to create a 2D grid and save it as ‘2D_coords.m’:

```
x = randi([0 99], 100, 1);
y = randi([0 99], 100, 1);
Y = horzcat(x, y);
```

- Run the following code to plot the image DB

```
tic
image_dir;
2D_coords;
imgScatter(Y, I);
toc
```

- Replace the 2D grid with the following uniform grid and run the above scatter plot again:

```
[x,y] = meshgrid(10:10:100,10:10:100);
x = x(:);
y = y(:);
Y = horzcat(x, y);
```

- Compute the normalized histograms of the 100 images and store them into an array `H`.
- Use the first image in `I` as the query image, compute the distance of each image to the query and store the distance in a vector `d`.
- Add a few lines of code in the `for` loop of the `imgScatter` function so that images are plotted according to their distance to the query image.
- Try the plot 200 images and plot them with overlap.
- Write a short report on different techniques of image DB visualization. Discuss the feasibility of visualizing an image DB using the same techniques as Google Map and Google Earth.

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OceanofPDF.com

Appendix

Deriving the Conditional Probability of a Gaussian Process

Given a set of data $\mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_N$ from a certain class C, and each feature vector $\mathbf{x}_i$ is a data point in R^D: $\mathbf{x}_i = (x_{i1}, x_{i2}, \ldots, x_{iD})$. A matrix $\mathbf{X} = D \times N = (\mathbf{d}_1, \mathbf{d}_2, \ldots, \mathbf{d}_D)^{\mathrm{T}}$ can be created as following:

$$\mathbf{X} = \begin{bmatrix} x_{11}, x_{21}, \ldots, x_{N1} \\ x_{12}, x_{22}, \ldots, x_{N2} \\ \ldots \\ x_{1D}, x_{2D}, \ldots, x_{ND} \end{bmatrix} = \begin{bmatrix} \mathbf{d}_1 \\ \mathbf{d}_2 \\ \ldots \\ \mathbf{d}_D \end{bmatrix} \tag{A.1}$$

$\mathbf{X}$ is a Gaussian process and $\mathbf{X}$ follows a multivariate normal distribution : $\mathbf{X} \sim \mathcal{N}(\boldsymbol{\mu}, \Sigma)$, where $\boldsymbol{\mu}$ and Σ are the *mean* and *variance* of $\mathbf{X}$ which are determined by (A.2) and (A.3) respectively.

$$\boldsymbol{\mu} = \begin{bmatrix} \boldsymbol{\mu}_1 \\ \boldsymbol{\mu}_2 \\ \ldots \\ \boldsymbol{\mu}_D \end{bmatrix} \tag{A.2}$$

$$\Sigma = \begin{bmatrix} \operatorname{cov}(\mathbf{d}_1, \mathbf{d}_1), \operatorname{cov}(\mathbf{d}_1, \mathbf{d}_2) \ldots, \operatorname{cov}(\mathbf{d}_1, \mathbf{d}_D) \\ \operatorname{cov}(\mathbf{d}_2, \mathbf{d}_1), \operatorname{cov}(\mathbf{d}_2, \mathbf{d}_2) \ldots, \operatorname{cov}(\mathbf{d}_2, \mathbf{d}_D) \\ \ldots \\ \operatorname{cov}(\mathbf{d}_D, \mathbf{d}_1), \operatorname{cov}(\mathbf{d}_D, \mathbf{d}_2) \ldots, \operatorname{cov}(\mathbf{d}_D, \mathbf{d}_D) \end{bmatrix} \tag{A.3}$$

where $\operatorname{cov}(\mathbf{d}_i, \mathbf{d}_j)$ is either a *covariance* or a *variance* :

$$\operatorname{cov}\left(\mathbf{d}_i, \mathbf{d}_j\right) = E\left[(\mathbf{d}_i - \mathbf{u}_i)\left(\mathbf{d}_j - \mathbf{u}_j\right)^T\right] = E[\mathbf{d}_i \mathbf{d}_j^T] - \mathbf{u}_i \mathbf{u}_j^T \tag{A.4}$$

$$\mathrm{var}\,(\mathbf{d}_i) = \mathrm{cov}\,(\mathbf{d}_i, \mathbf{d}_i) \tag{A.5}$$

and E is the expected value .

To predict a new data or a new set of data $\mathbf{X}_*$, $\mathbf{X}$ and $\mathbf{X}_*$ are concatenated and the concatenated data is a new GP which follows the following normal distribution :

$$\begin{pmatrix} \mathbf{X}_* \\ X \end{pmatrix} \sim \mathcal{N}\left(\begin{pmatrix} \mu_{\mathbf{X}_*} \\ \mu_{\mathbf{X}} \end{pmatrix}, \begin{pmatrix} \Sigma_{\mathbf{X}_*\mathbf{X}_*}, \Sigma_{\mathbf{X}_*\mathbf{X}} \\ \Sigma_{\mathbf{X}\mathbf{X}_*}, \Sigma_{\mathbf{X}\mathbf{X}} \end{pmatrix} \right) \tag{A.6}$$

Then, the probability of the new data $\mathbf{X}_*$ given the observed data $\mathbf{X}$ is given by (A.7):

$$p(\mathbf{X}_*|\mathbf{X}) = \mathcal{N}\left(\mu_{\mathbf{X}_*} + \Sigma_{\mathbf{X}_*\mathbf{X}}\Sigma_{\mathbf{X}\mathbf{X}}^{-1}\left(\mathbf{X} - \mu_{\mathbf{X}}\right), \Sigma_{\mathbf{X}_*\mathbf{X}_*} - \Sigma_{\mathbf{X}_*\mathbf{X}}\Sigma_{\mathbf{X}\mathbf{X}}^{-1}\Sigma_{\mathbf{X}\mathbf{X}_*} \right) \tag{A.7}$$

To prove (A.7), let's first formulate (A.6) into a general case of two multivariate normal distributions . Suppose $\mathbf{X}_1$ and $\mathbf{X}_2$ are the two partitions of $\mathbf{X}$:

$$\mathbf{X} = \begin{bmatrix} \mathbf{X}_1 \\ \mathbf{X}_2 \end{bmatrix} \tag{A.8}$$

where $\mathbf{X} \sim \mathcal{N}\,(\boldsymbol{\mu}, \Sigma)$, $\mathbf{X}_1 \sim \mathcal{N}\,(\boldsymbol{\mu}_1, \Sigma_{11})$ and $\mathbf{X}_2 \sim \mathcal{N}\,(\boldsymbol{\mu}_2, \Sigma_{22})$.

Then, the following are the partitions of $\boldsymbol{\mu}$ and Σ respectively:

$$\boldsymbol{\mu} = \begin{bmatrix} \mu_1 \\ \mu_2 \end{bmatrix} \tag{A.9}$$

$$\Sigma = \begin{bmatrix} \Sigma_{11} & \Sigma_{12} \\ \Sigma_{21} & \Sigma_{22} \end{bmatrix} \tag{A.10}$$

where Σ and Σ_{ij} are all the covariance matrices. Based on (A.4) and (A.5), it can be shown that the following properties of vector *variance* (*var*) and *covariance* (cov) are true [ref. 7 Chap. 7]:

(1)
$$\mathrm{var}\left(\mathbf{AX}+\mathbf{b}\right)=\mathbf{A}\mathrm{var}\left(\mathbf{X}\right)\mathbf{A}^{T} \tag{A.11}$$

(2)
$$\mathrm{var}\left(\mathbf{X}_1+\mathbf{X}_2\right)=\mathrm{var}\left(\mathbf{X}_1\right)+\mathrm{var}\left(\mathbf{X}_2\right)+\mathrm{cov}\left(\mathbf{X}_1,\mathbf{X}_2\right)+\mathrm{cov}\left(\mathbf{X}_2,\mathbf{X}_1\right) \tag{A.12}$$

(3)
$$\mathrm{cov}\left(\mathbf{AX}_1+\mathbf{b},\mathbf{X}_2\right)=\mathbf{A}\mathrm{cov}\left(\mathbf{X}_1,\mathbf{X}_2\right) \tag{A.13}$$

(4)
$$\mathrm{cov}\left(\mathbf{AX}_1+\mathbf{BX}_2,\mathbf{X}_2\right)=\mathbf{A}\mathrm{cov}\left(\mathbf{X}_1,\mathbf{X}_2\right)+\mathbf{B}\mathrm{var}\left(\mathbf{X}_2\right) \tag{A.14}$$

(5)
$$\mathrm{cov}\left(\mathbf{X}_1,\mathbf{X}_2\right)=\mathrm{cov}\left(\mathbf{X}_2,\mathbf{X}_1\right) \tag{A.15}$$

To compute the parameters of $p(\mathbf{X}_1|\mathbf{X}_2)$, we need to create an auxiliary random variable **C** which is both the linear combination of $\mathbf{X}_1$ and $\mathbf{X}_2$ and *independent* of $\mathbf{X}_2$ [ref. 8 Chap. 7]:

$$\mathbf{C}=\mathbf{X}_1+\mathbf{AX}_2 \tag{A.16}$$

Then, the matrix **A** can be found by letting cov($\mathbf{C}, \mathbf{X}_2$) = 0:

$$\begin{aligned}\mathrm{cov}\left(\mathbf{C},\mathbf{X}_2\right)&=\mathrm{cov}\left(\mathbf{X}_1+\mathbf{AX}_2,\mathbf{X}_2\right)\\&=\mathrm{cov}\left(\mathbf{X}_1,\mathbf{X}_2\right)+\mathbf{A}\mathrm{var}\left(\mathbf{X}_2\right)\\&=\Sigma_{12}+\mathbf{A}\Sigma_{22}=0\end{aligned} \tag{A.17}$$

which leads to

$$\mathbf{A}=-\Sigma_{12}\Sigma_{22}^{-1} \tag{A.18}$$

and

$$E\left(\mathbf{C}\right)=E\left(\mathbf{X}_1\right)+E\left(\mathbf{AX}_2\right)=\boldsymbol{\mu}_1+\mathbf{A}\boldsymbol{\mu}_2 \tag{A.19}$$

Therefore, we have

$$\begin{aligned}
E\left(\mathbf{X}_1|\mathbf{X}_2\right) &= E\left(\mathbf{C}-\mathbf{A}\mathbf{X}_2|\mathbf{X}_2\right)\\
&= E\left(\mathbf{C}|\mathbf{X}_2\right) - E\left(\mathbf{A}\mathbf{X}_2|\mathbf{X}_2\right)\\
&= E\left(\mathbf{C}\right) - \mathbf{A}\mathbf{X}_2\\
&= \boldsymbol{\mu}_1 + \mathbf{A}\left(\boldsymbol{\mu}_2 - \mathbf{X}_2\right)\\
&= \boldsymbol{\mu}_1 + \Sigma_{12}\Sigma_{22}^{-1}\left(\mathbf{X}_2 - \boldsymbol{\mu}_2\right)
\end{aligned} \tag{A.20}$$

where $E(\mathbf{AX}_2|\mathbf{X}_2) = \mathbf{AX}_2$ is due to both $\mathbf{A}$ and $\mathbf{X}_2$ are constants. $E(\mathbf{X}_1|\mathbf{X}_2)$ is the *mean* of $p(\mathbf{X}_1|\mathbf{X}_2)$.

By using (A.12) and (A.17), we have the following:

$$\begin{aligned}
\mathrm{var}\left(\mathbf{X}_1|\mathbf{X}_2\right) &= \mathrm{var}\left(\mathbf{C}-\mathbf{A}\mathbf{X}_2|\mathbf{X}_2\right)\\
&= \mathrm{var}\left(\mathbf{C}|\mathbf{X}_2\right) + \mathrm{var}\left(\mathbf{A}\mathbf{X}_2|\mathbf{X}_2\right) + \mathrm{cov}\left(\mathbf{C}, -\mathbf{A}\mathbf{X}_2\right) + \mathrm{cov}\left(-\mathbf{A}\mathbf{X}_2, \mathbf{C}\right)\\
&= \mathrm{var}\left(\mathbf{C}|\mathbf{X}_2\right) + \mathrm{var}\left(\mathbf{A}\mathbf{X}_2|\mathbf{X}_2\right) - \mathbf{A}\mathrm{cov}\left(\mathbf{C}, \mathbf{X}_2\right) - \mathbf{A}\mathrm{cov}\left(\mathbf{X}_2, \mathbf{C}\right)\\
&= \mathrm{var}\left(\mathbf{C}|\mathbf{X}_2\right)\\
&= \mathrm{var}\left(\mathbf{C}\right)
\end{aligned} \tag{A.21}$$

where $\mathrm{var}(\mathbf{AX}_2|\mathbf{X}_2) = \mathbf{A}\mathrm{var}(\mathbf{X}_2|\mathbf{X}_2)\mathbf{A}^T$ and $\mathrm{var}(\mathbf{X}_2|\mathbf{X}_2) = \mathrm{E}[(\mathbf{X}_2 - \mathrm{E}(\mathbf{X}_2|\mathbf{X}_2))^2|\mathbf{X}_2] = 0$.

Therefore, by combining (A.11)–(A.15), (A.18) and (A.21), we have:

$$\begin{aligned}
\mathrm{var}\left(\mathbf{X}_1|\mathbf{X}_2\right) &= \mathrm{var}\left(\mathbf{C}\right)\\
&= \mathrm{var}\left(\mathbf{X}_1 + \mathbf{A}\mathbf{X}_2\right)\\
&= \mathrm{var}\left(\mathbf{X}_1\right) + \mathbf{A}\mathrm{var}\left(\mathbf{X}_2\right)\mathbf{A}^T + \mathbf{A}\mathrm{cov}\left(\mathbf{X}_1, \mathbf{X}_2\right) + \mathbf{A}\mathrm{cov}\left(\mathbf{X}_2, \mathbf{X}_1\right)\\
&= \Sigma_{11} + \Sigma_{12}\Sigma_{22}^{-1}\Sigma_{22}\Sigma_{22}^{-1}\Sigma_{12} - 2\Sigma_{12}\Sigma_{22}^{-1}\Sigma_{21}\\
&= \Sigma_{11} - \Sigma_{12}\Sigma_{22}^{-1}\Sigma_{21}
\end{aligned} \tag{A.22}$$

To summarize the above, we have obtained both the *mean* and *variance* of $p(\mathbf{X}_1|\mathbf{X}_2)$:

$$\begin{aligned}
E\left(\mathbf{X}_1|\mathbf{X}_2\right) &= \boldsymbol{\mu}_1 + \Sigma_{12}\Sigma_{22}^{-1}\left(\mathbf{X}_2 - \boldsymbol{\mu}_2\right)\\
\mathrm{var}\left(\mathbf{X}_1|\mathbf{X}_2\right) &= \Sigma_{11} - \Sigma_{12}\Sigma_{22}^{-1}\Sigma_{21}
\end{aligned}$$

By substituting $\mathbf{X}_1$ and $\mathbf{X}_2$ with $\mathbf{X}_*$ and $\mathbf{X}$ respectively, (A.6) is proved.

An alternative proof of (A.7) is to use Bayesian theorem by working out the joint probability $p(\mathbf{X}_1, \mathbf{X}_2)$ and the marginal probability $p(\mathbf{X}_1)$ [ref. 9 Chap. 7].

$$\begin{aligned} p(\mathbf{X}_1, \mathbf{X}_2) &= \frac{1}{(2\pi)^{D/2}|\Sigma|^{1/2}} \exp\left\{-\frac{1}{2}\left[(\mathbf{X}_1-\mu_1)^T, (\mathbf{X}_2-\mu_2)^T\right]\begin{bmatrix}\Sigma_{11}\Sigma_{12}\\ \Sigma_{21}\Sigma_{22}\end{bmatrix}^{-1}\begin{bmatrix}\mathbf{X}_1-\mu_1\\ \mathbf{X}_1-\mu_1\end{bmatrix}\right\} \\ &= \frac{1}{(2\pi)^{\frac{m}{2}}|\Sigma_{11}|^{\frac{1}{2}}} \exp\left\{-\frac{1}{2}(\mathbf{X}_1-\mu_1)^T \overset{-1}{\underset{11}{\Sigma}} (\mathbf{X}_1-\mu_1)\right\} \\ &\quad \times \frac{1}{(2\pi)^{n/2}|\mathbf{A}|^{1/2}} \exp\left\{-\frac{1}{2}(\mathbf{X}_2-\mathbf{b})^T \mathbf{A}^{-1}(\mathbf{X}_2-\mathbf{b})\right\} \\ &= \mathcal{N}(\mathbf{X}_1, \boldsymbol{\mu}_1, \Sigma_{11}) \times \mathcal{N}(\mathbf{X}_2, \mathbf{b}, \mathbf{A}) \\ &= p(\mathbf{X}_1) \times p(\mathbf{X}_2) \end{aligned} \tag{A.23}$$

where $m + n = D$ and

$$\mathbf{A} = \Sigma_{22} - \Sigma_{21}\Sigma_{11}^{-1}\Sigma_{12} \tag{A.24}$$

$$\mathbf{b} = \boldsymbol{\mu}_2 + \Sigma_{21}\Sigma_{11}^{-1}(\mathbf{X}_2 - \boldsymbol{\mu}_2) \tag{A.25}$$

Therefore, the conditional probability of $p(\mathbf{X}_2|\mathbf{X}_2)$ is given as following:

$$\begin{aligned} p(\mathbf{X}_2|\mathbf{X}_1) &= \frac{p(\mathbf{X}_1, \mathbf{X}_2)}{p(\mathbf{X}_1)} \\ &= \mathcal{N}(\mathbf{X}_2, \mathbf{b}, \mathbf{A}) \end{aligned} \tag{A.26}$$

By substituting $\mathbf{X}_1$ and $\mathbf{X}_2$ with $\mathbf{X}$ and $\mathbf{X}_*$ respectively, (A.7) is also proved.

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